

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : C12N 15/31, C07K 14/22, 16/12, C12Q 1/68, A61K 39/095, G01N 33/50		A2	(11) International Publication Number: WO 99/57280																								
			(43) International Publication Date: 11 November 1999 (11.11.99)																								
(21) International Application Number: PCT/US99/09346																											
(22) International Filing Date: 30 April 1999 (30.04.99)																											
(30) Priority Data: <table border="0"><tr><td>60/083,758</td><td>1 May 1998 (01.05.98)</td><td>US</td></tr><tr><td>60/094,869</td><td>31 July 1998 (31.07.98)</td><td>US</td></tr><tr><td>60/098,994</td><td>2 September 1998 (02.09.98)</td><td>US</td></tr><tr><td>60/099,062</td><td>2 September 1998 (02.09.98)</td><td>US</td></tr><tr><td>60/103,749</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr><tr><td>60/103,794</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr><tr><td>60/103,796</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr><tr><td>60/121,528</td><td>25 February 1999 (25.02.99)</td><td>US</td></tr></table>		60/083,758	1 May 1998 (01.05.98)	US	60/094,869	31 July 1998 (31.07.98)	US	60/098,994	2 September 1998 (02.09.98)	US	60/099,062	2 September 1998 (02.09.98)	US	60/103,749	9 October 1998 (09.10.98)	US	60/103,794	9 October 1998 (09.10.98)	US	60/103,796	9 October 1998 (09.10.98)	US	60/121,528	25 February 1999 (25.02.99)	US		
60/083,758	1 May 1998 (01.05.98)	US																									
60/094,869	31 July 1998 (31.07.98)	US																									
60/098,994	2 September 1998 (02.09.98)	US																									
60/099,062	2 September 1998 (02.09.98)	US																									
60/103,749	9 October 1998 (09.10.98)	US																									
60/103,794	9 October 1998 (09.10.98)	US																									
60/103,796	9 October 1998 (09.10.98)	US																									
60/121,528	25 February 1999 (25.02.99)	US																									
(71) Applicants (for all designated States except US): CHIRON CORPORATION [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US). THE INSTITUTE FOR GENOMIC RESEARCH [US/US]; 9212 Medical Center Drive, Rockville, MD 20850 (US).		(US). MASIGNANI, Vega [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). MORA, Marirosa [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). PETERSEN, Jeremy [US/US]; Arlington, VA (US). PIZZA, Mariagratia [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RAPPUOLI, Rino [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RATTI, Giulio [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCALATO, Enzo [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCARSELLI, Maria [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). TETTELIN, Herve [US/US]; Gaithersburg, MD (US). VENTER, J., Craig [US/US]; Rockville, MD (US).																									
(72) Inventors; and (75) Inventors/Applicants (for US only): FRASER, Claire [US/US]; Rockville, MD (US). GALEOTTI, Cesira [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). GRANDI, Guido [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). HICKEY, Erin [US/US]; Gaithersburg, MD		(74) Agent: HARBIN, Alisa, A.; Chiron Corporation, Intellectual Property - R440, P.O. Box 8097, Emeryville, CA 94662-8097 (US).																									
		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).																									
		Published Without international search report and to be republished upon receipt of that report.																									
(54) Title: NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS																											
(57) Abstract <p>The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.</p>																											
<div style="text-align: right;">919 (46 kDa)</div> <div style="text-align: right;">A) PURIFICATION</div> <div style="text-align: right;"><p>M1 919</p></div>																											

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav	TM	Turkmenistan
BF	Burkina Faso	GR	Greece		Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's	NZ	New Zealand		
CM	Cameroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakhstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

BACKGROUND

Neisseria meningitidis is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

N. meningitidis causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al.* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al.* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [*eg.* Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (*eg.* Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (e.g. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least n consecutive amino acids from the sequences and, depending on the particular sequence, n is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis etc.) and in various forms (eg. native, fusions etc.). They are preferably prepared in substantially pure or isolated form (ie. substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins)

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least n consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence, n is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (I) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Methodology - Summary of standard procedures and techniques.

General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning: A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

All publications, patents, and patent applications cited herein are incorporated in full by reference.

Expression systems

The *Neisseria menB* nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, Gibberellins: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Repr.* 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet.*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to

those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO

Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human (α) interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15 μm in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with CaCl_2 or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by

electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Eur. Cong. Biotechnology* 1:412.

v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.

Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCI/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci. USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guilliermondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

Bacteriol. 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; *Pichia*]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular *Neisserial* protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular *Neisserial* protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisserial* sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria menB* proteins.

Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and

are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example, ^{125}I may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with ^{125}I , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance

or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection).

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) RibiTM adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (DetoxTM); (3) saponin adjuvants, such as StimulonTM (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence in vivo can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ

described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human

immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomuroid, as described in Wu &

Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP- 0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

Delivery Methods

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Polynucleotide and polypeptide pharmaceutical compositions

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

A. Polypeptides

One example are polypeptides which include, without limitation: asioloorosomuroid (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

B.Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

C.Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

D.Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, *eg.* Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See *eg.* Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

E.Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol. (supra)*; Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin[®], and lipofectAMINE[®] are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are

assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

Nucleic Acid Hybridisation

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated T_m of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to 10^{-9} to 10^{-8} g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy

yeast gene can be detected with an exposure time of only 1 hour starting with 1 µg of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of 10^8 cpm/µg. For a single-copy mammalian gene a conservative approach would start with 10 µg of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than 10^8 cpm/µg, resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature (T_m) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4[\%(G + C)] - 0.6(\%\text{formamide}) - 600/n - 1.5(\%\text{mismatch}).$$

where C_i is the salt concentration (monovalent ions) and n is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are 42°C for a probe which is 95% to 100% homologous to the target fragment, 37°C for 90% to 95% homology, and 32°C for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

Nucleic Acid Probe Assays

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [*eg.* see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

Chromosomal DNA Preparation

N.meningitidis strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl₃/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	(<i>Bam</i> HI- <i>Nde</i> I)
	<u>CGCGGATCCGCTAGC</u>	(<i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	(<i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	(<i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	(<i>Xho</i> I)
	<u>CCCGCTCGAG</u>	(<i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) <u>AAAGAATTC</u>	(<i>Eco</i> RI)
	(AAA) <u>AAAGGTACC</u>	(<i>Kpn</i> I)
3'-end primer tail:	(AAA) <u>AAACTGCAG</u>	(<i>Pst</i> I)
	(AAA) <u>AAATCTAGA</u>	(<i>Xba</i> I)

5' or 3'-end primer tail: AAAGCATGC (*Sph*I) AAAAAAGTCGAC (*Sal*I)

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridized to the sequence to be amplified. The melting temperature depended on the number and type of hybridising nucleotides in the whole primer, and was determined for each primer using the formulae:

$$T_m = 4 (G+C) + 2 (A+T) \quad (\text{tail excluded})$$

$$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N \quad (\text{whole primer})$$

The melting temperatures of the selected oligonucleotides were usually 65-70°C for the whole oligo and 50-55°C for the hybridising region alone.

Table 1 shows the forward and reverse primers used for each amplification. In certain cases, the sequence of the primer does not exactly match the sequence of the predicted ORF. This is because when initial amplifications were performed, the complete 5' and/or 3' sequences for some meningococcal B ORFs were not known. However the corresponding sequences had been identified in *Gonococcus* or in *Meningococcus A*. Hence, when the *Meningococcus B* sequence was incomplete or uncertain, *Gonococcal* or *Meningococcal A* sequences were used as the basis for primer design. These sequences were altered to take account of codon preference. It can be appreciated that, once the complete sequence is identified, this approach will no longer be necessary.

Oligonucleotides were synthesized using a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2.0ml NH₄OH, and deprotected by 5 hours incubation at 56°C. The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were centrifuged and the pellets resuspended in either 100µl or 1.0ml of water. The OD₂₆₀ was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration adjusted to 2-10pmol/µl.

Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a template in the presence of 20-40µM of each oligonucleotide primer, 400-800µM dNTPs solution, 1x PCR buffer (including 1.5mM MgCl₂), 2.5 units *Taq*I DNA polymerase (using

Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H₂O or 10mM Tris, pH 8.5.

Digestion of PCR fragments

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-

terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40 µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30 µl or 50 µl with either H₂O or 10mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD₂₆₀ of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10 µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200 µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50 µl of 10mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD_{260nm} and the concentration adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

Cloning

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

ratio of 3:1 fragment/vector was ligated using 0.5 μ l of NEB T4 DNA ligase (400 units/ μ l), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boheringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100 μ l *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800 μ l LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200 μ l of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100 μ g/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30 μ l. 5 μ l of each individual miniprep (approximately 1g) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20 μ l, that included 0.5 μ l T4 DNA ligase (400 units/ μ l, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boheringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100 μ l of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800 μ l LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200 μ l of the supernatant and plated onto LB ampicillin (100mg/ml) agar.

Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD₆₀₀ ranged between 0.1 and 0.15. The flasks were incubated at 30°C into gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

GST-fusion proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD₂₈₀ of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M") (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD_{280nm} of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD_{280nm} of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

His-fusion soluble proteins large-scale purification.

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

His-fusion insoluble proteins large-scale purification.

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D₅₅₀ 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni²⁺-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD₂₈₀ of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D₂₈₀ of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD₂₈₀ was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

Purification of His-fusion proteins.

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD_{550nm} reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni²⁺-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD_{280nm} of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD_{280nm} of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions

collected until the $O.D_{280nm}$ indicated all the recombinant protein was obtained. 20 μ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

His-fusion proteins renaturation

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 μ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 μ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

Purification of proteins

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 μ l buffer M1 (PBS pH 7.2). 25 μ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M NaH_2PO_4] overnight at 4°C. The

supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

Mice immunisations

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)₃ as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

ELISA assay (sera analysis)

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H₂O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA was considered positive when OD₄₉₀ was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN₃ in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

phenildiamine and 10 μ l of H₂O₂) were added to each well and the plates were left at room temperature for 20 minutes. 100 μ l of 12.5% H₂SO₄ was added to each well and OD₄₉₀ was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD₄₉₀ value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD₄₉₀ of 0.4 was higher than 1:400.

FACScan bacteria Binding Assay procedure.

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD₆₂₀. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN₃) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD₆₂₀ of 0.07. 100 μ l bacterial cells were added to each well of a Costar 96 well plate. 100 μ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 μ l/well of blocking buffer in each well. 100 μ l of R-Phicoerytrin conjugated F(ab)₂ goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 μ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 μ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

OMV preparations

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice (50% duty cycle, 50% output). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

Whole Extracts preparation

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

Western blotting

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

Bactericidal assay

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD₆₂₀ was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD₆₂₀ of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward)	CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse)	GGCAGGGAATGGCGGATTAAAG
919.1	(forward)	AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCCT
919.6	(reverse)	CAAATAAGAAAGGAATTTTG or GGTATCGCAAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° (in according to Tm of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTTGATCCAACC

- 919.1 (forward) AAAATGCCTCTCCACGGCTG or
CTGCGCCCTGTGTAAATCCCCT
- 919.2 (forward) ATCCTTCCGCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAATC
- 919.5 (forward) GCGCGTGGATTATTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or
GGTATCGCAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAGTGCCG
- 919.8 (reverse) TAAAAAAAGTTTCGACAGGG
- 919.9 (reverse) CCGTCCGCTGTCTCGCCC
- 919.10 (reverse) TCGTCCGGCGGGGTCGGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 1: Oligonucleotides used for PCR for Examples 2-10

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTtagAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
	Reverse	CCCGCTCGAG-GACCGCGTTGTGCGAAA <SEQ ID 3032>	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC <SEQ ID 3036>	XhoI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the

designated sequences being compared, the designated sequence controls and is the actual sequence being compared.

ORF: contig:

279 gnm4.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3039>:
m279.seq

```

1   ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCG GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACC GG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCCCTGCA ATCACGATTT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GGCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 3040; ORF 279>:
m279.pep

```

1   ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAATAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPA
151 SK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3041>:
g279.seq

```

1   atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgtcg gcggcggtt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgcggt ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcggcggc gttgcctgca atcacgactt gtccgggcga
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcactt tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 3042; ORF 279.ng>:
g279.pep

```

1   MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAATAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	: : : : : : : :					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60

	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
	: :					
g279	ITTCPGELKLTASTTSPCADSAQICLTCSKSKPKMAAIAPTPCGTADCISSARRRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPASKX					
	:					
g279	SAKSNASAATSAVYSPRLCPATAAGVLPPTSKX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3043>:

```
a279.seq
1  ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNN GGGCTTCGCG
51  GAGTTTGTCT GCGGCGGGTT TCATGAGGCT GCAATGGGA GGTACNGACA
101 CNGGCAGCGG CAGGCGCGGT TTGGCGCCGG CTTCTTTGGC GGCAAGCATA
151 GCGCGCTCGA CGGCGGCGGC ATTGCCTGCA ATCACGACTT GTCCGGGCGA
201 GTTGAAGTTG ACGGCTTCAA CCACTTCATC CTGTGCGGAT TCGGCGCAAA
251 TTTGTTTAC CTGTTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGCGCGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCAACN AGTGC GTGT
401 ATTGCGCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCGCT
451 TCCGAATAG
```

This corresponds to the amino acid sequence <SEQ ID 3044; ORF 279.a>:

```
a279.pep
1  MTXICGLIS TVXRASASLS AAGFMRLQWE GTDTGSGRAR LAPASLAASI
51  ARSTAAALPA ITTCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPAAT SAVYSPXLCP ATAAGVLPPA
151 SE*
```

m279/a279 ORFs 279 and 279.a showed a 88.2% identity in 152 aa overlap

	10	20	30	40	50	60
m279.pep	ITRICGLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAMARPTAAALPA					
	: : :					
a279	MTXICGLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
	: :					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPASKX					
	:					
a279	SAKSNAPAATSAVYSPXLCPATAAGVLPASEX					
	130	140	150			

519 and 519-1 gnm7.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3045>:

```
m519.seq (partial)
1  ..TCCGTTATCG GCGTATGGA GTTGACAAA ACGTTTGAAG AACGCGACGA
51  AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGCTTgGG
101 GTGTGAAGGT TTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
201 CCGTATCGCC GAATCCGAAG GTCGTAAAT CGAACAAATC AACCTTGCCA
```

```

251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTGTC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCCGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
551 TGATTTCTGC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3046; ORF 519>:

```

m519.pep (partial)
1  .SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLLISAGMK IIDSSKTAK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3047>:

```

g519.seq
1  atggaat tttt tcattat cttt gttggcagcc gtcgccgttt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatat tttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgctc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgctgctctc gccctcgatg aagccgccgg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgccgccct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcataaaaa attttcgccga gaagcaaaaa cggccaaata
951 a

```

This corresponds to the amino acid sequence <SEQ ID 3048; ORF 519.ng>:

```

g519.pep
1  MEFFIILLAA VAVFGKFSV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGQAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAN
251 RQIAAALQTO SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
301 NFRRHEKFSP EAKTAK*

```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

```

m519/g519

m519.pep                               10      20      30
                                      SVIGRMELDKTFEERDEINSTVVAALDEAA
g519      YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
              90      100      110      120      130      140

m519.pep              40      50      60      70      80      90
GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE

```

```

a519.seq
  1  ATGGAATTTT  TCATTATCTT  GCTGGCAGCC  GTCGTTGTTT  TCGGCTTCAA
51  ATCCTTTTGT  GTCATCCCAC  AGCAGGAAGT  CCACGTTGTC  GAAAGGCTCG
101 GCGGCTTTCCA TCGCGCCCTG  ACGGCCGTT  TGAATATTTT  GATTCCCTTT
151 ATCGACCGCG  TCGCCTACCG  CCTTTCGTT  AAAGAAATCC  CTTTAGACGT
201 ACCCAGCCAG  GTCTGCATCA  CGCGCGACAA  TACGCAGCTG  ACTGTTGACG
251 GTATCATCTA  TTTCCAAGTA  ACCGACCCCA  AACTCGCCTC  ATACGGTTCG
301 AGCAACTACT  TTATGGCGAT  TACCCAGCTT  GCCCAAACGA  CGCTGCGTTC
351 CGTTATCGGG  CGTATGGAAT  TGGACAAAA  GTTTGAAGAA  CGCGACGAAA
401 TCAACAGCAC  CGTCGTCTCC  GCCCTCGATG  AAGCCGCGGG  AGCTTGGGGT
451 GTGAAGGTTT  TGCGTTATGA  GATTAAAGAC  TTGGTCCGCG  CGCAAGAAAT
501 CCTTCGCTCA  ATGCAGGCGC  AAATTACTGC  TGAACGCGAA  AAACGCGCCC
551 GTATCGCCGA  ATCCGAAGTT  CGTAAATCG  AACAAATCAA  CCTTGGCAGT
601 GGTGACGCG  AAGCCGAAAT  CCAACAATC  GAAGCGGAGG  CTCAGGCTGC
651 GGTCAATGCG  TCAATGCCG  AGAAAAATCG  CCGCATCAAC  CGCGCCAAAG
701 GTGAAGCGGA  ATCCTTGCGC  CTTGTTGCCG  AAGCCAATGC  CGAAGCCATC
751 CGTCAAATTG  CCGCCGCCCT  TCAAACCCAA  GGCGGTGCGG  ATGCGGTCAA
801 TCTGAAGATT  CGGGAACAAT  ACGTCGCGCG  GTTCAACAT  CTTGCCAAAG
851 AAAGCAATAC  GCTGATTATG  CCGGCCAAT  TTGCCGACAT  CCGGACCGCT
901 ATTTCTGCCG  GTATGAAAAT  TATCGACAGC  AGCAAAACCG  CCAAATAA

```

```
a519.pep
  1  MEFFFIILLAA VVVFGEKSFV VIPQQEVHVV ERLGRFHRL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTILRSVIG RMELDKTTEE REINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GOREAEIQQS EGEAAQAVNA SNAEKIARIN RAKEAESLR LVAEANAEAI
251 RQIAAALQTS GGDAVNLLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKLIDS SKTAK*
```

[illegible]

```

m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAFAIRQIAAALQTQGGADAV
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519           IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAFAIRQIAAALQTQGGADAV
                210      220      230      240      250      260

                160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                ||||||||||||||||||||||||||||||||||||||||||||||||||
a519           NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51  ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GCGGTTTCCA TCGCGCCCTG ACGGCGCGTT TGAATATTTT GATTCCTTT
151 ATCGACGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCGAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEEFIILLVA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGQAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAFAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCTTT
151 ATCGACGCGG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCGAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGT AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG

```

851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep
 1 MEFFIILLAA VAVFGFKSFV VIPQOEHVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVA YRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLSYGS
 101 SNYIMAITQL AQTTLR SVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLR YEIKD LVPPQEILRA MQAQITAERE KRARIAESEGRKIEQINLAS
 201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

g519-1.pep	10	20	30	40	50	60
m519-1	10	20	30	40	50	60
g519-1.pep	70	80	90	100	110	120
m519-1	70	80	90	100	110	120
g519-1.pep	130	140	150	160	170	180
m519-1	130	140	150	160	170	180
g519-1.pep	190	200	210	220	230	240
m519-1	190	200	210	220	230	240
g519-1.pep	250	260	270	280	290	300
m519-1	250	260	270	280	290	300
g519-1.pep	310					
m519-1	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT
 201 ACCCAGCCAG GTCTGCATCA CGCGGACAA TACGCGCTG ACTGTTGACG
 251 GTATCATCTA TTTCCAAGTA ACCGACCCA AACTCGCTC ATACGTTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGTCGCTTC
 351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA

```

401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATG CCGCGCCCT TCAAACCCAA GCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVFQFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDR VAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPK LASYGS
101 SNYIMAITQL AQTTLR SVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLR YEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

```

a519-1.pep 10 20 30 40 50 60
MEFFIILLAAVVVFQFKSFVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS
|||||:|||||
m519-1 10 20 30 40 50 60
MEFFIILLVAVVFQFKSFVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHS

a519-1.pep 70 80 90 100 110 120
KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLR SVIG
|||||:|||||
m519-1 70 80 90 100 110 120
KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLR SVIG

a519-1.pep 130 140 150 160 170 180
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAITAERE
|||||:|||||
m519-1 130 140 150 160 170 180
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQQAITAERE

a519-1.pep 190 200 210 220 230 240
KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
|||||:|||||
m519-1 190 200 210 220 230 240
KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR

a519-1.pep 250 260 270 280 290 300
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
|||||:|||||
m519-1 250 260 270 280 290 300
LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

a519-1.pep 310
ISAGMKIIDSSKTAKX
|||||:|||||
m519-1 310
ISAGMKIIDSSKTAKX
310

```

```
m576.seq.. (partial)
1 .. ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
51 GCAATGAAG GAACAGGGCG CCGAAATCGA TTGAAAGTCT TTTACCGAAG
101 CCATCGAGCG AGGTGTATGAC GCGAAAGAAA TCAAATGAC CGAAGAGCAG
151 GCTCAGGAAG TCATGATGAA ATTCTTTCAG GAACAACAGG CTAAGCCGT
201 AGAAAAACAC AAGCGCGGAG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251 TTCTGAAAG AAAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCGGCG
301 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC GACCAAAGA
351 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401 TCGACAGCAG CAAGGCCAAT GCGCGCCCGG TCACCTTCCC TTTGAGCCAA
451 GTGATTCCGG GTTGACCGA AGCGGTACAG CTTCTGAAAG AAGCGCGCGA
501 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTCGGG
551 GCGACAAAT CCGTCCGAAG GCCACTTTGG TATTTGATGT GAAACTGGTC
601 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAAGTCGA
651 CATCAAAAAA GTAAATTAA
```

m576.pep.. (partial)

1	..MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ
51	AQEVMMKFLQ	EQQAKAVEKH	KADAKANEKE	GEAFLKENAA	KDGVKTTASG
101	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	GTVFDSSKAN	GGPVTFFPLSQ
151	VIPGWTEGVQ	LKLEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFVDKLV
201	KIGAFENAPA	KOPAOVDIKK	VN*		

g576.seq.. (partial)

```
1  ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaagtctt ttaccgatgc catgcaggca gtgtatgacg
101 gcaaaagaaat caaaatgacc gaagagcaga cccaggaaat gatgatgaaa
151 ttctctgagg agcagcagcg taaagccgta gaaaaaacac aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gatatcgtta ccgtggaata
351 cgaaggccgc ctgattgacg taccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc tacccgcgac aggggtcggg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgtgca aaatcggcgc acccggaaaac
601 gcgcccgcga agcagccgga tcaagtgcac atcaaaaaag taatatta
```

g576.pep.. (partial)

1	..MGVDIGRSLK	QMKEQGAEID	LKVFETDAMQA	VYDGKEIKMT	EEQAQEVMMK
51	FLQEQQAKAV	EKKHADAKAN	KEKEAFLKE	NAEDGVKTT	ASGLQYKITK
101	QGEKGQPTKD	DIVTVEYEGR	LIDGTVFDSS	KANGGPATFP	LSQVIPGWE
151	GVRLLEKGE	ATFYIPSNLA	YREQGAGEKI	GNATLVFVDV	KLVKIGAPEN
201	APAKOPDOVD	IKKNV*			

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

m576.pep

10 20 30 40 50 60

MQQASYAMGVDIGRSLKQMKQEGAEIDLKVFTEAMQAVYDGKEIKMTEEQAEVMMKFLQ

|||||

```

g576          MGVDIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLO
              10      20      30      40      50

              70      80      90      100     110     120
m576.pep      EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTTASGLQYKITKQEGKQPTKDDIV
              |||||
g576          EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTTASGLQYKITKQEGKQPTKDDIV
              60      70      80      90      100     110

              130     140     150     160     170     180
m576.pep      TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
              |||||
g576          TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE
              120     130     140     150     160     170

              190     200     210     220
m576.pep      QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN
              |||||
g576          QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN
              180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1   ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGGCGCAAAA AAGAAGCCGC CCCC GCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATACCCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTCCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1   MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLO EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

m576.pep          10      20      30
                  MQQASYAMGV DIGRSLQMK EQGAEIDLKV
                  |||||
a576              30      40      50      60      70      80
CGKKEAAPASASEPAAASSAQGDTSSIGSTMQQASYAMGV DIGRSLQMK EQGAEIDLKV

              40      50      60      70      80      90
m576.pep      FTEAMQAVYDGKEIKMTEEQAQEVMMKFLOEQQAKAVEKHKADAKANKEKGEAFLKENAA
              |||||
a576          FTEAMQAVYDGKEIKMTEEQAQEVMMKFLOEQQAKAVEKHKADAKANKEKGEAFLKENAA
              90      100     110     120     130     140

```

```

      100      110      120      130      140      150
m576.pep  KDGVKTTASGLQYKITKQEGEKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ
a576      KDGVKTTASGLQYKITKQEGEKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ
      150      160      170      180      190      200

      160      170      180      190      200      210
m576.pep  VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
a576      VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA
      210      220      230      240      250      260

      220
m576.pep  KQPAQVDIKKVN
a576      KQPAQVDIKKVN
      270

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

```

m576-1.seq
1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

```

m576-1.pep
1  MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

```

g576-1.seq
1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCCTGCAG GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCACTACA AAATCACCAA ACAGGGTGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG

```

701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

g576-1.pep

1 MNTIFKISAL TL~~SAAL~~ALSA CGKKEAAPAS ASEPA~~ASAA~~ QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
 151 LQYKITYQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGFN ATLVFDVKLV
 251 KIGAPENAPA KQPDQVDIKK VN*

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TL SAAL ALSA	CGKKEAAPAS	ASEPA ASAA	QGDTSSIGST	MQQASYAMGV
m576-1	MNTIFKISAL	TL SAAL ALSA	CGKKEAAPAS	ASEPA ASAA	QGDTSSIGST	MQQASYAMGV
	10	20	30	40	50	60
	70	80	90	100	110	120
g576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
	130	140	150	160	170	180
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITYQGE	GKQPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITYQGE	GKQPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
	190	200	210	220	230	240
g576-1.pep	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGFN
m576-1	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGVR	LLKEGGEATF	YIPSNLAYRE	QGAGEKIGFN
	190	200	210	220	230	240
	250	260	270			
g576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

a576-1.seq

1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCGCC TGCGGCAAAA AAGAAGCCGC CCGCGCATCT GCATCCGAAC
 101 CTGCGCGCGC TTCTTCCGCG CAGGCGGACA CCTCTCGAT CGGCAGCACG
 151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
 201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
 251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
 301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
 351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGCG
 451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
 551 TCGACAGCAG CAAAGCCAAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
 601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGCGGCGA
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG

701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLQOMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
 101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVTFTASG
 151 LQYKITQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
 251 KIGAPENAPA KQPAQVDIKK VN*

a576-1/m576-1 ORFs 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISAL <u>TL</u> SAALALSAACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISAL <u>TL</u> SAALALSAACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a576-1.pep	DIGRSLQOMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAQAEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLQOMKEQGAEIDLKVFTTEAMQAVYDGKEIKMTEEQAQAEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLENAAKDGVTFTASGLQYKITQGEKGKOPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVTFTASGLQYKITQGEKGKOPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVQLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq

1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CCGCCGCCAT
 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
 101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
 151 GGAACGACGG TCGGCGGCGG CGGGGCCGTC TATACCGTTG TACCGCACCT
 201 GTCCCTGCCC CACTGGGCGG CGCAGGATT TCGCCAAAAGC CTGCAATCCT
 251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
 301 TGCGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCTTTCAGG CAAAACAGTT
 351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
 401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG

```

451 CGGACGGCAC AAGCCCGCTT CCCGATTTC GGTATTCCCG ACGATTTTAT
501 CTCGTCCCC CTGCTGCGG GTTTCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCcG ATTCCCCATC ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCGATACT CGGTACGCC
751 GAAGACCCTG TCGAACTTTT TTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAATCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGc CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

m919.pep

```

1  MKKYLFRAL YGIAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51  GTTVGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMOGI KSYMQRNPQR LAEVLGQNPS YIFFRELAYS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

g919.seq

```

1  ATGAAAAAAC ACCTGCTCCG CTCGCCCTG TACGGcatCG CCGCCgccAT
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAGC CTGCAATCCT
251 TCCGCCCTCG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTC AAC CCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCagg tgcaggcaAC GGAAGcCTTG
401 Caggtagcgt TACCGCTAT TACGAACCGG TGCTGAAGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCGTCCCCG CTGCTGCGG GTTTCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCATCCT Cggttagcgc
751 GAagaccCcG tcgaacttTT TTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCcg tccggcaaat acatCCGCAt cggATagcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcatc aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCGTCCG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTG TCGCCACCGC CCATCCGGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

```

g919.pep
  1 MKKHLLRSAL YGIAAAILAA CQSRSIQTFP QPDTSVINGP DRPAGIPDPA
 51 GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGVPVAGLG
351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

m919/g919

m919.pep	10	20	30	40	50	60
	MKKYLFRALYGIAAAILAACQSKSIQTFPQDTSVINGPDRPVGIPDPAGTTVGGGGAV					
g919	MKKHLLRSALYGIAAAILAACQSRSIQTFPQDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
m919.pep	70	80	90	100	110	120
	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120
m919.pep	130	140	150	160	170	180
	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGIIPDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRTERARFPIYGIIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGTHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
	190	200	210	220	230	240
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
	250	260	270	280	290	300
m919.pep	310	320	330	340	350	360
	KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIIFRELAYSNDGPVAGLGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIIFRELAYSNEGVPVAGLGTPLMGEYAGA					
	310	320	330	340	350	360
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPL FVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPL FVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420

```

              430      440
m919.pep      QKTTGYVWQLLPNGMKPEYRPX
              |||||
g919           QKTTGYVWQLLPNGMKPEYRPX
              430      440

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCGGCCCTG TCGGCATCG CCGCGCCAT
51 CCTCGCGGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCGCCC
151 GGAACGACGG TCGGCGGCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGGCCCAAG CCTTCAAAC CCCCGTCCAT TCCGTTCAAG CAAAACAGTT
351 TTTTGAACGC TATTTACGC CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCTGCCG GTTTGCGGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCCCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTACGCC
751 GAAGACCCCG TCGAACTTT TTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCAAG TTTTGGGGCA AAACCCACG TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTATTGT TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CCGTATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```

a919.pep
1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQGSGRLKTP SGKYIRIGYA DKNEHPVYSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

```

              10      20      30      40      50      60
m919.pep      MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
              |||||
a919           MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m919.pep      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
              |||||
a919           YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
              70      80      90      100     110     120

```

	130	140	150	160	170	180
m919.pep	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA					
a919	YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pep	LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFE GSRFLPYHTRNQINGGAL					
a919	LVRI RQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFE GSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pep	DGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
a919	DGKAPILGYAEDPVELFFMHIQGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pep	KLGQTS MQGIKSYMRQNPQRLAEVLGQNPSYIFFREL AGSSNDGPVGALGTPLMGEYAGA					
a919	KLGQTS MQGIKAYMQNPQRLAEVLGQNPSYIFFREL TGSSNDGPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pep	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK					
a919	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pep	QKTTGYVWQLLPNGMKPEYRPX					
a919	QKTTGYVWQLLPNGMKPEYRPX					
	430	440				

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCGG CCAATTGCTG
151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
401 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
451 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
501 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
551 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
601 xxxxxxX CAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAAGCACG GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGTTGGC GCGTGTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```

1051 GCAACCGGCG CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

This corresponds to the amino acid sequence <SEQ ID 3076; ORF 121>:

m121.pep

1 METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL Axxxxxxxxxxxx xxxxxxxxxxxxxx
151 xxxxxxxxxxxxxx xxxxxxxxxxxxxx xxxxxxxxxxxxxx xxxxxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3077>:

g121.seq

1 ATGGAAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51 GCGGATGCC GTGCTGGTAC GGATGGACGG CCGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCT TACCCTGACC GGTGCGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCAC AGACGAACGT CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCGCCTGT ACAGCGCAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACAGCGCCGA ACACGGTtac AGCATACAGC TTGCCGATTT
351 GCGCTGCTG GCGGAACGa cgcggatttT TACCGTCggc gacttcCGCA
401 GCGCGACCT TGCTGCCGCG GGacaAGGTG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CCGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cacTGGcagc TGCTTTACGA CAAAacggt gcAAAGgcgg cacAAGGCAA
651 catatTGCcg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTTCAC
701 AACCCcacc aaAAAGCACG GGgcGCGaac TgtttgcccT AAattggctc
751 gaaacctAcc ttgacggcgg cgaaccga tacgacgtat tgcggacgct
801 ttcccgattc accgcgcaaA ccgTttggga cgcggtctca CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGCGG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATTtg
1001 cgtggttgC GCGTGTGG ATTAACGCA TTCCCGTAG TCCGCACAAA
1051 GCGACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

This corresponds to the amino acid sequence <SEQ ID 3078; ORF 121.ng>:

g121.pep

1 METQLYIGIM SGTSMGADA VLVRMDGGKW LGAEGHAFTP YPDRLLRRKLL
51 DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVWDAYS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	: : : : :					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	: : : : :					

```

g121      HRSRMLSQELSRLYAQTAAEELCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
           70      80      90      100      110      120
           130      140      150      160      170      180
m121.pep  AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      AELTRIFTVGDFRSRDLAAGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA
           130      140      150      160      170      180
           190      200      210      220      230      240
m121.pep  XXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
           190      200      210      220      230      240
           250      260      270      280      290      300
m121.pep  GRELFAINWLETYLDGGENRYDVLRTLRSRFTAQTVCDVASHAAADARQMYICDGGIRNPV
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVWDVASHAAADARQMYICGGGIRNPV
           250      260      270      280      290      300
           310      320      330      340      350      360
m121.pep  LMADLAECFGRVSLHSTADLNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      LMADLAECFGRVSLHSTAE LNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
           310      320      330      340      350      360

m121.pep  XAGYYXX
           | : : : :
g121      GAGYYXX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTACCCCC TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGCG GACTTCCGCA
401 GCCGCGACCT TCGCGCCGCG GGACAAGGCG CGCCGCTCGT CCCGCTTTT
451 CACGAAGCCC GTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCGACGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGCG AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCGG TATTTGCGAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATT ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCC TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCC
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGADA VLIRMDGKWK LGAEGHAFTP YPGRLLRKL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGP NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRSF TAQTVFDAVS HAAADARQMY ICGGGIRNPV

```

301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

m121/a121 ORFs 121 and 121.a showed a 74.0% identity in 366 aa overlap

m121.pep	10	20	30	40	50	60
	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTYPYGRRLRRQLLDLQDTGADEL					
a121	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTYPYGRRLRRQLLDLQDTGADEL					
	10	20	30	40	50	60
m121.pep	70	80	90	100	110	120
	HRSRILSQELSRLYAQTAELCSQNLAPSDITALGCHGQTVRHAPHEHGYISQLADLPPL					
a121	HRSRILSQELSRLYAQTAELCSQNLAPSDITALGCHGQTVRHAPHEHGYISQLADLPPL					
	70	80	90	100	110	120
m121.pep	130	140	150	160	170	180
	XX					
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVPAPFHEALFRDDRETRAVLNIGGIANISVLPDPA					
	130	140	150	160	170	180
m121.pep	190	200	210	220	230	240
	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121.pep	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV					
a121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDPQWVEA AAFAWMAACWVNRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYX					
a121	GAGYYYX					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3081>:

m121-1.seq

1	ATGGAACAC	AGCTTTACAT	CGGCATCATG	TCGGGAACCA	GCATGGACGG
51	GGCGGATGCC	GTACTGATAC	GGATGGACGG	CGGCAAATGG	CTGGGCGCGG
101	AAGGGCACGC	CTTTACCCCC	TACCCCGGCA	GGTTACGCCG	CCAATTGCTG
151	GATTTGCAGG	ACACAGGCGC	AGACGAACTG	CACCGCAGCA	GGATTTTGTC
201	GCAAGAACTC	AGCCGCCTAT	ATGCGCAAAC	CGCCGCCGAA	CTGCTGTGCA
251	GTCAAAACCT	CGCACCGTCC	GACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTTAC	AGCATACAGC	TTGCCGATTT
351	GCCGCTGCTG	GCGGAACGGA	CGCGGATTTT	TACCGTCGGC	GACTTCCGCA
401	GCCGCGACCT	TGCGGCCGCG	GGACAAGGCG	CGCCACTCGT	CCCCGCCTTT
451	CACGAAGCCC	TGTTCCGCGA	CAACAGGGAA	ACACGCGCGG	TACTGAACAT
501	GCGCGGGATT	GCCAACATCA	GCGTACTCCC	CCCCGACGCA	CCCGCCTTCG
551	GCTTCGACAC	AGGGCCGGGC	AATATGCTGA	TGGACGCGTG	GACGCAGGCA
601	CACTGGCAGC	TTCTTTACGA	CAAAAACGGT	GCAAAGGCGG	CACAAGGCAA
651	CATATTGCCG	CAACTGCTCG	ACAGGCTGCT	CGCCACCCG	TATTTGCGAC
701	AACCCACCCC	TAAAAGCACG	GGGCGCGAAC	TGTTTGCCCT	AAATTGGCTC
751	GAAACCTACC	TTGACGCGCG	CGAAAACCGA	TACGACGTAT	TGCGGACGCT
801	TTCCCGTTTT	ACCGCGCAAA	CCGTTTGCGA	CGCCGCTCA	CACGCAGCGG

```

851 CAGATGCCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

```

m121-1.pep
1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQLL
51  DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGP NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

```

m121-1.pep      10      20      30      40      50      60
METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTYPGRLLRQLLDLQDTGADEL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121             10      20      30      40      50      60
METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTYPDRLLRKLDDLQDTGTDEL

m121-1.pep      70      80      90      100     110     120
HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121             70      80      90      100     110     120
HRSRMLSQELSRLYAQTAAELLCSONLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL

m121-1.pep     130     140     150     160     170     180
AERTRIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDNRETRAVLNIGGIANISVLPPDA
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121            130     140     150     160     170     180
AELTRIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPFGA

m121-1.pep     190     200     210     220     230     240
PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121            190     200     210     220     230     240
PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST

m121-1.pep     250     260     270     280     290     300
GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDAYSHAAADARQMYICGGGIRNPV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121            250     260     270     280     290     300
GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAYSHAAADARQMYICGGGIRNPV

m121-1.pep     310     320     330     340     350     360
LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121            310     320     330     340     350     360
LMADLAECFGTRVSLHSTAELNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL

m121-1.pep      XAGYYYY
|||||
g121             GAGYYYY

```

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

```

a121-1.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

```

```

51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCGG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAATG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCGCTG ACGCGCAAAC CGCCGCGGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCGGCA
401 GCCGCGACCT TGCGGCGGGC GGACAAGGCG CGCCGCTCGT CCCCCTTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CCGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACCCACCCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGATTG ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCC TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCGCACAATA
1051 GCAACCGCGC CATCAAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPESHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAFWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLDLQDTGADEL					
a121-1	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLDLQDTGADEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEHGYISQLADLPLL					
a121-1	HRSRMLSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPESHSYSVQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDNRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTPGNMMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGNMMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFDAVS HAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFDAVS HAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

```

          310      320      330      340      350      360
m121-1.pep  LMADLAECFGTRVSLHSTADLNLDPOWVEAAAXFAWLAACWINRIPGSPHKATGASKPCIL
          |||||:|||||:|||||:|||||:|||||:|||||
a121        LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWMAACWVNRI PGSPHKATGASKPCIL
          310      320      330      340      350      360

m121-1.pep  XAGYXX
          |||||
a121        GAGYXX

```

128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

```

m128.seq (partial)
1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCG GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGTG TCGCACCTCA ACTGCGTCG CGACACGCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAACTC AACCAC
1  TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51  wGTCAAAAAA TAyTTCcCyG TCGGCAAwGT ATTAACCGGA CTGTTCGCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCCGTC
151 TGGCACAAAG ACGTGCCTTA TtTGAATTG CAACAAACG GCGAaMCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKA ATGGGACGCG GTCGAAGTGC CCAGCCAGTT
501 TATGAAAAAT TTCGTTTGGG AATACAATGT CTTGGCACA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCcC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAaG CGGCATGTTC yTsGTCCGCGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAAAGTCCA ACAGGTTTGA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTCCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCGGCCACA
901 GGCAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAAATC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3086; ORF 128>:

```

m128.pep (partial)
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

//
1  YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGfTEKTPV
51  WHKDVRXYEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSdGTL
101 QLPTAYLVCN FAPPVGGREA RLShDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQVL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT
301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHSGF DNAV*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

```

g128.seq
1  atgattgaca acgCActgct ccacttgggc gaagaaccCC GTTTTaatca
51  aatccaaacc gaagACAtca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCGGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TCGCGGATTT CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAACCGTC CTAGACGCGA .CGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCGCG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGccaaa CTGCTCGGCT TTAATAATTA CGCCGAATTG TCCTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAGGTTT TAAACTTCCT GCACGACCTC
901 GCCGCGCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAACACCTCG GTCTCGCGA CCCGCAGCCG TGGGACTTGA
1001 GCTACGCGCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTGCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCAAAACC
1201 ATCGGCGCGC TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGActaca AAGGCCGCGC CCGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTGCTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AacCGGCCAC GGA CTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAacggcgtA GAATGGGACG CGGTGGAAT GCCCAGCCAG
1501 TTTATGGAAA ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCGC
1551 CCACGAAGAA AccgGCGAGC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TcgCGCCCAA AAACCTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TCGATATGAT GATTACAGT GAAAGCGACG AATGCCGCTCT
1701 GAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GtcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCCGCAGG CTATTACAGC TACGCATGGG CCGAAGTCCt
1851 cAGCACCGAT GCCTACGCCG CCTTTGAAGA AAGcGACGac gtcGCCGCCA
1901 CAGGCAAACG CTTCTGGCAA GAAAtccttg ccgtcggcgg ctCCCGCAGC
1951 gcgCGCGAAT CTTCAAAGC CTTCCGCGGA CGCGAACC GAATAGACGC
2001 ACTGCTGCGC CAaagcggtT TCGACAACGC gGcttgA

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

```

g128.pep
1  MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 QQDIELYNRF KTIKNSPEFA TLSPAQTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTYG KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDVSRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYA AFESDD VAATGKRWFQ EILAVGGSRS

```

651 AESFKAFRG REPSIDALLR QSGFDNAA*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)
from *N. gonorrhoeae*:

m128/g128

g128.pep	10	20	30	40	50	60
	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
g128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
g128.pep	130	140	150	160	170	180
	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
g128.pep				340	350	360
	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
m128	YASEKLREAKYAFSETXVKKYFPVGXVLNG					
				10	20	30
g128.pep	370	380	390	400	410	420
	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
g128.pep	430	440	450	460	470	480
	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSGDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
g128.pep	490	500	510	520	530	540
	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
g128.pep	550	560	570	580	590	600
	LVRQMEFALFDMMIYSESDECRLLKNWQQVLDVSRKEVAVIQPEYNRNFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDDGRLKNWQQVLDVSRKKVAVIQPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
g128.pep	610	620	630	640	650	660
	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330

```

          670      679
g128.pep  IDALLRQSGFDNAAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACTCA ACTCCGTAC CGACACGCC GAACGCGCG
251 CGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCCAGATC
401 TGGCGGATTT CGTCCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAAC CGAAGGCGCG CAACTTTCCG CCAAATTTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAAA ACGTCCCGC
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCG CGGTTTTTTC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGAAA ATTTCTGTTT GGAATACAAT GTCTTGCGC AAATGTCCCG
1551 CCACGAAGAA ACCGGCGTTC CCTGCCGAA AGAACTCTT GACAAAATGC
1601 TCGCCGCCAA AAATTTCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGCGGCT ATTCCGACG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CTTTGAAGA AAGCGACGAT GTCGCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTA LLGFKNYAEL SLATKMADTP EQVLNLFHLD
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDVAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAARNFQ RGMFLVRQME

```

551 FALFDMMIYS EDDEGR LKNW QQVLD SVRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
 651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIGVGVSHLNCVADTPELRVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIGVGVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNHLHL					
	250	260	270	280	290	300
m128.pep						140
						YASEKLEAKYAFSETXVKKYFPVGX
a128	ARRAKPYAEKDLAEVKAFARESGLGLADLPWDLGYAGEKLEAKYAFSETEVKKYFPVGK					150
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPVWHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDVAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDVAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGR LKNWQQVLD SVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGR LKNWQQVLD SVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600

```

400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAAGYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
          610      620      630      640      650      660

460      470
m128.pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3091>:

```

m128-1.seq
1  ATGACTGACA  ACGCACTGCT  CCATTTGGGC  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AATCCGCCCT  GCAAACCGCC  ATCGCCGAAG
101 CGCGCGAACA  AATCGCCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTCT  AACCCTTGAC  CGGCATACCC  GAACGCTGCG  GCAGGATTTG
201 GGGCGTGGTG  TCGCACTTCA  ACTCCGTGCG  CGACACGCCC  GAACTGCGCG
251 CCGTCTATAA  CGAAGCTGAT  CCCGAAATCA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CACCGCTTC  AAAACATCA  AAAATCTCCC
351 CGAATTCGAC  ACCCTCTCCC  CCGCAAAAA  AACCAAATCT  AACACGATCA
401 TGCGCATATT  CGTCTCTCAG  GGC GCGGAAC  TGCCGCCCGA  ACAGCAGGCA
451 GAACTGGCAA  ATAGTCAAA  CGAAGGCGCG  CAACTTTCCG  CCAAATCTCT
501 CCAAACGCTC  CTACGCGCGA  CCGACGCGT  CGGCATTTAC  TTTGACGATT
551 CCGCACCGCT  TGCCGGCATT  CCGCAAGAGC  CGCTCGCCAT  GTTTGCGGCC
601 GCCGCGCAAA  GCGAAAGCAA  AACAGGCTAC  AAAATCGGCT  TGCAGATTCC
651 ACATCTACCT  GCGGTCATCC  AATACGCGCA  CAACCGCGAA  CTGCGCGAAC
701 AAATCTACCG  CGCTACGTT  ACCCGCGCCA  GCGAACTTTC  AGACGACGCG
751 AAATTCGACA  ACACCGCAA  CATCGACCG  ACGCTCGCAA  AGCCCTTGCA
801 AACCGCCAAA  CTGCTCGGCT  TCAAAAATA  CGCCGAATTG  TCGCTGGCAA
851 CCAAATGGC  GGACACGCC  GAACAAGTT  TAAACTTCTT  GCACGACCTC
901 GCCCGCGCG  CCAAACCTA  CGCCGAAAA  GACCTCGCCG  AAGTCAAAGC
951 CTTGCGCCG  GAAAGCCTGA  ACCTCGCGA  GTTGCAACCG  TGGGACTTGG
1001 GCTACGCCAG  CGAAAACTG  CGCGAAGCCA  AATACGCGTT  CAGCGAAACC
1051 GAAGTCAAAA  AATACTTCCC  CGTCGGCAA  GTATTAAACG  GACTGTTCCG
1101 CCAATCAAA  AAACCTACG  CATCTCGGAT  TACCGAAAA  ACCGTCCCCG
1151 TCTGTCACAA  AGACGTGCG  TAATTGTAAT  TGCAACAAAA  CGGCGAAACC
1201 ATAGGCGGCG  TTTATATGGA  TTTGTACGCA  CGCGAAGGCA  AACCGCGCGG
1251 CGCGTGGAT  AACGACTACA  AAGGCGCGCG  CCGTTTTTCA  GACGGCACGC
1301 TGCACCTGCC  CACCGCTTAC  CTCTGCTGCA  ACTTCGCCCC  ACCCGTTCGG
1351 GGCAGGGAAG  CCGCGCTGAG  CCACGACGAA  ATCTCATCT  TCTTCCACGA
1401 AACCGGACAC  GGGCTGCACC  ACCTGCTTAC  CCAAGTGGAC  GAACTGGGCG
1451 TATCTCGCAT  CAACGGCGTA  GAATGGGACG  CGGTGCAACT  GCCAGCCAG
1501 TTTATGAAA  ATTTGTTTG  GGAATACAAT  GTCTTGGCAG  AAATGTTCAG
1551 CCACGAGAA  ACCGCGTTT  CCTCGCGAA  AGAACTTCT  GCAAAAATGC
1601 TCGCCGCCAA  AAACCTCCAA  CGCGGCATGT  TCCTCGTCCG  GCAAAATGGAG
1651 TTCGCCCTCT  TTGATATGAT  GATTTACAGC  GAAGACGACG  AAGGCCGTCT
1701 GAAAACCTGG  CAACAGGTTT  TAGACAGCGT  GCGCAAAAAA  GTCGCGCTCA
1751 TCCAGCCGCG  CGAATAACA  CGTTTCGCCT  TGAGCTTCGG  CCACATCTTC
1801 GCAGGCGGCT  ATTCCGCAGG  CTATTACAG  TACGCGTGGG  GCGAAGTATT
1851 GAGCGCGGAC  GCATACGCG  CCTTTGAAGA  AAGCGACGAT  GTCGCGCCA
1901 CAGGCAAACT  CTTTGGGAC  GAAATCTCTG  CCGTCGCGCG  ATCGCGCAGC
1951 CGCGCAGAA  CTTTCAAAGC  TCTCGCGCG  CGGAACCGCA  GCATAGACGC
2001 ACTCTGCGC  CACAGCGGTT  TCGACAACGC  GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3092; ORF 128-1>:

m128-1.pcp.
1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHGTWA
51 NTVEPLTGIT ERVGRIWGVV SHLNSVADTP ELRAVYNELM PEITVFETEI

```

101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKSTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLNLGFAQIK KLYGIGFTEK TVPVWHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLLKNW QQVLDVSRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AESFKAFRG REPSIDALLR HSGFDNAV*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1 ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51 AATCAAAACC GAAGACATCA AACC CGCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACCGCTCG GCAGGATTTG
201 GGGCGTCTGT TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCACGACC
401 TCGCGGATTT CGTATTGAGC GGC GCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAA CAAAGGCGCG CAACTTTCCG CCAATTTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGT CCGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCG
601 GCCGCGCAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CAAAATGGC GGACACGCCC GAACAGGTTT TAACTTCCT GCACGACCTC
901 GCGCGCGCG CCAAACCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAACACCTCG GTCTCGCCGA CCGCAGCCG TGGGACTTGA
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTCGC
1101 CCAATCAAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TTTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGGCG TTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCGTCGGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1 MIDNALLHLG EEPRFNQIKT EDIKPAVQTA IAEARGQIAA VKAQTHTGWA
51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL NHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKSTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQQNGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

10 20 30 40 50 60

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGTWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRIWGVVSHLSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
m128-1	ERVGRIWGVVSHLSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSESKTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFDNTANIDRTLENALKTAKLLGFKNYAELSLATKMADTPEQVLNLFHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNLFHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDLSYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLDLQPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWM
m128-1	VINGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

a128-1.seq

1	ATGACTGACA	ACGCACTGCT	CCATTGGGC	GAAGAACCCC	GTTTTGATCA
51	AATCAAAACC	GAAGACATCA	AACCCGCCCT	GCAAACCGCC	ATTGCCGAAG
101	CGCGCGAACA	AATCGCCGCC	ATCAAAGCCC	AAACGCACAC	CGGCTGGGCA
151	AACACTGTCTG	AACCCCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTGGTG	TCGCACCTCA	ACTCCGTCAC	CGACACGCCC	GAACGCGCG
251	CCGCCTACAA	TGAATTAATG	CCCAGAAATTA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TCGAGCTGTA	CAACCGCTTC	AAAACCATCA	AAAATCCCC
351	CGAGTTCGAC	ACCTCTCTCC	ACGCGCAAAA	AACCAAATC	AACCACGATC
401	TGCGCGATT	CGTCCTCAGC	GGCGCGGAAC	TGCCGCCCGA	ACAGCAGGCA
451	GAATTGGCAA	AACTGCAAAC	CGAAGGCGCG	CAACTTCCG	CCAAATTCTC

```

501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTGGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTGACA ACACCGCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCCCCG GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGCGGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACC GGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAAC GCCCAGTCAG
1501 TTTATGAAA ATTTCTGTTG GGAATACAAT GTCTTGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AACTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTGCGCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGCGGCGT ATTCCGAGG CTATTACAGC TAGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCC CTTTGAAGA AAGCGACGAT GTCGCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA
51 NTVEPLTGIT ERVGRIVGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVEPLSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKREWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

```

          10      20      30      40      50      60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
|||||
m128-1 MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90      100     110     120
a128-1.pep ERVGRIVGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
|||||:|||||:|||||
m128-1 ERVGRIVGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90      100     110     120

          130     140     150     160     170     180

```

a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAEELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAEELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAAQSESKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLEAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLEAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDDEGRKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDDEGRKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670

206

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3097>:

m206.seq

1	ATGTTTCCCC	CGACAAAAC	CCTTTTCCTC	TGCTCAGCG	CACTGCTCCT
51	CGCCTCATGC	GGCAGGACCT	CCGGCAAACA	CCGCCAACCG	AAACCCAAAC
101	AGACAGTCCG	GCAAATCCAA	GCCGTCGCGA	TCAGCCACAT	CGACCGCACA
151	CAAGGCTCGC	AGGAACCTCAT	GTCCACAGC	CTCGGACTCA	TCGGCACGCC
201	CTACAAATGG	GGCGCGCAGCA	GCCACGCAAC	CGGCTTCGAT	TGCAGCGGCA
251	TGATTCAATT	CGTTTACAAT	AACGCCCTCA	ACGTCAAAGT	GCCGCGCACC
301	GCCCGCGACA	TGGCGGCGGC	AAGCCGAAA	ATCCCCGACa	GCCGcyTCAA
351	GGCCGGCGAC	CTCGTATTCT	TCAACACCGG	CGGCGCACAC	CGCTACTCAC
401	ACGTCGGACT	CTACATCGGC	AAAGGCGAAT	TCATCCATGC	CCCCAGCAGC
451	GGCAAAACCA	TCAAAACCGA	AAAACCTCTC	ACACCGTTTT	ACGCCAAAAA
501	CTACCTCGGC	GCACATACTT	TTTTTACAGA	ATGA	

This corresponds to the amino acid sequence <SEQ ID 3098; ORF 206>:

m206.pap..

```

1  MFPPDKTLFL  CLSALLLASC  GTTSGKHRQP  KPKQTVRQIQ  AVRISHIDRT
51  QGSQELMLHS  LGLIGTPYKW  GGSSTATGFD  CSGMIQFVYK  NALNVKLPR
101  ARDMAAASRK  IPDSRXKAGD  LVFFNTGGAH  RYSHVGLYIG  NGEFIHAPSS
151  GKTIKTEKLS  TPFYAKNYLG  AHTEFTE*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 3099>:

g206.seq

1	atgtttttccc	cgcacaaaac	cctttttctc	tgtctcgcg	cactgtcct
51	cgcctcatgc	ggcacgacct	ccggcaaaca	ccgccaaccg	aaacccaac
101	agacagtcgc	gcaaatccaa	gccgtccgca	tcagccacat	cggcgcgaca
151	caaggtccg	aggaactcat	gctccacagc	ctcggactca	tcggcacgcc
201	ctacaaatgg	ggcgcgcagc	gcaccgcagc	cggcttcgac	tgcagcggca
251	tgattcaatt	ggtttataaa	aacgccctca	acgtcaagct	gccgcgcacc
301	gcccgcgaca	tggcgcgcgc	aagccgcaa	atccccgaca	gccgcctcaa
351	ggcggcgac	atcgatttct	tcaaccaccg	cggcgcacac	cgctactcac
401	acgtcggact	ctacatcggc	aacggcgaat	tcatccatgc	ccccggcagc
451	ggcaaaaacca	tcaaaacgca	aaaactctcc	acacggtttt	acgccaaaaa
501	ctaccttgga	gcgcatacgt	tttttacaga	atga	

This corresponds to the amino acid sequence <SEQ ID 3100; ORF 206.ng>:

g206.pep

```

1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGPD CSGMIQLVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD IVFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTEFTE*

```

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/q206

	10	20	30	40	50	60
m206.pep	MFP	PD	KT	FL	CL	SALL
	AS	CG	TT	SG	KHR	QPK
	Q	T	V	R	Q	I
	Q	A	V	R	I	S
	H	I	D	R	T	O
	G	S	E	L	M	L
	H	S				
g206	M	F	P	D	K	T
	F	L	C	L	G	A
	L	L	A	S	C	G
	T	T	S	G	K	H
	R	Q	P	K	P	Q
	T	V	R	Q	I	Q
	A	V	R	I	S	H
	I	G	R	T	O	G
	S	E	L	M	L	H
	S					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	L	G	L	I	G	T
	P	Y	K	W	G	S
	S	T	A	T	G	F
	D	C	S	G	M	I
	Q	F	V	Y	K	N
	A	L	N	V	K	L
	P	R	T	A	R	D
	M	A	A	S	R	K
	I	P	D	S	R	X
	K	A	G	D		
g206	L	G	L	I	G	T
	P	Y	K	W	G	S
	S	T	A	T	G	F
	D	C	S	G	M	I
	Q	L	V	Y	K	N
	A	L	N	V	K	L
	P	R	T	A	R	D
	M	A	A	S	R	K
	I	P	D	S	R	L
	K	A	G	D		
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	L	V	F	F	N	T
	G	A	H	R	Y	S
	H	V	G	L	I	Y
	I	G	N	G	E	F
	I	H	A	P	S	S
	G	K	T	I	K	T
	E	K	L	S	T	P
	F	Y	A	K	N	Y
	L	G	A	H	T	F
	F	F	T	E	X	
g206	I	V	F	F	N	T
	G	A	H	R	Y	S
	H	V	G	L	I	Y
	I	G	N	G	E	F
	I	H	A	P	S	S
	G	K	T	I	K	T
	E	K	L	S	T	P
	F	Y	A	K	N	Y
	L	G	A	H	T	F
	F	F	T	E	X	

130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCCGACA GCCGCTTAA
351 GGCCGCGCAG CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT QGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT QGSQELMLHS					
	10	20	30	40	50	60
m206.pep	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT ARDMAAASRK IPDSRLKAGD					
a206	LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT ARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	LVFFNTGGAH RYSHVGLYIGN GEFIHAPSS GKTIKTEKLS TPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAH RYSHVGLYIGN GEFIHAPSS GKTIKTEKLS TPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGGC GGCGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTGTTTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GGCGGGCAAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGTT
551 CTTAGATCC CATCCCGCG TCAAACCTG CACCTGCGAA TGGCGGTAGC
```

```

601 AATTTTGGAA GGGTTGATTT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGGA TGAAGAAGTA CAGCTAAAT CAGAATTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGGCAGG
1201 TTTGCCGCAA AAGTCGATTT CGGCAGCAAA TCTGTGGACG GCATTATCGA
1251 CAGCGGCGAT GATTTGCATA TGGGTACGCA AAAATTCAAA GCCGCCATCG
1301 ATGGAACCGG CTTTAAGGGG ACTTGACGCG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCCC ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTTGCCGCGA
1451 AAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

```

m287.pep
1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQG QGAPSAQGSQ DMAAVSEENT GNNGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGGDDPSA GGQNAGNTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRVVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRLPAE MPLIPVQAD TLIVDGEAVS LTGHSNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMTQKFKF AAIDGNGFKG TWTENGSGDV
451 SGKFYGPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

```

g287.seq
1 atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcgtggcgc gatcgccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggcgcgcccc gttgttgctg aaaatgcggy ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgcgcgaagc
201 cgatacgagc gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 tttcggcaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgcga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 ccccgcgctc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 gttgaccac tgtaaaaggc attcttgtaa tgggtgataa ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaaagcat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagc gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gcttcgggcc
751 gagattccgc tgattccgt caatcaggcc gatacgctga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgc caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcgatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttgttgg
951 cacggcggcg tacaacggcg aagtgtgtga tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccc caaaagtcca tttcggcagc
1051 aaatctgtgg acggcattat cgacacgggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatggaaa cggctttaag gggacttgga
1151 cggaaaatgg cggcggggat gtttcgggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattcggc gtgtttgccc gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

```

g287.pep
1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV

```

```

51 LPKEKKDEEA AGGAPQADTQ DATAGEGSQD MAAVSAENTG NGGAATTNDP
101 KNEDAGAQND MPQNAAESAN QTGNNQAGS SDSAPASNPA PANGGSDFGR
151 TNVGNVVID GPSQNTLTH CKGDSNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGNTKYI IFYTDKPTR SARSRSLPA
251 EIPLIPVQA DTLIVDGEAV SLTGHSGNIF APEGNYRYLT YGAEKLPGGS
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSVDDGIIDSG DDLHMGTKF KAAIDGNGFK GTWTENGGGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFGF VFAGKKDRD*

```

m287/g287 ORFs 287 and 287.ng showed a 70.1% identity in 499 aa overlap

```

m287.pep      10      20      30      40      49
MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSE-----KETEA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
g287          10      20      30      40      50      60
MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEVLPKEKKDEEA
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

m287.pep      50      60      70      80      90     100     109
KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g287          70      80      90     100     110
AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTNDPNKNEDEVAQNMPQNA--
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

m287.pep     110     120     130     140     150     160     169
DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQDDPSAGGQNAAGTA
g287          -----

m287.pep     170     180     190     200     210     220     229
AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFGFVRLANGVLIDGPSQNTLTHCKGDS
::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g287         120     130     140     150     160     170
-ESANQTGNNQAGSSDSAPASNPAPANGGSDFGRNTNVGNVVIDGPSQNTLTHCKGDS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

m287.pep     230     240     250     260     270     280     289
CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP
|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g287         180     190     200     210     220     230
CNGDNLLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGNTKYIIFYTD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

m287.pep     290     300     310     320     330     340     349
KPTSFARFRRSARSRSLPAEMPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT
||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g287         240     250     260     270     280     290
KPPT-----RSARSRSLPAEIPLIPVQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLT
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

m287.pep     350     360     370     380     390     400     409
YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
g287         300     310     320     330     340     350
YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMEMENGRPYPSGGRFAAKVDFGS
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

m287.pep     410     420     430     440     450     460     469
KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGGSDVSGKFYGPAGEEVAGKYSYR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
g287         360     370     380     390     400     410
KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGGGDVSGRFYGPAGEEVAGKYSYR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|

m287.pep     470     480     489
PTDAEKGFGFVFAGKKEQDX

```

g287

|||||::||
PTDAEKGFGVVFAGKKDRDX
420 430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3107>:

a287.seq

```
1 ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
51 CTGTGGGGGC GCGGTGGCG GATCGCCCGA TGTTAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTACTG AAGATGTCGG GGAAGAGGTG
151 CTGCCGAAAG AAAAGAAAGA TGAGGAGCG GTGAGTGGTG CGCCGCAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CGGTCAAGAT ATGGCGGCAG
251 TTTCGGCAGA AAATACAGGC AATGGCGGTG CGGCAACAAC GGATAATCCC
301 GAAAATAAAG ACGAGGGACC GCAAAATGAT ATGCCGCAAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATCGGC ACAACCGGCA
451 AACCAACCGG ATATGGCAAA TGCGGCGGAC GGAATGCAGG GGGACGATCC
501 GTCGGCAGGG GAAAATGCCG GCAATACGGC AGATCAAGCT GCAATCAAG
551 CTGAAAACAA TCAAGTCGGC GGCTCTCAA ATCCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTTGACAGCG GTTCGGAAAA TGTAACGTTG ACACATTGTA
701 AAGACAAAGT ATGCGATAGA GATTCTTAG ATGAAGAAGC ACCACCAAAA
751 TCAGAATTTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA
801 AGACGAGCAA CGAGAGAATT TTGTCGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATTT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CGCGATTGAG CGGTCTGCA CGGTGAGGC GGTGCTTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GGCGGATACG CTGATTGTCG
1001 ATGGGGAAGC GGTGAGCCTG ACGGGGCATT CCGGCAATAT CTTGCGCCCG
1051 GAAGGGAATT ACCGCTATCT GACTTACGGG GCGGAAAAAT TGTCCGCGCG
1101 ATCGTATGCC CTCAGTGTGC AAGGCGAACC GGCAAAGGC GAAATGCTTG
1151 CCGGCACGGC CGTGTAACAAC GCGGAAGTGC TGCATTCCA TATGGAAGAC
1201 GGCCGTCCGT CCCCCTCCGG AGGCAGGTTT GCCGCAAGG TCGATTTCGG
1251 CAGCAAATCT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTT ACGGCCCGGC
1401 CCGCGAAGAA GTGGCGGGA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGCGCGATT CCGCGTGTTC GCCGCAAAA AAGAGCAGGA TTGA
```

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

a287.pep

```
1 MFKRSVIAMA CIVALSAACGG GGGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPQND MPQNAADTDS STPNHTPAPN MPTRDMGNQA PDAGESAQPA
151 NQPDMANAAD GMQDDPSAG ENAGNTADQA ANQAENNQVG GSQNPASSTN
201 PNATNGGSDF GRINVANGIK LDGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIIYKDKSAS
301 SSSARFRRSA RSRRLPAEM PLIPVQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMEN
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGD LHMGTQKFKA VIDGNGFKGT
451 WTENGGGDVVS GRFYGPAGEE VAGKYSYRPT DAERGGFGVF AGKKEQD*
```

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

```
10 20 30 40 49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETEA
|||||::|||
a287 MFKRSVIAMACIVALSAACGGGGGGSPDVKSADTLSKPAAPVVTEDEVGEEVLPKEKKDEEA
10 20 30 40 50 60

50 60 70 80 90 100 109
m287.pep KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
||||:| |:::||||| |||||:::|:|:|:| |||||
a287 VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPENKDEGPQNDMPQNAADT
70 80 90 100 110
```

	110	120	130	140	150	160	169
m287.pep	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDDPSAGGQNAGNTA						
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGDDPSAG-ENAGNTA						
	120	130	140	150	160	170	
	170	180	190	200	210	220	229
m287.pep	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFGVRDLANGVLIDGPSQNTLTHCKGDS						
a287	DQAAQAENNQVGGSQNPASSTPNPATNGGSDFGRINVANGIKLDSGSENVTLTHCKDKV						
	180	190	200	210	220	230	
	230	240	250	260	270	280	289
m287.pep	CSGNNFLDEEVQLKSEFEKLSADKISNYKKDGKNDKRVGLVADSVQMKGINQYIIFYKP						
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVIIYKD						
	240	250	260	270	280	290	
	290	300	310	320	330	340	
m287.pep	KP--TSFARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRY						
a287	KSASSSSARFRRSARSRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRY						
	300	310	320	330	340	350	
	350	360	370	380	390	400	
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF						
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF						
	360	370	380	390	400	410	
	410	420	430	440	450	460	
m287.pep	GSKSVDSGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSQKFGYPAGEEVAGKYS						
a287	GSKSVDSGIIDSGDDLHMGTKQFKAVIDGNGFKGTWTENGSGDVSQKFGYPAGEEVAGKYS						
	420	430	440	450	460	470	
	470	480	489				
m287.pep	YRPTDAEKGFGVFAGKKEQDX						
a287	YRPTDAEKGFGVFAGKKEQDX						
	480	490					

406

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3109>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACACGTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGTGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAACAA CTGAAAGCCC AAACAAAACCT GGAATATTTT GCAGTAGACA

```

```

701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPYR YETT AETTSAGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEAF
251 AYKENYALWM GPYKVSKEGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGQP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCTCCTT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPYR YETT AETTSAGGLTG LTTSLSTLNA PALSRTQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEAF
251 AYKENYALWM GPYKVSKEGIK PTEGLMVDFS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGQP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

```

          10      20      30      40      50      60
g406.pep  MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKDMDLQALHGR
          |||||||
m406      MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAAVKDMDLQALHGR

```

	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
	130	140	150	160	170	180
g406.pep	LTTSLSTLNAPALSRTQSDGSGSRSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	190	200	210	220	230	240
g406.pep	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVS KG IKPTEGLMVD FSDI QPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVS KG IKPTEGLMVD FSDIRPYGNHTGNSAPSVEADN					
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```
a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAAAC TGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA
```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```
a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVS ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
```

251 AYKENYALWM GPYKVSKEGK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN
 301 SHEGYGYSDE AVRRHRQQGP *

m406/a406 ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap

m406.pep	10	20	30	40	50	60
	MQARLLIPIILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
a406	MQARLLIPIILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
m406.pep	70	80	90	100	110	120
	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
	70	80	90	100	110	120
m406.pep	130	140	150	160	170	180
	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
m406.pep	190	200	210	220	230	240
	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVS PANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
m406.pep	250	260	270	280	290	300
	IKPKTNAFEAAAYKENYALWMGPYKVSKEGK PTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSKEGK PTEGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
m406.pep	310	320				
	SHEGYGYSDEVVRQHRQQGPX					
a406	SHEGYGYSDEAVRRHRQQGPX					
	310	320				

EXAMPLE 2

Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm

that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 3

Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 4

Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera

were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).. These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 5

Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

Immunol 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 8

Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

Table 2

225 gene variability: List of used *Neisseria* strains

Identification Strains number	Source / reference
Group B	
zo01_225 NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225 BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225 NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225 297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225 1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225 BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225 BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225 528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225 NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225 BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225 NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225 NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225 NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225 NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225 SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225 NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225 NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225 BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225 BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225 44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225 MC58	R. Moxon
zo96_225 2996	Our collection
Group A	
zo22_225 205900	R. Moxon
zo23_225 F6124	R. Moxon
z2491 22491	R. Moxon / Maiden <i>et al.</i> , 1998
Group C	
zo24_225 90/18311	R. Moxon
zo25_225 93/4286	R. Moxon

Others

zo26_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998
 zo27_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998
 zo28_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998
 zo29_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

Gonococcus

zo32_225 Ng F62 R. Moxon / Maiden *et al.*, 1998
 zo33_225 Ng SN4 R. Moxon

 fa1090 FA1090 R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
 NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z2491 <SEQ ID 3116>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRVPARRAGNA
 DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN*

Z001_225 <SEQ ID 3117>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDSRFLN*

Z002_225 <SEQ ID 3118>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDSRFLN*

Z003_225 <SEQ ID 3119>

MDSFFKPAVWAVLWLMFAVRLALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDSRFLN*

Z004_225 <SEQ ID 3120>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z005_225 <SEQ ID 3121>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z006_225 <SEQ ID 3122>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z007_225 <SEQ ID 3123>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z008_225 <SEQ ID 3124>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z009_225 <SEQ ID 3125>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z010_225 <SEQ ID 3126>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z011_225 <SEQ ID 3127>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z012_225 <SEQ ID 3128>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z013_225 <SEQ ID 3129>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFIQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z014_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z015_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z016_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z017_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z018_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z019_225 <SEQ ID 3135>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z020_225 <SEQ ID 3136>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPINRAPARRAGNADELIGSAMGLNEQPVLPVNRVPARRAGNA
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
MQHIKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN*

Z021_225 <SEQ ID 3137>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR
VKKNDP SRFLN*

Z022_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR

SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

ZO23_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

ZO24_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

ZO25_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

ZO26_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

ZO27_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

ZO28_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

ZO29_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
VKKN DPSRFLN*

ZO32_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

ZO33_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRSALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS
GFMQHIKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN*

ZO96_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG
 NADELIGSAMGLNEQPVLVNVNRPARRAGNADELIGNAMGLNEQPVLVNVNRPARRAGNA
 DELIGNAMGLLGIAYRYGGSISTGFDSCGFMQHIKFRAMGINLPRTSAEQARMGTPVAR
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
 VKKNDPSRFLN*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

Table 3

235 gene variability: List of used <i>Neisseria</i> strains		
Identification Strains number		Reference
Group B		
gnmzq01	NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02	BZ198	Seiler <i>et al.</i> , 1996
gnmzq03	NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04	1000	Seiler <i>et al.</i> , 1996
gnmzq05	1000	Seiler <i>et al.</i> , 1996
gnmzq07	BZ169	Seiler <i>et al.</i> , 1996
gnmzq08	528	Seiler <i>et al.</i> , 1996
gnmzq09	NGP165	Seiler <i>et al.</i> , 1996
gnmzq10	BZ133	Seiler <i>et al.</i> , 1996
gnmzq11	NGE31	Seiler <i>et al.</i> , 1996
gnmzq13	NGE28	Seiler <i>et al.</i> , 1996
gnmzq14	NGH38	Seiler <i>et al.</i> , 1996
gnmzq15	SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16	NGH15	Seiler <i>et al.</i> , 1996
gnmzq17	NGH36	Seiler <i>et al.</i> , 1996
gnmzq18	BZ232	Seiler <i>et al.</i> , 1996
gnmzq19	BZ83	Seiler <i>et al.</i> , 1996
gnmzq21	MC58	Virji <i>et al.</i> , 1992
Group A		
gnmzq22	205900	Our collection

gnmzq23 F6124 Our collection
 z2491 Z2491 Maiden *et al.*, 1998

Group C

gnmzq24 90/18311 Our collection
 gnmzq25 93/4286 Our collection

Others

gnmzq26 A22 (group W) Maiden *et al.*, 1998
 gnmzq27 E26 (group X) Maiden *et al.*, 1998
 gnmzq28 860800 (group Y) Maiden *et al.*, 1998
 gnmzq29 E32 (group Z) Maiden *et al.*, 1998
 gnmzq31 *N. lactamica* Our collection

Gonococcus

gnmzq32 Ng F62 Maiden *et al.*, 1998
 gnmzq33 Ng SN4 Our collection

fa1090 FA1090 Dempsey *et al.* 1991

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>

MKPLILGLAAVLALSACQVRKAPDLDTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVGAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ01 <SEQ ID 3150>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANNLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ02 <SEQ ID 3151>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTTSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ03 <SEQ ID 3152>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ04 <SEQ ID 3153>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ05 <SEQ ID 3154>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ07 <SEQ ID 3155>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ08 <SEQ ID 3156>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ09 <SEQ ID 3157>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMMLAST
AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITITEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ10 <SEQ ID 3158>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ11 <SEQ ID 3159>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ13 <SEQ ID 3160>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ14 <SEQ ID 3161>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ15 <SEQ ID 3162>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ28 <SEQ ID 3173>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ29 <SEQ ID 3174>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

GNMZQ31 <SEQ ID 3175>

MKPLILGLAAVLALSACQVQKAPDFDYTAFKESKPASILVVPPLNESPDVNGTWGMLAST
 AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKAAAYDLLSPYSHNGILKGPRFVEEQPK*

GNMZQ32 <SEQ ID 3176>

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

GNMZQ33 <SEQ ID 3177>

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK*

22491 <SEQ ID 3178>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

Table 4

287 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
--	------------------

Group B

287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992

Group A

z2491	Z2491	Maiden <i>et al.</i> , 1998
-------	-------	-----------------------------

Gonococcus

fa1090	FA1090	Dempsey <i>et al.</i> 1991
--------	--------	----------------------------

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

287_14 <SEQ ID 3179>

MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNO
 TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGSDSCSGNNFLDEEV
 QLKSEFEKLSADKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTSFAF
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFTENGSRPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMGTKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_2 <SEQ ID 3180>

MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAADTDSLTPNHTPAS
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNO
 TAGSQNPASSTNPSATNSGGDFGRITNVGNSVVIDGPSQNTLTHCKGSDSCSGNNFLDEEV
 QLKSEFEKLSADKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTSFAF
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTGAEKLP
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFTENGSRPSRGRFAAKVDFGSKSVDGII
 DSGDGLHMGTKFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKG
 GFGVFAGKKEQD*

287_21. <SEQ ID 3181>

MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNMPQNAAGTDSSTPNHTPDP
 NMLAGNMENQATDAGESSQPANQPDMAANTADGMQGGDDPSAGGQAGNTAAQGANQAGNNQ
 AAGSSDPIPASNPAPANGGNSNFRVLDLAVGLIDGPSQNTLTHCKGSDSCSGNNFLDEEV
 QLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTSFAFRRS

ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD
DLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGFV
FAGKKEQD*

287_9 <SEQ ID 3182>

MFKRSVIAMACIVALSACGGGGGGSPDVKSADTLSPKPAAPVVTEDVGEVLPKEKKDEEA
VSGAPQADTQDATAGKGGQDMAAVSAENTGNGGAATTDNPENKDEGPQNDMPQNAADTDS
STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMAADGMQGGDDPSAGENAGNTADQA
ANQAENNQVGGSONPASSTNPATNGGSDFRINRVANGIKLDSGSENVTLTHCKDKVCDR
DFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVITYKDKSAS
SSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYG
AEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKS
VDGIIDSGDDLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPT
DAEKGFGFVFAKKEQD*

FA1090 <SEQ ID 3183>

MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA
AGGAPQADTQDATAGEGSDMAAVSAENTGNGGAATTDNPKNEDAGAQNMPQNAAESAN
QTGNNQAGSSDSAPASNAPANGGSDFRTNVGNSSVVIDGPSQNTLTHCKGDSNGDN
LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVEKNGTNKYVITYKDKPPT
SARSRRSLPAEIPVQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
YALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKSVVDGIIDSG
DDLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPTDAEKGFGFV
VFAGKKDRD*

Z2491 <SEQ ID 3184>

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVSEKETEAKEDAPQAGSQG
QGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGTDSSTPNHTPDP
NMLAGNMENQATDAGESQPANQPDMAADGMQGGDDPSAGGQAGNTAAQGANQAGNNQ
AAGSSDPIPASNPAPANGGSGNFRVLDLGVLDGPSQNTLTHCKGDSNGNFLDEEV
QLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMGKINQYIIFYKPKPTSFARFRS
ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLPGGSY
ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD
DLHMGTOQKFAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGFGFV
FAGKKEQD*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

Table 5

519 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
------------------------	--------------------

number**Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

Group A

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Others

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

Gonococcus

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090_519 <SEQ ID 3185>
MEFFIILLAAVAVFGKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGANGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANAETIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Z2491_519 <SEQ ID 3186>

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV01_519 <SEQ ID 3187>

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV02_519 <SEQ ID 3188>

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV03_519 <SEQ ID 3189>

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV04_519 <SEQ ID 3190>

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV05_519 <SEQ ID 3191>

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV06_519ASS <SEQ ID 3192>

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV07_519 <SEQ ID 3193>

MEFFIILLVAVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV11_519 <SEQ ID 3194>

MEFFIILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV12_519 <SEQ ID 3195>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV18_519 <SEQ ID 3196>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV19_519 <SEQ ID 3197>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV20_519ASS <SEQ ID 3198>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM
ISAGMKIIDSSKTAK*

ZV21_519ASS <SEQ ID 3199>

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV22_519ASS <SEQ ID 3200>

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV26_519 <SEQ ID 3201>

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
LVAEANAFAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV27_519 <SEQ ID 3202>

MEFFIILLVAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA EAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV28_519 <SEQ ID 3203>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA EAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV29_519ASS <SEQ ID 3204>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTIVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREPEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA EAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSNKTAK*

ZV32_519 <SEQ ID 3205>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA EAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

ZV96_519 <SEQ ID 3206>

MEFFIILLAAVAVFGFKSFVVIPOQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR
LVAEANA EAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
ISAGMKIIDSSKTAK*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

Table 6

919 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
------------------------	--------------------

number**Group B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11asbc	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

Group A

zm22	205900	R. Moxon
zm23asbc	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

Group C

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

Others

zm26	A22 (group W)	R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26 (group X)	R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800 (group Y)	R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32 (group Z)	R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

Gonococcus

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon
fa1090	FA1090	R. Moxon

References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3207>

MKKHLLRSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
YFTPWQVAGNGSLAGTVTGYYEPVLKGDGRTERARFPIYGIPTDDFISVPLPAGLRGGKN
LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSGNEGVPVAGLGTPLMGEYAGA
IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPENGMPPEYRP*

Z2491 <SEQ ID 3208>

MKKYLFRALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNDGVPVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPENGMPPEYRP*

ZM01 <SEQ ID 3209>

MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELTSNDGVPVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPENGMPPEYRP*

ZM02 <SEQ ID 3210>

MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELTSNDGVPVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPENGMPPEYRP*

ZM03 <SEQ ID 3211>

MKKYLFRALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYYEPVLKGDGRRTAQARFPIYGIPTDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
KLGQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFRELTSNDGVPVAGLGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPENGMPPEYRP*

ZM04 <SEQ ID 3212>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM05 <SEQ ID 3213>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM06 <SEQ ID 3214>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM07 <SEQ ID 3215>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM08N <SEQ ID 3216>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM09 <SEQ ID 3217>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROQTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELTSNSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM10 <SEQ ID 3218>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIROQTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGSRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM11ASBC <SEQ ID 3219>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM12 <SEQ ID 3220>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM13 <SEQ ID 3221>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAEQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM14 <SEQ ID 3222>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSRNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM15 <SEQ ID 3223>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDLAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNHQQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM16 <SEQ ID 3224>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPGRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM17 <SEQ ID 3225>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM18 <SEQ ID 3226>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM19 <SEQ ID 3227>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM20 <SEQ ID 3228>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM21 <SEQ ID 3229>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM22 <SEQ ID 3230>

MKKYLFRAALCGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGQTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM23ASBC <SEQ ID 3231>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTVTGYEYEPVLKGDDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTSKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM24 <SEQ ID 3232>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM25 <SEQ ID 3233>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM26 <SEQ ID 3234>

MKKYLFRAALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGTSMQGIKAYMQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM27BC <SEQ ID 3235>

MKKYLFRAALYGISAAAILAACQSKSIQTFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGETAGK
MKEPGYVWQLLPNGMKPEYRP*

ZM28 <SEQ ID 3236>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGTSMQGIKAYMRQNPQRLAEVLGQNPSYIFFRELGSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
YFTPWQVAGNGSLAGTGTGYEYEPVLKGDDRTAQARFPIYGI PDDFISVPLPAGLRSGKA
LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA
VDRHYITLGAPLFVATTHPITRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
QKTTGYVWQLLPNGMKPEYRP*

ZM31ASBC <SEQ ID 3238>

MKKHLFRAALYGIAAAILAACQSKSIQTFFPQPDTSIIKGPDRPAGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYVFFRELAGSGNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM32ASBC <SEQ ID 3239>

MKKHLRSALYGIAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKA
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYI FFRELAGSGDGPVGALGTPLMGGYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM33ASBC <SEQ ID 3240>

MKKHLRSALYGIAAAILAACQSRSIQTFFPQPDTSVINGPDRPAGIPDPAGTTVAGGGAV
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKSYMRQNPBKLAEVLGQNPSYI FFRELAGSGNEGPVGALGTPLMGEYAGA
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAILAACQSKSIQTFFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER
 YFTPWQVAGNGSLAGTVTGYEPEVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRSGKA
 LVRI RQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVVSIGRYMADKGYL
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYI FFRELAGSSNDGPVGALGTPLMGEYAGA
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK
 QKTTGYVWQLLPNGMKPEYRP*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 7: Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF primer Sequence		Restriction sites
001	Forward CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI-
	Reverse CCCGCTCGAG-TGCCGTCTTGTCAC	NdeI
003	Forward CGCGGATCCCATATG-GTCGTATTCGTGGC	XhoI
	Reverse CCCGCTCGAG-AAAATCATGAACACGCGC	BamHI-
005	Forward CGCGGATCCCATATG-GACAATATTGACATGT	NdeI
	Reverse CCCGCTCGAG-CATCACATCCGCCCC	XhoI
006	Forward CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI-
	Reverse CCCGCTCGAG-AGTTCCGGCTTTGATGT	NdeI
007	Forward CGCGGATCCCATATG-GCCGACAACAGCATCAT	XhoI
	Reverse CCCGCTCGAG-AAGGCGTTCATGATATAAG	BamHI-
008	Forward CGCGGATCCCATATG-AACAACAGACATTTTG	NdeI
	Reverse CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009	Forward CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI-
	Reverse CCCGCTCGAG-TGGCTTTTGCCACGTTTT	NdeI
011	Forward CGCGGATCCCATATG-AAGACACACCGCAAG	XhoI
	Reverse CCCGCTCGAG-GGCGGTCAGTACGGT	BamHI-
012	Forward CGCGGATCCCATATG-CTCGCCCGTTGCC	NdeI
	Reverse CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013	Forward CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI-
	Reverse CCCGCTCGAG-CTGATTCGGCAAAAAATCT	NdeI
018	Forward CGCGGATCCCATATG-CAGCAGAGGCAGTT	XhoI
	Reverse CCCGCTCGAG-GACGAGGCGAACGCC	BamHI-
019	Forward AAAGAATTC-CTGCCAGCCGCAAGACCCCGGC	NdeI
	Reverse AAAGTGCAG-TCAGCGGGCGGGGACAATGCCCAT	XhoI
023	Forward AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	Eco RI
	Reverse AAAGTGCAG-TTACCCCCAAATCACTTTAACTGA	Pst I
025	Forward AAAGAATTC-TGCGCCACCAACAGCCTGCTCC	Eco RI
	Reverse AAAGTGCAG-TCAGAACGCGATATAGCTGTTCCG	Pst I
031	Forward CGCGGATCCCATATG-GTCTCCCTTCGCTT	BamHI-
	Reverse CCCGCTCGAG-ATGTAAGACGGGGACAAC	NdeI
032	Forward CGCGGATCCCATATG-CGGCGAAACGTGC	XhoI
		BamHI-

	Reverse	CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward	CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
	Reverse	CCCGCTCGAG-ATTTGCCGCATCCCGAT	BamHI-
034	Forward	CGCGGATCCCATATG-GCCGAAAACAGCTACGG	NdeI
	Reverse	CCCGCTCGAG-TTTGACGATTTGGTTCAATT	XhoI
036	Forward	CGCGGATCCCATATG-CTGAAGCCGTGCG	BamHI-
	Reverse	CCCGCTCGAG-CCGGA CTGCGTATCGG	NdeI
038	Forward	CGCGGATCCCATATG-ACCGATTTCGCCA	XhoI
	Reverse	CCCGCTCGAG-TTCTACGCCGTACTGCC	BamHI-
039	Forward	CGCGGATCCCATATG-CCGTCCGAACCGC	NdeI
	Reverse	CCCGCTCGAG-TAGGATGACGAGGTAGG	XhoI
041	Forward	CGCGGATCCCATATG-TTCGTGCGCGAACCGC	BamHI-
	Reverse	CCCGCTCGAG-GCCCAAAA ACTCTTTCAA	NdeI
042	Forward	CGCGGATCCCATATG-ACGATGATTTGCTTGC	XhoI
	Reverse	CCCGCTCGAG-TTTGCAGCCTGCATTTGAC	BamHI-
043	Forward	AAAAAAGGTACC-ATGGTTGTTCAAATCAAATATC	NdeI
	Reverse	AAACTGCAG-TTATTGCGCTTACCTTCCGCCG	XhoI
043a	Forward	AAAAAAGGTACC-GCAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse	AAAAAACTGCAG- TTAATCCTGCAACACGAATTCGCCCCGTCCG	Pst I
044	Forward	CGCGGATCCCATATG-CCGTCCGACTAGAG	Kpn I
	Reverse	CCCGCTCGAG-ATGCGCTACGGTAGCCA	Pst I
046	Forward	AAAGAATTC-ATGTCGGCAATGCTCCCGACAAG	BamHI-
	Reverse	AAACTGCAG-TCACTCGGCGACCCACACCGTGAA	NdeI
047	Forward	CGCGGATCCCATATG-GTCATCATA CAGGCG	XhoI
	Reverse	CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	Eco RI
048	Forward	AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	Pst I
	Reverse	AAACTGCAG-TCAAGATTCGACGGGGATGATGCC	Eco RI
049	Forward	AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	Pst I
	Reverse	AAACTGCAG-AAGGCGTATCTGAAAAAATGGCAG	BamHI-
050	Forward	CGCGGATCCCATATG-GGCGCGGGCTGG	NdeI
	Reverse	CCCGCTCGAG-AATCGGGCCATCTTCGA	XhoI
052	Forward	AAAAAAGAATTC-ATGGCTTTGGTGGCGGAGGAAAC	Eco RI
	Reverse	AAAAAAGTCGAC-TCAGGCGGCGTTTTCACCTTCCT	Sal I
052a	Forward	AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTTTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCAAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGAATTTTGGCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCCTTTTCATTTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTTTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGTTCTGCCAGTTTCAG	XhoI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGAAAGTCAACACCCATTATCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAACACTACTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCGTCGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Pst I
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
108a	Forward	AAAAAAGAATTC-GGTAACACATTCGGCAGCTTAGACGGTGG	Eco RI
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Pst I
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTATGGG	Eco RI
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTTT	Pst I
111	Forward	CGCGGATCCCATATG-TGTTCGGAACAAACCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAAA	XhoI
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	XhoI
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAACTGGAAGTCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	XhoI
122	Forward	CGCGGATCCCATATG-GTCATGATTAATAATCCGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATT	XhoI
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	Eco RI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	Pst I
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGCACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGCCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-

	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	XhoI
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Eco RI
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCGGG	Pst I
	Reverse	AAACTGCAG-TTAAAGTGTTCGGAGCCGGC	Eco RI
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	Pst I
	Reverse	CCCGCTCGAG-GACCGCGTTGTCTGAAA	BamHI-
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	NdeI
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	XhoI
132	Forward	AAAGAATTC-ATGGAACCTTCAAAACCTTAATTTG	Eco RI
	Reverse	AAAAAACTGCAG-TCACCATGTCCGCAATTTGAAAAAC	Pst I
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	BamHI-
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	NdeI
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	XhoI
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	BamHI-
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCCAATTCGATCC	NdeI
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	XhoI
137a	Forward	AAAAAAGAATTC-GGCCGCAAACACGGCATCGGCTTCCT	Kpn I
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Pst I
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Pst I
141	Forward	AAAGAATTC-ATGAGCTTCAAAACCGATGCCGAAATCGC	Xba I
	Reverse	AAACTGCAG-TCAGAACAAGCCGTGAATCACGCC	Eco RI
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTTCATG	Pst I
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	BamHI-
143	Forward	AAAAAAGAATTC- ATGCTCAGTTTCGGCTTTCTCGGCGTTCAGAC	NdeI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	XhoI
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Eco RI
	Reverse	AAAAAATCTAGA-TCGGCATCGGCCGGCATATGTCCG	Pst I
146	Forward	AAAAAAGAATTC- CGCCAAGTCGTCATTGACCACGACAAAGTC	Xba I
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAACTGGG	Eco RI
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTTGGAAAC	Pst I
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Eco RI
148	Forward	AAAAAAGAATTC- ATGGCGTTAAAAACATCAAACCTTGAACACGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Eco RI
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	Xba I
			BamHI-

	Reverse	CCCGCTCGAG-AACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	NdeI
151	Forward	AAAAAAGAATTC-	XhoI
		ATGAAACAAATCCGCAACATCGCCATCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTAAAGTGGCGGCG	Pst I
152	Forward	AAAAAAGAATTC-	Eco RI
		ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG-	Pst I
		TTACGCCGACGAAATACTCAGACTTTTCGG	
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTCGGG	XhoI
155	Forward	AAAAAAGAATTC-ATGAAATCGGTATCCACGCGAGTC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTCAGCAT	Pst I
156	Forward	AAAAAAGAATTC-GCACAGCAAACGGTTTTGAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Pst I
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAAACACAATATCCCCGC	XhoI
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	Eco RI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTCCAGTTC	Xba I
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTTGGCCGCCTTCTTT	XhoI
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGCAGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGTTTCCGTCAAACCTGC	XhoI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	BamHI-
			NheI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTCGCG	XhoI
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI-
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	NdeI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCGT	XhoI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	BamHI-
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI-
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	NdeI
218	Forward	CGCGGATCCCATATG-GTCGCGGTCGATC	XhoI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	BamHI-
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	NdeI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI-
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	NdeI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	XhoI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	BamHI-
226	Forward	AAAGAATTC-CTTGCGATTATCGTGCGCACGCG	NdeI
	Reverse	AAACTGCAG-TCAAAATCCCAAAACGGGGAT	XhoI
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	Eco RI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	Pst I
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	NdeI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	XhoI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	BamHI-
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAGGCGGTTTGGG	NdeI
	Reverse	AAAAAACTGCAG-TCAAGGTTTTTCTGATTGCCGCCGC	XhoI
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI-
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	NdeI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	XhoI
			BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
			BamHI-
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	NdeI
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	NdeI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTTGTCTAAGTTCCTGATATG	NheI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
			EcoRI-
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	NdeI
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	NdeI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	XhoI
			EcoRI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTG	XhoI
			BamHI-
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	NdeI
243	Forward	CGCGGATCCCATATG-ACGATTTTTTCGATGCTGC	HindIII
			BamHI-
	Reverse	CCCGCTCGAG-CGACTTGGTACCGCG	NdeI
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	NdeI
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	NdeI
248	Forward	CGCGGATCCCATATG-CGAAACAGAACT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	NdeI
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	NdeI
253	Forward	AAAAAAGAATTC-ATGATTGACAGGAACCGTATGCTGCG	XhoI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Eco RI
			Pst I

253a	Forward	AAAAAAGAATTC-AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	AAAAAAGAATTC-ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI-
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	NdeI
			XhoI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	BamHI-
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	NheI
			XhoI
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCTCTG	BamHI-
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	NdeI
			XhoI
258	Forward	AAAAAAGAATTC-GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	AAAAAAGAATTC-GCGAAGGCGGTGGCGCAAGGCGA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI-
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	NdeI
			XhoI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	BamHI-
	Reverse	CCCGCTCGAG-AACAGGGCGACACCCT	NdeI
			XhoI
261	Forward	AAAAAAGAATTC-CAAGATACAGCTCGGGCATTTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	Pst I
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	BamHI-
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	NdeI
			XhoI
264	Forward	AAAAAAGGTACC-GCCGACGCAGTGGTCAAGGCAGAA	Kpn I
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCCG	Pst I
265	Forward	AAAAAAGAATTC-GCGGAGGTCAAGAGAAGGTGTTTG	Eco RI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAATGGG	Pst I
266	Forward	AAAGAATTC-CTCATCTTTGCCAACGCCCCCTTC	Eco RI
	Reverse	AAACTGCAG-CTATTCCTGTTGCGCGTGTGCCA	Pst I
267	Forward	AAAGAATTC-TTCTTCCGATTTCGATGTTAATCG	Eco RI
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Pst I
269	Forward	AAAGAATTC-TGCAAACCTTGCGCCACGTGCCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
269a	Forward	AAAAAAGAATTC-GACTTTATCCAAAACACGGCTTCGCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
270	Forward	AAAGAATTC-GCCGTCAAGCTCGTTTTGTGCAATG	Eco RI
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Pst I
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	BamHI-
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	NdeI
			XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTTGGTTACGGAC	BamHI-
	Reverse	CCCGCTCGAG-TTTGCTTTTCAGTATTATTGAA	NdeI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCATCACGATGATGCG	XhoI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Eco RI
277	Forward	AAAAAAGAATTC-ATGCCCCGCTTTGAGGACAAGCTCGTAGG	Pst I
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Eco RI
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Pst I
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Eco RI
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Kpn I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTCGTCATAGTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Pst I
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT	BamHI-
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	NdeI
280	Forward	AAAAAAGGTACC-GCCCCCTGCCGTTGTAACCAG	XhoI
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	Kpn I
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Pst I
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Eco RI
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTTCCGG	Xba I
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Eco RI
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Xba I
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Eco RI
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	Pst I
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	BamHI-
284	Forward	CGCGGATCCCATATG-TTTGCCTGCAAAAGAATCG	NdeI
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAACTG	XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTTCCGAAAA	BamHI-
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	NdeI
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	XhoI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC	EcoRI-
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	NheI
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	XhoI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-TTGATTTTTGCGGATGATT	NdeI
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTTGTCAGAAC	XhoI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	Eco RI
295	Forward	CGCGGATCCCATATG-AACCGGCCGGCCTCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	NdeI
297	Forward	AAAAAAGAATTC-GCATAATTGCTTCGACAGAGAG	XhoI
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	Eco RI
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	Pst I
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Eco RI
299	Forward	CGCGGATCCGCTAGC-CTACCTGTGCGCTCCG	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	NheI
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	XhoI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	Eco RI
305	Forward	AAAAAAGGTACC-GAATTTTACCGATTTCAGCACCGGA	Pst I
	Reverse	AAAAAACTGCAG-TCATTCCCACTTATCCAGCCTGACAG	Kpn I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Pst I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Kpn I
306	Forward	CGCGGATCCCATATG-TTTATGAACAAATTTTCCC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	NdeI
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	NdeI
311	Forward	AAAAAAGGTACC-ATGTTCAGTTTTGGCTGGGTGTTT	XhoI
	Reverse	AAACTGCAG-ATGTTTCATATTCCCTGCCTTCGGC	Kpn I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Pst I
	Reverse	AAACTGCAG-TCAGTTTTTCATCGATTGAACCGG	Kpn I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Pst I
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Eco RI
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	Pst I
			BamHI-
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	NdeI
402	Forward	AAAAAAGAATTC-GTGCCTCAGGCATTTTCATTTACCCTTGC	XhoI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Xba I
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Eco RI
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	Xba I
			BamHI-
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	NdeI
			XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGTGTGATGTTACCCC	XhoI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	XhoI
503	Forward	CGCGGATCCCATATG-TGTTGCGGGAAAGGCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI- NdeI
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	HindIII
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	XhoI
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	XhoI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	XhoI
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGCGCCCAGCCGT	XhoI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	Eco RI
	Reverse	AAACTGCAG-TCAAATTCAGACTCTGCCAC	Pst I
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	XhoI
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTCAAGTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	XhoI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	HindIII
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	BamHI- NdeI

Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
525 Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
527 Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTTCG	Eco RI
Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
529 Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
530 Forward	CGCGGATCCCATATG-AGTGCGAGCGCGG	BamHI- NdeI
Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
531 Forward	AAAAAAGAATTC-TATGCCGCCGCTACCAAATCTACGG	Eco RI
Reverse	AAAAAACTGCAG-TTAAACAGCGCCGTGCCGACGACAAG	Pst I
532 Forward	AAAAAAGAATTC-ATGAGCGGTCAGTTGGGCAAAGGTGC	Eco RI
Reverse	AAAAAACTGCAG-TCAGTGTTCAGTGGTTCGGTATCAAA	Pst I
532a Forward	AAAAAAGAATTC-TTGGGTGTCGCGTTTGAGCCGGAAGT	Eco RI
Reverse	AAAAAACTGCAG-TCAGTGTTCAGTGGTTCGGTATCAAA	Pst I
535 Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
537 Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
538 Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
539 Forward	CGCGGATCCGCTAGC-GAGGATTTGCAGGAAA	BamHI- NheI
Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
542 Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
Reverse	AAACTGCAG-TTACCGCGAACCGGTCAGGAT	Pst I
543 Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
543a Forward	AAAAAAGAATTC-GGCAAACTCGTCATGAATTTGC	Eco RI
Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
544 Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCCGACCTGCACGG	Eco RI
Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
544a Forward	AAAAAAGAATTC- GCAAATGACTATAAAAAACAAAACTTCCAAGTACTTGC	Eco RI
Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
547 Forward	AAAGAATTC-ATGTTTCGTAGATAACGGATTTAATAAAAC	Eco RI
Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
548 Forward	AAAGAATTC-GCCTGCAAACCTCAAGACAACAGTGCGGC	Eco RI

	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCCCGCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTGGGAATATGCCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCCAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTTCATTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGTGTTCATTTCCGC	XhoI
574	Forward	CGCGGATCCCATATG-TGTTTGCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCGGG	XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCG	XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTTCGTACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACTTCCCCCGAAGTG	XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	XhoI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCCAGTCGTTGAA	Xba I
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Pst I
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Pst I
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTTCTGTTTTGGA	Pst I
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	XhoI
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	BamHI-

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
			XhoI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Pst I
589	Forward	AAAAAAGAATTC- ATGCAACAAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACCTGAACGGACTC	BamHI- NheI
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	XhoI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCTGACACTCGCG	Pst I
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGGAGGCGGAGAAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Pst I
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	XhoI
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	BamHI- NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	HindIII
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	XhoI
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	BamHI- NheI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	XhoI
603	Forward	AAAAAAGAATTC-CTGTCCTCGCGTAGGCGGGGACGGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	Pst I
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	BamHI- NheI
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	XhoI
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	Pst I
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Pst I
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCATCATCAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTCGCGTTC	Pst I
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	BamHI- NdeI

	Reverse	CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward	CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward	CGCGGATCCCATATG-CCGTCTCAAAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward	CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward	CGCGGATCCCATATG-TCCGTCGTGAGCGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward	AAAAAAGAATTC-ATGTCAAACACAATCAAAATGGTTGTCGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward	AAAAAAGAATTC-GGGCTTCTCGCCGCTCGCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTTTGTGTTTAAAACGAGATA	Pst I
622	Forward	CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGTCCAAATGATAAATCTG	XhoI
624	Forward	CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGATTCCGGGCCTGCGC	XhoI
625	Forward	CGCGGATCCCATATG-TTTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCAAAATTACCGCCTT	XhoI
627a	Forward	AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward	AAAAAAGGTACC-GCCTTACAAACATGGATTTTGCGTTC	Kpn I
	Reverse	AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAA	Pst I
629a	Forward	AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACAACACCGCCGTCCGGTTCAAACC	Pst I
630a	Forward	AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward	AAAAAAGAATTC- ATGACCCAGCGACGGGTCGGCAAGCAAAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATCCACTATAATCCTGTTGCT	Pst I
638	Forward	AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse	AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward	CGCGGATCCCATATG-ATGCTTTATTTTGTTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward	CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI XhoI Eco RI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	
644	Forward	AAAAAAGAATTC- ATGCCGTCTGAAAGGTCGGCGGATTGTTGCC	
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Pst I
645	Forward	AAAAAAGAATTC-GTGAACAGAGCAACACGTTAAATCG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCGC	Pst I
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Pst I
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Pst I
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGCGGAAACTGCCGCCGTC	Pst I
650	Forward	AAAAAAGAATTC-ATGTCCAAACTCAAACCATCGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Pst I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Kpn I
	Reverse	AAAAAACTGCAG-TTATTTGCCCAGTTGGTAGAATGCGGC	Pst I
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGGTAATTTTCATCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCGA	Pst I
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Eco RI
	Reverse	AAAAAACTGCAG-CTACGATTTCCGCGATTTCACATCGT	Pst I
657	Forward	AAAAAAGAATTC-GCAGAATTTGCCGACCGCCATTTGTGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	Pst I
658	Forward	CGCGGATCCCATATG-GTGTCCGGAATTGTG	BamHI- NdeI XhoI Eco RI
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTCCGCGTCGGGC	Pst I
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	BamHI- NdeI XhoI Eco RI
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	BamHI- NdeI XhoI Eco RI
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTTGCCGACGATTTC	Pst I
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTCGTATTCGTCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	Pst I

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTAAAAAACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-AAAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTAGGAGCTTTTGAACGCGTCGGACTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCGC	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAATAAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTTCGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI

694	Forward	CGCGGATCCCATATG-TTGGTTCCGCATCCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	XhoI
695	Forward	CGCGGATCCCATATG-TTGCTCAAACCTCGTCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCACACGGCT	XhoI
696	Forward	CGCGGATCCCATATG-TTGGGTGCCGGCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC-GCATCGACAGACGGTGTGTCGTGGAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTTGGATACTTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	XhoI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Pst I
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	XhoI
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTTTTGCCGGATAATATGGCGGGTGCG	Pst I
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	BamHI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	XhoI
708	Forward	CGCGGATCCGCTAGC-CCTTTTAAGCCATCCAAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	XhoI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGGTTTCGGTCAG	XhoI
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTTGCC	XhoI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	XhoI
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	XhoI

725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	XhoI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCGATGTTTAGCGTCC	XhoI
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTGTCGGTTTGGGTATC	HindIII
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	BamHI- NheI
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	XhoI
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	EcoRI- NdeI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGCTTGCCTCCTTTAC	XhoI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGAGATTTTGAATCAAAGAG	XhoI
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	XhoI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACCGAACA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGCGAGAATT	XhoI
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCCGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	XhoI
743	Forward	CGCGGATCCCATATG-GACGGTGTGTGCCTGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	XhoI
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-

	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
747	Forward	CCGGAATTCTAGCTAGC-CTGACCCCTTGGG	XhoI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	EcoRI-
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	NheI
	Reverse	CCCGCTCGAG-TTCAAGCCGAGTATGC	HindIII
750	Forward	CGCGGATCCCATATG-TGTCGCCCGAACCTG	BamHI-
	Reverse	CCCGCTCGAG-CTTTTCCCCGCCGCAA	NdeI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGTT	XhoI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	BamHI-
759	Forward	CGCGGATCCGCTAGC-CGCTTCACACACACCAC	NdeI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	NheI
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	XhoI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	BamHI-
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	NdeI
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	XhoI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTA	BamHI-
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	NdeI
	Reverse	CCCGCTCGAG-TTTCTGTACAGCAGGGG	XhoI
768	Forward	CGCGGATCCCATATG-GCCCCGCAAAAACCCG	BamHI-
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	NdeI
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	XhoI
	Reverse	CCCGCTCGAG-GCGTTTGTGCGAGATTTTC	BamHI-
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	NdeI
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	XhoI
772	Forward	CGCGGATCCCATATG-TTTGCGGCGTTGGTGG	BamHI-
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	NdeI
774	Forward	CGCGGATCCCATATG-TCCGTTTCACCCGTTCC	XhoI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	BamHI-
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	NdeI
			XhoI
			BamHI-
			NdeI

	Reverse CCCGCTCGAG-GGCGTTGTTCCGATTTCG	XhoI
900	Forward CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI- NdeI
	Reverse CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	XhoI
901	Forward CGCGGATCCCATATG-CCCGATTTTTTCGATG	BamHI- NdeI
	Reverse CCCGCTCGAG-AAAATGGAACAATACCAGG	XhoI
902	Forward. CCGGAATTCTACATATG-TTGCACTTTCAAAGGATAATC 2	EcoRI- NdeI
	Reverse CCCGCTCGAG-AAAAATGTACAATGGCGTAC	XhoI
903	Forward CCGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	EcoRI- NheI
	Reverse CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
904	Forward AAAAAAGGTACC-ATGATGCAGCACAATCGTTTC	Kpn I
	Reverse AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
904a	Forward AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
	Reverse AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
905	Forward CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI- NdeI
	Reverse CCCGCTCGAG-CCACTGATAACCGACAGAT	XhoI
907	Forward CGCGGATCCCATATG-GGCGCGCAACGTGAG	BamHI- NdeI
	Reverse CCCGCTCGAG-ACGCCACTGCCAGCG	XhoI
908	Forward AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	Eco RI
	Reverse AAACTGCAG-TTAATATGGTTTTGTCGTTTCG	Pst I
909	Forward CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	BamHI- NdeI
	Reverse CCCGCTCGAG-TCGGTTTTGAACTTTGGTTTT	XhoI
910	Forward AAAGAATTC-GCATTTGCCGGCGACTCTGCCGAGCG	Eco RI
	Reverse AAACTGCAG-TCAGCGATCGAGCTGCTCTTT	Pst I
911	Forward AAAGAATTC-GCTTTCCGCGTGGCCGGCGGTGC	Eco RI
	Reverse AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTCCGC	Pst I
912	Forward AAAAAAGAATTC- CAAATCCGTCAAAACGCCACTCAAGTATTGAG	Eco RI
	Reverse AAAAAACTGCAG-TTACAGTCCGTCCACGCCTTTTCGC	Pst I
913	Forward CGCGGATCCCATATG-GAAACCCGCCCGC	BamHI- NdeI
	Reverse CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	XhoI
915	Forward CGCGGATCCCATATG-TGCCGGCAGGCGGAA	BamHI- NdeI
	Reverse CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
914	Forward AAAGAATTC-GACAGAATCGGCGATTGGAAGCACG	Eco RI
	Reverse AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
916	Forward CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI- NdeI
	Reverse CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCCGCCTTCACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTTCGGG	NdeI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	XhoI
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	BamHI-
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCGTGAATCC	NdeI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	XhoI
922	Forward	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	Eco RI
	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	Pst I
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NheI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	XhoI
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTC	BamHI-
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	NdeI
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	XhoI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Eco RI
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTGCCCCGACAACAACGCGACG	Eco RI
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAACCGCCAATCCGCGGACAC	Eco RI
936	Forward	CGCGGATCCCATATG-GCCGCCGTGCGCGC	Pst I
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	BamHI-
937	Forward	AAAAAAGAATTC-CCGTTTACATTCAAACCGGCGCAAC	NdeI
	Reverse	AAAAAACTGCAG-TTAAAATGTATGCTGTACGCCAAA	XhoI
939a	Forward	AAAAAAGAATTC-GGTTCCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	Eco RI
	Reverse	CCCGCTCGAG-TTAGAACCGCATTGTC	BamHI-
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	NdeI
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	XhoI
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI-

	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward	CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
	Reverse	GCCCAAGCTT-GGGTCGTTTGTGCGTC	BamHI-
959	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	NdeI
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	HindIII
961	Forward	CGCGGATCCCATATG-GCCACAAGCGACGACG	BamHI-
	Reverse	CCCGCTCGAG-CCACTCGTAATTGACGC	NdeI
972	Forward	AAAAAAGAATTC- TTGACTAACAGGGGGGAGCGAAATTA AAAAC	XhoI
	Reverse	AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Eco RI
973	Forward	AAAAAAGAATTC-ATGGACGGCGCACAACCGAAAAC	Xba I
	Reverse	AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Eco RI
982	Forward	CGCGGATCCCATATG-GCAGCAAAAGACGTAC	Pst I
	Reverse	CCCGCTCGAG-CATCATGCCGCCCATCC	BamHI-
983	Forward	CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	NdeI
	Reverse	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward	CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
	Reverse	CCCGCTCGAG-TAATAAACCTTCTATGGGC	NdeI
988	Forward	CGCGGATCCCATATG-TCTTTAAATTTACGGGAAAAAG	XhoI
	Reverse	GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	BamHI-
989	Forward	CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	NdeI
	Reverse	CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	HindIII
990	Forward	CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	EcoRI-
	Reverse	CCCGCTCGAG-AAACAGCCATTTGAGCGA	NdeI
992	Forward	CGCGGATCCCATATG-GACGCGCCCGCCCG	XhoI
	Reverse	CCCGCTCGAG-CCAAATGCCCAACCATTC	BamHI-
993	Forward	CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	NdeI
	Reverse	CCCGCTCGAG-GAACACATCGCGCCCG	XhoI
996	Forward	CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	BamHI-
	Reverse	CCCGCTCGAG-TCTAAACCCCTGTTTCTC	NdeI
997	Forward	CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	XhoI
	Reverse	CCCGCTCGAG-GACGGCATCGCTCAGG	EcoRI-
			NheI
			XhoI

Underlined sequences indicate restriction recognition sites.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1>:

```
g001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG GTGTCGGCGA ACGAGGTGTC
 51  CCGCAGGGCT TCGCCCCGA TGGTGCTGGT CATCTGCCAG ACGCTGCCGA
101  AACGCGATAC TTAAACGGC TCGGTACGC ATACTTTACC GGTTCGGCG
151  ATTTTGCCGA GGTCGTTGCG CAGCAAATCG ACAATCATCA CGTTTCGGC
201  GCGGTTTTTC GGGTCGGTTT GTAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301  CCGTCTGAAG CGATGTTGAG GAAGAGTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCGGCTTCAT CGGGCAGGTG GGACAATACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 2; ORF 001.ng>:

```
g001.pep
  1  MLPOGKAARR VSANEVSGRA CARMVLVICQ TLPKRDTLNG SGHTTLPVWA
 51  ILPRSLRSKS TIITFSARFF GSVNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEAMLRKSS GEKHSVHAD C PASSGRWDNT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3>:

```
m001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
 51  CGGcAssCTT ss.GCTTGA yGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101  AACGCGATAC TTAAACGGT TCGGTACGC ATACTGTGCC GGTTCGGCG
151  ATTTTGCCGA GATCGTTACG CAGCAAATCG ACAATCATCA CGTTTCGGC
201  GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301  CCGTCCGAAC CGATTTTGAG GAAGAGTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CCCTCCGCAT CGGGCAGGTG GGACAAGACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 001>:

```
m001.pep
  1  MLPOGKAARR MSANEVCGXL XAWXVLVICQ TLPKRDTLNG SGHTTVPVWA
 51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 5>:

```
a001.seq
  1  ATGCTGCCGC AGGGGAAGGC GCGCGGAGG ATGTCGGCGA ACGAGGTGTC
 51  CCGCAAGGCT TGGGCTTGA TGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101  AACGCGATAC TTAAACGGT TCGGTACGC ATACTGTGCC GGTTCGGCG
151  ATTTTGCCGA GGTCGTTACG CAGCAAATCG ACAATCATCA CGTTTCGGC
201  GCGGTTTTTC GGGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251  CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTCCGT GCTGATGGTG
301  CCGTCCGAAC CGATTTTGAG GAAGAGTCG GCGGAGAAAC ACAGCGTCCA
351  CGCGGATTGC CTTGTGCAT CGGGCAGGTG GGACAAAACG GCATAG
```

This corresponds to the amino acid sequence <SEQ ID 6; ORF 001.a>:

```
a001.pep
  1  MLPOGKAARR MSANEVCGKA WAWMVLVICQ TLPKRDTLNG SGHTTVPVWA
 51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101  PSEPILRKSS GEKHSVHAD C PASGRWDKT A*
```

m001/a001 96.2% identity over a 131 aa overlap

```

              10      20      30      40      50      60
m001.pep  MLPOGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGHTTVPVWAILPRSLRSKS
|||||
a001.pep  MLPOGKAARRMSANEVCGKAWAWMVLVICQTLPKRDTLNGSGHTTVPVWAILPRSLRSKS
```

	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
a001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
a001.pep	PCASGRWDKTAX					
	130					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 001 shows 89.3% identity over a 131 aa overlap with a predicted ORF (ORF 001.ng) from *N. gonorrhoeae*:

m001/g001

	10	20	30	40	50	60
m001.pep	MLPQGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS					
g001	MLPQGKAARRVSA NEVSGRACARMVLVICQTLPKRDTLNGSGTHTLPVWAILPRSLRSKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSAREFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
g001	TIITFSAREFFGSVCNSAARRSSCPSPKIGAVPFIGSVLMVPSEAMLRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
g001	PASSGRWDNTAX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 7>:

g003.seq

```

1  ATGGTCGTAT TCGTGGCTGA AGGCGTATTC GGTGCGCTG TTTTGGGTCA
51  CTTGGTATTG CTCTTCGGTC AGGGTGC GTT TGAGTTCGGC GTCAC TCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTG CCTTGC GG TG CGGT CGGT
151 TTTGCCCGGC AGCGGTTCTG CGGCTTTCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAGG TAGTCCTGAT GGTATTCCTC GGCCTCGTAG
251 AAGTTTTTCA GCGGTTTCGT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTCG GCGGGGTCGG
351 TGTAGTACAC GCCGCTGCGG TATTGCGTGC CGGTGTCGTT ACCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAA TAATATTGCA GGATGTCGTC
451 CAGGCTGagt TTGTCGGCAT CGTaggtcac tTTGACGGTC TCGGCATGAC
501 CCGTATGGCG GTaggacact tctTCgtanc TcGGGtTTTC CGTgttGCCG
551 TTGGCgttac cGGATACCGC gtcaACCACG CCGTcgtatgc gttggaAATa
601 ggCTTCCAAG ccccaaaaagc agccgccggc gaagtaa atg gtgcccgtgt
651 tcatgattGC TGa

```

This corresponds to the amino acid sequence <SEQ ID 8; ORF 003.ng>:

g003.pep

```

1  MVVFVAEGVF GRAVLGHLVL LFGQGA FEFG VTRFFIRCRV EAFALRCGFG
51  FARQRFVGF D VDVA VAVGV FNQVLMVFL GVVEVFQRFV FNNEGQLVFL
101 LLAFEGGGDD GFFGGVG VVH AA AVL RAGVV TLFVEAGRIN DAEIILQD VV

```

151 QAEFVGIVGH FDGLGMTRMA VGHFFVRVFR VAVGVTGYRV NHAVDAL EIG
201 FQAPKAAAGE VNGARVHDC

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

m003.seq
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA
51 CTTGgTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCACCTCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGCAGGG CGGTCTTGGT
151 TTTGCCCGGC AGCGGTTCGT CAGCkTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGk CGGCGATGAC GGCTTTTTTCG kCGGGGTCGG
351 TGAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTGACGGTT TCGGCGTGCG
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA
601 GGCTTCCAAG CCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

m003.pep Length: 221
1 MVVFVAEGIF GRAVLGNLXL LFGQGAFFFG VTRFFIRCRV EAFALRGGLG
51 FARQRFVSXA DVDVAVAVGV FNQVVLMLVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGGGDD GFFXGVGVVH AAVLRTGVV ALFVEAGRIN DAEEILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVDAL E
201 GFQAPEAAXG EVNGARVHDF *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

a003.seq
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA
51 CTTGGTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCACCTCGGT
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGCAGGTG CGGTCTTGGT
151 TTTGCCCGGC AGCGGTTCGT CGGCTTTGCG GATATCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG
251 AAGTTTTTCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTTG
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTTCG GCGGGGTCGG
351 TGAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC
451 TAGGCTGAGT TTGTCGGCAT CGTAGGTCAC TTGACGGTT TCGGCGTGCG
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGG
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGAAATA
601 GGCTTCCAAG CCCAGAAGC AGCCGCCGGC GAGGTAGATG GTGCGCGTGT
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

a003.pep
1 MVVFVAEGIF GRAVLGNLVL LFGQGAFFFG VTRFFIRCRV EAFALRCGLG
51 FARQRFVGFA DIDVAVAVGV FNQVVLMLVFL GIVEVFQRLV FNNEGQLVFL
101 LLAFEGGGDD GFFGGGVVH AAVLRTGVV ALFVEAGRIN DAEEILQDVV
151 *AEFVGIVGH FDGFGVARMA VGHVFIARIF RVAVGVAGYR VNHAVDAL E
201 GFQAPEAAAG EVDGARVHDF *

m003/a003 95.9% identity over a 220 aa overlap

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXLLFGQGAFFFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
a003	MVVFVAEGIFGRAVLGNLVLFLFGQGAFFFGVTRFFIRCRVEAFALRCGLGFARQRFVGFA					
	10	20	30	40	50	60

	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGXGDDGFFXGVGVVH					
a003	DIDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGGDDGFFGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
a003	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDLEIGFQAPEAAAXGEVNGARVHDFX					
a003	RVAVGVAGYRVNHAVDLEIGFQAPEAAAGEVDGARVHDFX					
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVFVFAEGIFGRAVLGNLXLLFGQGAFFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
g003	MVFVFAEGVFGRAVLGHLVLLFGQGAFFGVTRFFIRCRVEAFALRCGFGFARQRFVGFA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGXGDDGFFXGVGVVH					
g003	DVDVAVAVGVFNQVVLVFLGVVEVFQRFVFNNEGQLVFLLLAFEGGDDGFFGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEEILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
g003	AAAVLRAGVVTLFVEAGRINDAEIILQDVVQAEFVGIVGHFDGLGMTRMAVGHFFV-RVF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDLEIGFQAPEAAAXGEVNGARVHDFX					
g003	RVAVGVGTGYRVNHAVDLEIGFQAPKAAAGEVNGARVHDC					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

```

1  ATGgtagAAC GGCATATCCA GCATTTCGGG AACGGTCATC TTCATTGAT
51  GCGCCCATGC CAACAagtga gccAAAtgtT CGGCGGCAGG GCCTacgatT
101 TCCGCGCCGA TAAagcggcc gGTGgctTTT tcgGCataca ggcgcaTatg
151 gCCTTTGTTT ACCAgcatca cgcggtcgcg accttgaTTT TTGAACGATA
201 CTTCGCCgaT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTCAAAC CGACAAAGCC GATTTCGgga ctggttaaACA CCACGCCAAT
301 GGTgctgctgg cGCAAAACCGC TGCCGATATt cgGtagcgg ccccgcggtta
351 ttgccccggca atcttaacctt ggctcgcgggc ttcatGCAGC AGGGGCagtt
401 ggttgacgc gtcgccccgca ataAAGATAT GCGGAATgct ggtCTGCATg
451 gtCAGCGGAT CGGCAACGGG tacgccgcgc gcgtctttgT CGATATTGAT
501 GTTTTCCAAA CCGATATtgT CAACGTTTCGG ACGGCgACCT ACGGCTGCCA

```

```

551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTTG ACCTCGGTTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTCGCCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCCG ATGATTCCGC CCAAACCGAA AATTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

g004.pep

```

1 MVERHIQHLR NGHLLMRPC QQVSQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVYQHHAHA TLIFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAN
101 GAAAQTAADI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTFR ASLSILMFSK PILSTFGRRP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMPF MIPKPKIST
251 FTFKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

m004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTTCAGAC CGACAAAGCC GATTTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGCAATC TTGCCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTTAG CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTTCGGAAT GCCGCCGATG ATTCGCCCA AACCAGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

m004.pep

```

1 MVERHIQHLR NGHLLMCPs QQVRQMFGR AYDFRADKAA GGFFGIQAHM
51 AFVHQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHHAD
101 GAAPQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPA KICGILVCMV
151 SGSATGTFR SFSILIFSKP ILSTFGRRPT AASIYSATN PFSPPSCSQWT
201 STLPSASSLT SVLASRCSFN SSPNTAFASS ETTGSEMPFM IPEKPKISTF
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

a004.seq

```

1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
51 GTGCCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCCGG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGG CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGCAATC TTGCCTTGGT CGGCGGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCCCGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGTT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCGTC GAGTTTGACC TCGGTTTTAG CATCCAAATG
651 CAGTTTCAAT TCTTCACCGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTTCGGAAT GCCGCCGATG ATGCCACCA AACCAGAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

```
a004.pep
  1 MVERHIQHLR NGHLLHMCPS QQVRQMFGR TYDFCADEAA GGFFGIQAHM
 51 AFVYQHAAA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGEHYAD
101 GAAAQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPAI KICGILVCIV
151 SGSATGTPRA SFSILMFSKP ILSTFGRRPT AASIYSATNT PFSPPSCSQWT
201 STLPSASSLA SVLASKCSFN SSPNTAFASS ETTGSEMPPM MPPKPKISTF
251 TPKRCNA*
```

m004/a004 94.9% identity over a 257 aa overlap

```

      10      20      30      40      50      60
m004.pep MVERHIQHLRNGHLLHMCPSQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
a004      MVERHIQHLRNGHLLHMCPSQQVRQMFGRRTYDFCADEAAGGFFGIQAHMAFVYQHAAA
      10      20      30      40      50      60

      70      80      90     100     110     120
m004.pep ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI
a004      ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGEHYADGAAAQTAADIRVAAALSPAI
      70      80      90     100     110     120

      130     140     150     160     170     180
m004.pep LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTTPRASFSILIFSKPILSTFGRRPT
a004      LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTTPRASFSILMFSKPILSTFGRRPT
      130     140     150     160     170     180

      190     200     210     220     230     240
m004.pep AASIYSATNTPFSPSCSQWTSTLPSASSLTVLASRCSFNSSPNTAFASSETTGSEMPPM
a004      AASIYSATNTPFSPSCSQWTSTLPSASSLASVLASKCSFNSSPNTAFASSETTGSEMPPM
      190     200     210     220     230     240

      250
m004.pep IPPKPKISTFTPKRCNAX
a004      :|||||
MPPKPKISTFTPKRCNAX
      250
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

m004/g004

```

      10      20      30      40      50      60
m004.pep MVERHIQHLRNGHLLHMCPSQQVRQMFGRAYDFRADKAAGGFFGIQAHMAFVHQHHAAA
g004      MVERHIQHLRNGHLLHMRPCQQVSMFGGRAYDFRADKAAGGFFGIQAHMAFVYQHAAA
      10      20      30      40      50      60

      70      80      90     100     110     119
m004.pep ALVFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA
g004      :||:|||||
TLIFERYFADDKFVGLVLRGNLRFQTDKADLRTGKHHANGAAAQTAADIRVAAPRYCPA
      70      80      90     100     110     120

      120     130     140     150     160     170     179
m004.pep ILPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTTPRASFSILIFSKPILSTFGRRP
```

```

|||||
g004      ILPWSAASCSRGSWLDASPAIKICGMLVCMVSGSATGTTPRASLSILMFSPILSTFGRRP
           130      140      150      160      170      180

180      190      200      210      220      230      239
m004.pep  TAASIYSATNTFFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
           |||||
g004      TAANIYSATNTFFSPSCSQWTSTLPSASSLTSVLASRCSFNSSPNTAFASSETTGSEMP
           190      200      210      220      230      240

240      250
m004.pep  MIPPKPKISTFTPKRCNAX
           |||||
g004      MIPPKPKISTFTPKRCNA
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 19>:

```

g005.seq
1  ATGGGGATGG ACAATATTGA TATGTTTCATG CCTGAACAAG AGGAAATCCA
51  ATCAATGTGG AAAGAAATTT TACTGAATTA CGGTATTTTC CTGCTCGAAC
101 TGCTTACCGT GTTCGGCGCA ATTGCGCTGA TTGTGTTGGC TATCGTACAG
151 AGTAAGAAAC AGTCGGAAAG CGGCAGTGTC GACTGACAG ATTTTTCGGA
201 AAATTATAAA AAACAGCGGC AATCGTTGA AACATTCTTT TTAAGCGAGG
251 AAGAGACAAA ACATCAGGAA AAAAAAGAAA AGAAAAAGGA AAAGGCGGAA
301 GCCAAAGCAG AGAAAAAGCG TTTGAAGGAG GCGGGGAGA AATCTGCCGA
351 AACGCAAAAA TCCCGCCTTT TTGTGTTGGA TTTTGACGGC GATTTGTATG
401 CACACGCCGT AGAATCCTTG CGTCATGAGA TTACGGCGGT GCTTTTGATT
451 GCCAAGCCTG AAGATGAGGT TCTGCTCAGA TTGGAAGTC CGGGCGGCGT
501 GGTTACGGT TACGGTTTGG CGGCTTCGCA GCTTAGGCGT TTGCGCGAAC
551 GCAATATTCC GCTGAcggtc gccgTCGATA AGGTCGCGGC AAGCGcggc
601 tatatgatgg cgtgtgtgGC GGATAAAATT GTTCCGctc cgtttgcggt
651 catcggttcg gtgggtgtgg tgGcggaagt gcCGAATATC CaccgCctGT
701 TGAAAAACA TGATATTGAT GTGGATGTGA TGACGGCGGG CGAATTTAAG
751 CGCACGGTTA CTTTTATGGG TGAAATACG GAAAAGGGCA AACAGAAATT
801 CCGCAGGAA CTGGAGGAAA CGCATCAGTT GTTCAAGCAG TTTGTCAGTG
851 AAAACCGCCC CGGGTTGGAT ATTGAAAAAA TAGCGACGGG CGAGCATTGG
901 TTCGGCCGGC AGGCGTTGGC GTTGAAGTTG ATTGACGAGA TTTCGACCAG
951 TGATGATTG TTGTTGAAAG CGTTTGAAAA CAAACAGGtt aTCGAAGTGA
1001 AATATCAGGA GAAGCGAAGC CTGATCCAGC GCATTGTTTT GCAGGCGGAA
1051 GCTTCCGTTG AAAAGTTGTT TGCCAAACTT GTCAACCGGC GAGCGGATGT
1101 GATGTAG

```

This corresponds to the amino acid sequence <SEQ ID 20; ORF 005.ng>:

```

g005.pep
1  MGMDNIDFM PEQEEIQSMW KEILLNYGIF LLELLTVFGA IALIVLAIVQ
51  SKKQSESGSV VLTDSENYK KQRQSFETFF LSEEETKHQE KKEKKKEKAE
101  AKAEKKRLKE GGEKSAETQK SRLFVLDFDG DLYAHAVESL RHEITAVLLI
151  AKPEDEVLLR LSPGGVVHG YGLAASQLRR LRERNIPLTV AVDKVAASGG
201  YMMACVADKI VSAPFAVIGS VGVVAEVPNI HRLLKKHDID VDVMTAGEFK
251  RTVTFMGENT EKGKQKFRQE LEETHQLFKQ FVSENRPGLD IEKIATGEHW
301  FGRQALALNL IDEISTDDL LLKAFENKQV IEVKYQEKRS LIQRIGLQAE
351  ASVEKLFACL VNRRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 21>:

```

m005.seq
1  ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51  GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101  CCGTGTTCCG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151  AAACAGTCGG AWAGCGGCAG TGTCGTACTG ACGGATTTTT CGGAAAATTA
201  TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251  CACAACATCA GGAAAAAGAG GAAAAGAAA AGGAAAAGGC GGAAGCCAAA

```

```

301 GCAGAGAAAA A.CGTTTGAA GGAGGGTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATGCTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGGTGGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGG GGCAACAGA AATCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTG AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTGTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

m005.pep

```

1 MDNIDMFPE QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQXSGSVVL TDFSENYKKQ RQSFEAFFLS GEEAQHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFVLXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIGLQAEAS
351 VEKLFKILVN RRADVM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

a005.seq

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAAGTGTCTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AAAGCGGCAG TGTCGTACTG ACGGATTTT CGGAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAACATCA GGAAGAAAGAG GAAAGAAAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGGTGGG GAGAAATCTT CCGAAACGCA
351 AAAATCCCGC CTTTTGTGT TGGATTTGA CGGCGATTG TATGCACACG
401 CCGTAGAATC CTTGCGTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCTGCT TAGATTGGAA AGTCCGGGCG GCGTGGTTCA
501 CGGTACGGT TTGGCGGCTT CGCAGCTTAG GCGTTTTCGC GAACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTTCC GCTCCGTTT CGATTGTCGG
651 TTCGGTGGGT GTTGTAGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGGAAGG GGCAACAGA AATCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTG AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTT AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAAAGT TGTGTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

a005.pep

```

1 MDNIDMFPE QEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSESGSVVL TDFSENYKKQ RQSFEAFFLS GEEAKHQEKE EKKKEKAEAK
101 AEKKRLKEGG EKSSQTQKSR LFVLDFDGL YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRRLR ERNIPLTAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```

301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEQSLI QRIGLQAEAS
 351 VEKLFKLVN RRADVM*

m005/a005 79.2% identity over a 366 aa overlap

m005.pep	MDNIDMFMEQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSVVL
a005	MDNIDMFMEQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESXSGSVVL
m005.pep	TDFSENYKKQRQSFEAFFLSGEEAQHQEKEKKKEKAEAKAEKKRLKEGGEKSAETXKSR
a005	TDFSENYKKQRQSFEAFFLSGEEAKHQEKEKKKEKAEAKAEKKRLKEGGEKSSSETQKSR
m005.pep	LFVLXX
a005	LFVLDFDGLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPGGVVHGYGLAASQLRRLR
m005.pep	XXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSGVVAEVPNIHRLKKHDIDVD
a005	ERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAIVGSGVVAEVPNIHRLKKHDIDVD
m005.pep	VMTAGEFKRTVTFMGENTKQKQFRQLEETHQLFKQFVSENRPQLDIEEVATGEHWFG
a005	VMTAGEFKRTVTFMGENTKQKQFRQLEETHQLFKQFVSENRPQLDIEEVATGEHWFG
m005.pep	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEQSLIQRIGLQAEASVEKLFKLVN
a005	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEQSLIQRIGLQAEASVEKLFKLVN
m005.pep	RRADVMX
a005	RRADVMX

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

m005.pep	MDNIDMFMEQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSXSGSV
g005	MGMDNIDMFMEQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESXSGSV
m005.pep	VLTDFSENYKKQRQSFEAFFLSGEEAQHQEKEKKKEKAEAKAEKKRLKEGGEKSAETXK
g005	VLTDFSENYKKQRQSFETFFLSEETKHQEKKEKKKEKAEAKAEKKRLKEGGEKSAETQK

	120	130	140	150	160	170
m005.pep	SRLFVLXX					
			:			
g005	SRLFVLDFDGLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPPGVVHGYGLAASQLRR					
		130	140	150	160	170 180
	180	190	200	210	220	230
m005.pep	XXXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDID					
	:					
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
		190	200	210	220	230 240
	240	250	260	270	280	290
m005.pep	VDVMTAGEFKRTVTFMGENTEKQKQFRQLEETHQLFKQFVSENRPQLDIEEVATGEHW					
g005	VDVMTAGEFKRTVTFMGENTEKQKQFRQLEETHQLFKQFVSENRPGLDIEKIATGEHW					
		250	260	270	280	290 300
	300	310	320	330	340	350
m005.pep	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFACL					
g005	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKRSLIQRIQLQAEASVEKLFACL					
		310	320	330	340	350 360
	360					
m005.pep	VNRRADVMX					
g005	VNRRADVMX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

g006.seq

1	ATGCTGCTGG	TGCTggaatt	ttggttCGGc	gtGtCGGCGG	TGGGCatact
51	tgCGTTGTTT	TTATGGCttt	TGCCACGTTT	TGCCGCCATC	AGCGAAAACC
101	TGTATTTC	CCTGAACAAC	AGCTTGGAAC	gcgACAACCA	CTTTATCCGA
151	AAAGGCGACG	AGCGGCAGCT	GTACCGCCAT	TACGGACTGG	TTTCGCGCCT
201	GCGTGTGCTG	ATTTCACAAC	GCGAAGCCTT	CGGCTATCTC	TGCGTCGGCG
251	CGGCGATGGG	TATTTTGTTT	GGCTTTGCTT	TTGTGATGAT	GACGCTCAAA
301	GGCTACGGCA	GCGCGGGGCA	TATTTATTCG	GTCGGCACTT	ATCTGTGGAT
351	GTTTGCCATG	AGTTTGACG	ATGTGCCGCG	ATTGGTCGAA	CAATATCCA
401	ATTTGAAAGA	CATCGGACAA	CGGATAGAGT	GGTCGGAACG	GAACATCAAA
451	GCCGGAATT	GA			

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

g006.pep

1	MLLVLEFWFG	VSAVGILALF	LWLLPRFAAI	SENLYFRLNN	SLERDNHFIR
51	KGDERQLYRH	YGLVSRRLVL	ISNREAFGYL	CVGAAMGILF	GFAFVMMTLK
101	GYGSAGHIYS	VGTYLWMFAM	SLDDVPRLVE	QYSNLKDIGO	RIEWSERNIK
151	AGT*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

m006.seq

1	ATGCTGCTGG	TGCTGGAATT	TTGGGTCGGC	GTGTCGGCGG	TGGGCATACT
51	TGCGTTGTTT	TTATGGCTTT	TGCCACGTTT	TGCCGCCATC	AGCGAAAACC
101	TGTATTTC	CCTGAACAAC	AGCTTGGAAC	GCGACAACCA	CTTTATCCGA
151	AAAGGCGACC	GGCGGCAGCT	GTACCGCCAT	TACGGACTGC	TTGCGCGCCT
201	GCGTGTGCTG	ATTTCACAAC	GCGAAGCCTT	CGGCTATCTC	TGCGTCGGCA
251	CGGCGATGGG	TATTTTGTTT	GGCTTTGCTT	TTGTGATGAT	GACGCTCAAA
301	GGCTACAGCA	GCGCGGGGCA	TGTCTATTTC	GTCGGCACTT	ATCTGTGGAT

351 GTTTGCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
 401 ATTTGAAAGA CATCGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
 451 GCCGGAACCTGA

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

m006.pep
 1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
 51 KGDRRQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
 101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSNLKDIGQ RIEWSERNIK
 151 AGT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

a006.seq
 1 ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT
 51 TCGGTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC
 101 TGTATTCCG CCTGAAGAAC AGCTTGGAAC GCGACAACCA CTTTATCCGA
 151 AAAGGCGACG AGCGGCAGCT GGACCGCCAT TACGGAAGTC TTGCGCGCCT
 201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGCTCGGCA
 251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
 301 GGCTACAGCA GCGCGGGGCA TGTCTATTCG GTCGGCACTT ATCTGTGGAT
 351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA
 401 ATTTGAAAGA CATCGACAA CGGATAGAGT GGTGGAACG GAACATCAAA
 451 GCCGGAACCT GA

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

a006.pep
 1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR
 51 KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK
 101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSNLKDIGQ RIEWSKRNIK
 151 AGT*

m006/a006 96.7% identity over a 153 aa overlap

m006.pep	10	20	30	40	50	60
	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDRRQLYRH					
a006	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLKNSLERDNHFIRKGDERQLDRH					
	10	20	30	40	50	60
m006.pep	70	80	90	100	110	120
	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAM					
a006	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAI					
	70	80	90	100	110	120
m006.pep	130	140	150			
	SLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSNLKDIGQRIEWSKRNIKAGTX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

m006/g006

m006.pep	10	20	30	40	50	60
	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIRKGDRRQLYRH					

g006-i.seq

g006-1.pep

m006-1.seq

1	ATGTGGA AAA	TGTTGAAACA	CATAGCCCAA	ACCCACC GCA	AGCGATTGAT
51	TGGCACATT	TCCCTGGTCG	GACTGGA AAA	CCTTTTGATG	CTGGTGTATC
101	CGGTGTTTG	CGCGCGGGCG	ATCAATGCCG	TGATTGCGGG	GGAGGTGTGG
151	CAGGCGTTG	TGTACGCTTT	GGTGTGCTT	TTGATGTGGC	TGGTGGGTGG
201	GGTGCGGCG	ATTGCCGATA	CGCGCACGTT	TACGCGGAT	TATACCGAAA
251	TCGCCGTGCC	GGTCGTGTTG	GAACAGCGGC	AGCGACAAGT	CCCGCATTTC
301	CGCGTAACT	CGCGGGTGTG	CTGTCGCGT	GAGTTTGTCA	GCTTTTTTGA
351	AGAACACCTG	CCGATTGCCG	CGACATCGT	CGTATCCATA	TTCCGCGCGT
401	GCATCATGCT	GCTGGTGCTG	GAATTTTGGG	TCGGCGTGTG	GGCGGTGGGC
451	ATACTTGCGT	TGTTTTTATG	GCTTTTGCCA	CGTTTTTGCC	CCATCAGCGA
501	AAACCTGTAT	TTCCGCTCGA	ACAAAGTCT	GGAACGGCAC	AACCACTTTA
551	TCGGA AAAAG	CGACCGGCGG	CAGCTGTACT	GCCATTACGG	ACTGCTTTGG
601	CGCCTGCGTG	TGCTGATTTC	CAACCGCGAA	GCCTTCGGCT	ATCTCTGCGT

```

651 CGGCACGGCG ATGGGTATTT TGTCGGCTT TGCTTTGTG ATGATGACGC
701 TCAAAGGCTA CAGCAGCGCG GGGCATGTCT ATTCGGTCGG CACTTATCTG
751 TGGATGTTTG CCATGAGTTT GGACGACGTG CCGCGATTGG TCGAACAATA
801 TTCCAATTTG AAAGACATCG GACAACGGAT AGAGTGGTCG GAACGGAACA
851 TCAAAGCCGG AACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 34; ORF 006-1>:

```

m006-1.pep
  1 MWKMLKHIAQ THRKLIGTF SLVGLENLLM LVYPVFGGRA INAVIAGEVW
  51 QALLYALVVL LMWLVGAVRR IADTRTFTRI YTEIAPVVVL EQRQRQVPHS
 101 AVTARVALSR EFVSFFEEHL PIAATSVVSI FGACIMLLVL EFWVGVS AVG
 151 ILALFLWLLP RFAAISENLY FRLNNSLERD NHFIRKGD RR QLYRHYGLLA
 201 RLRVLISNRE AFGYLCVGT A MGILFGFAFV MMTLKGYS SA GHVYSVGTYL
 251 WMFAMSLDDV PRLVEQYSNL KDIGQRIEWS ERNIKAGT*

```

m006-1/g006-1 95.5% identity in 288 aa overlap

m006-1.pep	10	20	30	40	50	60
	MWKMLKHIAQTHRKLIGTFSLVGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL					
g006-1	10	20	30	40	50	60
	MWKMLKHIAKTHRKLIGTFSPVGLENLLMLGYPVFGGWAINAVIAGR VQALLYALVVF					
m006-1.pep	70	80	90	100	110	120
	LMWLVGAVRR IADTRTFTRI YTEIAPVVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
g006-1	70	80	90	100	110	120
	LMWLVGAARR IADTRTFTRI YTEIAPVVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
m006-1.pep	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERD					
g006-1	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERD					
m006-1.pep	190	200	210	220	230	240
	NHFIRKGD RR QLYRHYGLLARLV LISNREAFGYLCVGTAMGILFGFAFVM T LKGYSSA					
g006-1	190	200	210	220	230	240
	NHFIRKGD RR QLYRHYGLVSR LV LISNREAFGYLCVGAAMGILFGFAFVM T LKGYGSA					
m006-1.pep	250	260	270	280	289	
	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
g006-1	250	260	270	280		
	GHIYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 35>:

```

a006-1.seq (partial)
  1 ..AGCCAAAACC ACCGCAAGCG ATTGATTGGC ACATTTTTC TGGTCGGACT
  51 GGAAAACCTT TTGATGCTGG TGTATCCGGT GTTTGGCGGC TGGGCGATTA
 101 ATGCCGTGAT TGCAGGCGAG GCGTGGCAGG CGTTGCTGTA CGCTTTGGTT
 151 GTGCTTTTGA TGTGGCTGGT CCGTGGCGCG CCGCGGATTG CCGATACGCG
 201 CACGTTTACG CGGATTTATA CCGAAATCGC CGTGCCGGTT GTGTTGGAAC
 251 AGCGGCAGCG GCAAGTCCCG CATTCGGCGG TAACTGCGCG GGTGCGCCTG
 301 TCGCGTGAGT TTGTCAGCTT TTTTGAAGAA CACCTGCCGA TTGCCGCGAC
 351 ATCCGTCGTA TCCATATTCG GCGCGTGCAT CATGCTGCTG GTGCTGGAAT
 401 TTTGGGTCGG CGTGTGCGCG GTGGGCATAC TTGCGTTGTT TTTATGGCTT
 451 TTGCCACGTT TTGCCGCCAT CAGCGAAAAC CTGTATTTC GCCTGAAGAA
 501 CAGCTTGGA A CGCGACAACC ACTTTATCCG AAAAGGCGAC GAGCGGCAGC
 551 TGGACCGCCA TTACGGACTG CTTGCGCGCC TGCGTGTGCT GATTTC AAC
 601 CGCGAAGCCT TCGGCTATCT CTGCGTCGGC ACGGCGATGG GTATTTGTT
 651 CGGCTTTGCT TTTGTGATGA TGACGCTCAA AGGCTACAGC AGCGCGGGG

```

701 ATGTCTATTC GGTCCGCACT TATCTGTGGA TGTTGCCAT AAGTTGGAC
 751 GACGTGCCGC GATTGGTCGA ACAATATTC AATTGAAAG ACATCGGACA
 801 ACGGATAGAG TGGTCGAAAC GGAACATCAA AGCCGGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

a006-1.pep (partial)
 1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL
 101 SREFVSFFEE HLPAAATSVV SIFGACIMLL VLEFWVGSA VGILALFLWL
 151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRLVISN
 201 REAFGYLCVG TAMGILFGFA FVMMLTKGYS SAGHVYSVGT YLWMFAISLD
 251 DVPRLVEQYS NLKDIGQRIE WSKRNIKAGT *

a006-1/m006-1 95.7% identity in 280 aa overlap

	10	20	30	40	50
a006-1.pep	SQNHRKRLIGTFFLVGLENLMLVYPVFGGWAINAVIAGQAWQALLYALVVL				
m006-1	MWKMLKHIAQTHRKRLLIGTFFSLVGLENLMLVYPVFGGRAINAVIAGEVWQALLYALVVL				
	10	20	30	40	50
	60	70	80	90	100
a006-1.pep	LMWLVGAAARRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
m006-1	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVP HSAVTARVALSREFVSFFEEHL				
	70	80	90	100	110
	120	130	140	150	160
a006-1.pep	PIAATSVVSIFGACIMLLVLEFWVGSAVGILALFLWLLPRFAAISENLYFRLKNSLERD				
m006-1	PIAATSVVSIFGACIMLLVLEFWVGSAVGILALFLWLLPRFAAISENLYFRLNNSLERD				
	130	140	150	160	170
	180	190	200	210	220
a006-1.pep	NHFIRKGDERRQLDRHYGLLARLRLVISNREAFGYLCVGTAMGILFGFAFVMMLTKGYSSA				
m006-1	NHFIRKGDERRQLDRHYGLLARLRLVISNREAFGYLCVGTAMGILFGFAFVMMLTKGYSSA				
	190	200	210	220	230
	240	250	260	270	280
a006-1.pep	GHVYSVGTLYWMFAISLDDVPRLVEQYSNLKDIGQRIEWSKRNIKAGTX				
m006-1	GHVYSVGTLYWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

g007.seq
 1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTGTGCT GCCTCTGcgc
 51 CGCcGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT
 101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC
 151 ACTGCGtTTC CTccgctTTT CCggtcgGac tgtattatga acaAACCGCa
 201 cgTCctgctg cacagcatgg tcaaaggcAt cgacgggaca ttcaaagtgg
 251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgcca tcagcgATGC
 301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

g007.pep
 1 MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG
 51 TAFPPLFRSD CIMNKPVLL HSMVKGIDGT FKVERQNLRR IYARNRHQRC
 101 GHCRRRHLYH ERL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:

m007.seq

```

1 ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTC.
251 AACGGCAAAA CCTACAACGG ATTCATGCCC GCAACGCCA TCAGCGATGC
301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 40; ORF 007>:

m007.pep

```

1 MNTTRLPTAL VLGCFCAAA AADNSIMTKG QK VYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVXRQNLQR IHARNRHQRC
101 GHCRRRHLHY ERL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 41>:

a007.seq

```

1 ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTC.
251 AACGGCAAAA CCTACAACGG ATTCATGCCC GCCACTGCCA TCAGCGATGC
301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 42; ORF 007.a>:

a007.pep

```

1 MNTTRLPTAL VLGCCLAAA AADNSIMTKG QK VYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVXRQNLQR IHARHCHQRC
101 GHCRRRHLHY ERL*

```

m007/a007 97.3% identity over a 113 aa overlap

	10	20	30	40	50	60
m007.pep	MNTTRLPTALVLGCFCAAA	SAADNSIMTKGQK	VYESNCVACHGKKGEGRG	TMFPPLYRSD		
a007	MNTTRLPTALVLGCLCAA	SAADNSIMTKGQK	VYESNCVACHGKKGEGRG	TMFPPLYRSD		
	10	20	30	40	50	60
	70	80	90	100	110	
m007.pep	FIMKKPQVLLHSMVKGINGT	IKVXRQNLQRIHARNRHQRC	GHCRRRHLHYERLX			
a007	FIMKKPQVLLHSMVKGINGT	IKVXRQNLQRIHARHCHQRC	GHCRRRHLHYERLX			
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 007 shows 86.7% identity over a 113 aa overlap with a predicted ORF (ORF 007.ng) from *N. gonorrhoeae*:

m007/g007

	10	20	30	40	50	60
m007.pep	MNTTRLPTALVLGCFCAAA	SAADNSIMTKGQK	VYESNCVACHGKKGEGRG	TMFPPLYRSD		
g007	MNTTRLPTAFILCCLCAA	SAADNSIMTKGQK	VYESNCIACHGKKGEGRG	TAFPLFRSD		
	10	20	30	40	50	60
	70	80	90	100	110	
m007.pep	FIMKKPQVLLHSMVKGINGT	IKVXRQNLQRIHARNRHQRC	GHCRRRHLHYERLX			

g007 CIMNKPHVLLHSMVKGIDGTFKVERQNLRRYYARNRHQRCGHCHRRRLHYHERL
 70 80 90 100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 43>:

g007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCATCGCC TGCCACGGCA AGAAAGGGA AGGGCGCGGC
151 ACTGCGTTTC CTCCGCTTTT CCGGTCGGAC TATATTATGA ACAAACCGCA
201 CGTCCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGGC AAAAAAAC.
```

This corresponds to the amino acid sequence <SEQ ID 44; ORF 007-1.ng>:

g007-1.pep (partial)

```

1  MNTTRLPTAF ILCLCAAAS AADNSIMTKG QKYESNCIA CHGKKGEGRG
51 TAFPFLFRSD YIMNKPVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKG KKN...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 45>:

m007-1.seq

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGC AAAAAAACT
401 AA
```

This corresponds to the amino acid sequence <SEQ ID 46; ORF 007-1>

m007-1.pep

```

1  MNTTRLPTAL VLGCFAAAS AADNSIMTKG QKYESNCVA CHGKKGEGRG
51 TMFPFLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKS KKN*
```

m007-1 / g007-1 91.7% identity in 133 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFAAASAADNSIMTKGQKYESNCVACHGKKGEGRGTMFPFLYRSD					
g007-1	MNTTRLPTAFILCLCAAASAADNSIMTKGQKYESNCIACHGKKGEGRGTAFPFLFRSD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGTIKVNKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	: : : : : : : : : :					
g007-1	YIMNKPVLLHSMVKGINGTIKVNKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
	:					
g007-1	TEKDVQAKGKKN					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 47>:

a007-1.seq (partial)

```

1  ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC
51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT
101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA
```

```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAACA GGCAAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

a007-1.pep (partial)

```

1 MNTTRLPTAL VLGLCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGLCAAAS	AAADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
a007-1	MNTTRLPTALVLGLCAAAS	AAADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKGINGT	IKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV				
a007-1	FIMKKPQVLLHSMVKGINGT	IKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV				
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
a007-1	TEKDVQAKNKK					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

g008.seq

```

1 ATGAACAACA GACATTTTGC CGTCAtcgCC TTGGGCAGCA ACCTTGACAA
51 CCCCACACAA CAAATacgcg gcgcattaga cgcgctctcg tcccatcctg
101 acatccggct tgaaCaggtt tcctcactgt aTatgaccgc acctgtcgggt
151 tacgAcaaTC agcccgATTT CATCaatgcc gTCTgcaccg TTCCACCAC
201 CtTGGACGGC ATTGcccTGC TTGCCgaACT CAaccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCCGCC TTACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAATACG GAAAGGTTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGACA GGTA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

g008.pep

```

1 MNNRHFAVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51 YDNQPDFINA VCTVSTLDG IALLAELNRI EADFGRETSF RNAPRTLDD
101 IIDFDGISSD DPLRLPHPR AHERSFVIRP LAEILPDFIL KGYKVVVELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

m008.seq

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCTCAA CAGGTACGCG CCGCATTTGA CACGCTGTCG TCCCATCTGT
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATTT TGTCAATGCC GTCTGCACCG TTCCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAct CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GkATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACctTGCC

```

```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTGTTTTA GGAAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAAAT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

m008.pep

```

1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFRERSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHGKVAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 53>:

a008.seq

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATT CGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAAT CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT TCACGCGAC GACCCCGGAC TCACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CACACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTATTTTG GGAAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

a008.pep

```

1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
51 YDNQPDFVNA VCTVSTTLDG IALLAELNRI EADFRERSF RNAPRTLDLD
101 IIDFDGISSD DPRLTLPHPR AHERSFVIRP LAEILPDFIL GKHGKVAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYDNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYDNQPDFVNA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m008.pep	VCTVSTTLDGIALLAELNRIEADFRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLDGIALLAELNRIEADFRERSFRNAPRTLDLDIIDFDGISSDDPRLTLPHPR					
	70	80	90	100	110	120
	130	140	150	160		
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

m008/g008

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHPDIRLKQASSLYMTAPVGYDNQPDFVNA					
g008	MNNRHFAVIALGSNLDNPAQQIRGALDALSSHPDIRLEQVSSLYMTAPVGYDNQPDFINA					

	10	20	30	40	50	60
m008.pep	70	80	90	100	110	120
	VCTVSTTLDGIALLAELNRIEADFRGRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
g008	70	80	90	100	110	120
	VCTVSTTLDGIALLAELNRIEADFRGRERSFRNAPRTLXLDIIDFDGISSDDPRLTLPHPR					
m008.pep	130	140	150	160		
	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
g008	130	140	150	160		
	AHERSFVIRPLAEILPDFILGKYGKVVELSKRLGNQGIRLLPDRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

g009.seq

```

1  ATGCCCCGCG CTGCCGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GCGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGAAA TCAGCACACG CAGGCGCGAA ACCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTcg cGTTCCAAGC
201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AaaGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

g009.pep

```

1  MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFAVGNQHT QARNQSVMAV
51  QLPLVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

m009.seq

```

1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTA
151 CAGCTGCCGC CGGTCGCCTT TTCGGATAAA GTGGTTGTcg CGTTCGAAGC
201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A

```

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

m009.pep

```

1  MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFAVGNQHT QARKQSVMAV
51  QLPPVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

m009/g009

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
g009	MPRAAVAFAERHHHKSKAEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
m009.pep	70	80				
	VVVAFAQVVQAEIQVFADGGKTWQKPX					
g009	70	80				
	VVVAFAQVVQAEIQVFADGGKTWQKPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
1  ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
51  CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAT TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTCG CGTTCCAAGC
201 TGTCTTCAG  GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
1  MPRAAVAFAER HHHKSKEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
51  QLPLVAFSDK  VVVAFAQVLO AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKEQNTHRRADAEIAEGFVGNQHTQARKQSVMAVQLPPVAFSDK					
a009	MPRAAVAFAERHHHKSKEQNTHRRADAEIAEGFVGNQHTQARKQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFAQVQAEIQVFADGGKTWQKPX					
	:					
a009	VVVAFAQVLOAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
1  ATGGGTTTTC CTGTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTGTTC TAAAGTGTTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GCGGGTATTT CCGCTCTCTT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTTCGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTGC TATTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGCGGAG GCGGATATTC TGTGAacgc
801 cgacggcgaa cgcTTTATGG AAcgctatgc GCcgACCGta aAagaCTTGG
851 CTTCTCGCga cgtGGTTTCA CgcgcGatgG CGatggaAAT ctatgaaggt
901 cgcggctgTG GtaaaAAcaA agaCCacgtC TTACTGAAAA TCGACcAtAt
951 cggTGcAGAA AAAATTATGG AAAAAGTCCG GGCATCCGC GAGATTTCa
1001 TTCagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc ggttgTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCg aCCAATTATC ACGGTGAAGT
1101 TGTGTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTCCGTAC ACGGTGCGAA CCGTTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDRWHMY DTVKGSWDLG DQDAIEFMCR AAPEAVIELE
101 HMGMPPFDRVE SGKIYQRPFG GHAEHKGRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENGDVVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGCKNKDHF LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPPIVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

```

m010.seq (PARTIAL)
1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTTGT CTAAAGTGTT
51  CCCGACCCGT TCGCATACCG TAGCGGCGCA GGGCGGTATT TCCGCCTCTn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCGTG
151 AAAGGTTCCG ACTGGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAAA ATTTATCAGC GTCCTTTCGG CGGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAGAACGC GYCTGTGCGG TTGCCGACCG
351 TACAGGTCAT GCGATGCTGC ATACTTTGTA CCAACAAAAC GTCCGTGCCA
401 ATACGCAATT CTTGTGGAA TGGACGGCAC AAGATTTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACGCCCATG GAAATGGAAA CCGCGGAAGT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGGCGGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCGC CGATGGTTTG
601 GGTATTTGTG CGCGTGCAGG TATCCCGTTG GAAGACATGG AATTCTGGCA
651 ATTCCAGCCG ACCGGCGTGG CGGGTGCGGG CGTGTGATT ACCGAA...

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

```

m010.pep (PARTIAL)
1  ..XQLSKSGLNC AVLSKVFPTR SHTVAAQGGI SASXGNVQED RWDWHMYDTV
51  KGSDDLGDQD AIEFMCRAP EAVIELEHMG MPFDRVESGK IYQRPFGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQQN VRANTQFFVE WTAQDLIRDE
151 NGDVVGV TAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMFVQFQF TGVAGAGVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

```

a010.seq
1  ATGGGCTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTG TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTGTGCG GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTCCA
1001 TTCAAGTTCG CCGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CCGTATTCCG ACCAACTACC ATGGCGAAGT
1101 TGTGTTTCCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTGGGT
1201 ACCAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCT TTGCTGCTA

```

```

1301 ATGCCGCGA ACTGACCCGC CAACGTATCG AGCGTTTGA CAATCAAAC
1351 GATGGTAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GGCGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TCGCGACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTC AATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKV F PTRSHTVAAQ
51  GGISASLGNV QEDRW DWHMY DTVKGS DWLG DQDAIEFMCRA APEAVIELE
101 HMGMPPDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNV RANTQF FVEWTAQDLI RDENG DVVGV TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RCGCKNKD HV LLKIDHIGAE KIMEKLP GIR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWK P LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVM AIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKR VY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

                                10      20      30
m010.pep                      XQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASXGNV
                                |||||
a010      MGFPVRKFDAVIVGGGGAGLRAXLQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRW DWHMYDTVKGSDWLG DQDAIEFMCRA APEAVIELEHMGMPDRVESGKIYQRPFG
                                |||||
a010      QEDRW DWHMYDTVKGSDWLG DQDAIEFMCRA APEAVIELEHMGMPDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAEHGKRAVERXCAVADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVGV
                                |||||
a010      GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNV RANTQFFVEWTAQDLIRDENG DVVGV
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                |||||
a010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
                                |:|
a010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPT VKDLASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 010 shows 98.7% identity over a 231 aa overlap with a predicted ORF (ORF 010.ng) from *N. gonorrhoeae*:

m010.pep/g010.pep

```

                                10      20      30
m010.pep                      XQLSKSGLNCAVLKVFPTRSHTVAAQGGISASXGNV
                                |||
g010      MGFPVRKFDIVVGGGAGLRAALQLSKSGLNCAVLKVFPTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRWDMYDITVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                |||
g010      QEDRWDMYDITVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAENGKRAVERXCAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV
                                |||
g010      GHTAENGKRAVERACAVADRTGHAMLHTLYQQNVRANTQFFVEWTAQDLIRDENGDVVGV
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                |||
g010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
                                |:|
g010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

```

1   ATGGGTTTTC CTGTTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTGTGC TAAAGTGTTT CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAGAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCT TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGCGGT ACGGCGCGAG GCGGTATTTC TGTGAACGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTGGTTTCA CGCGCATGG CGATGGAAAT CTATGAAGGT
901 CGCGGCTGTG GTAAAACAAA AGACCACGTC TTAAGTAAAA TCGACCATAT
951 CCGTGAGAAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCT
1001 TTCAGTTTGC CGGTATCGAT CCGATTAAAG ACCCGATTCC GGTGTGCGCG
1051 ACTACCACT ATATGATGGG CGGCATTCCG ACCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT

```

1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep
 1 MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVFP TRSHTVAAQ
 51 GGISASLGNV QEDRDWHMY DTVKGSDDLW QDAIEFMCR AAEPAVIELE
 101 HMGMFPDRVE SGKIYQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY
 151 QQNVRAQTQF FVEWTAQDLI RDENGDVGVV TAMEMETGEV YIFHAKAVMF
 201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
 251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
 301 RCGGKKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP
 351 TTHYMMGGIP TNYHGEVVVP QGDEYEVFVK GLYAAGECAC ASVHGANRLG
 401 TNSLLDLVVF RPTPR*

g010-1 / P10444

sp|P10444|DHSA_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942
 (AE000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 191/303 (63%), Positives = 238/303 (78%)

Query: 1 MGFPVRKFDAVIVXXXXXXXXXXXXXSKGLNCVLSKVFP TRSHTVAAQGGISASLGNV 60
 M PVR+FDAV++ S+SG CA+LSKVFP TRSHTV+AQGGI+ +LGN
 Sbjct: 1 MKLPVREFDAVVIGAGGAGMRAALQISQSGQTCALLSKVFP TRSHTVSAQGGITVALGNT 60
 Query: 61 QEDRDWHMYDTVKGSDDLWQDAIEFMCR AAEPAVIELEHMGMFPDRVESGKIYQRPFG 120
 ED W+WHMYDTVKGS++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG
 Sbjct: 61 HEDNWEWHMYDTVKGS DYIGDQDAIEYMKCTGPEAILELEHMG LPPSRLDDGR IYQRPFG 120
 Query: 121 GHAEHGKRAVERACAVADRTGHAMLHTLYQQNVRAQTQFFVEWTAQDLIRDENG DVGVV 180
 G + G R A ADRTGHA+LHTLYQQN++ +T F E W A DL++++G VVG
 Sbjct: 121 GQSKNFGGEQAARTAAADRTGHALLHTLYQQNLKNHTTIFSEWYALDLVKNQDGA VVGC 180
 Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240
 TA+ +ETGEV F A+A + ATGG GRIY S+TNA++NTGDG+G+ RAG+P++DME WQ
 Sbjct: 181 TALCIETGEVVYFKARATV LATGGAGRIYQSTTNAHINTGDGVGM AIRAGVPVQDMEMWQ 240
 Query: 241 FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG 300
 FHPTG+AGAGVL+TEG RGE G LLN GERFMERYAP KDLA RDVV+R++ +EI EG
 Sbjct: 241 FHPTGIAGAGVLTEGCRGEGGYLLNKHGERFMERYAPNAKDLAGRDVVAR SIMIEIREG 300
 Query: 301 RGC 303
 RGC
 Sbjct: 301 RGC 303

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169
 Identities = 53/102 (51%), Positives = 62/102 (60%)

Query: 309 HVLLKIDHIGAEKIMEKLPGIREISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368
 H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +
 Sbjct: 310 HAKLKLDHLGKEVLESRLPGILELSRTFAHVDVPVKEPIPIPTCHYMMGGIPTKVTGQAL 369
 Query: 369 VPQGDEYEVFVKGLYAAGECACASVHGANRLGTNSLLDLVVF 410
 +V V GL+A GE AC SVHGANRLG NSLLDLVVF
 Sbjct: 370 TVNEKGEDVVVPG LFAVG E IACVSVHGANRLG GNSLLDLVVF 411

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..
 1 ATGGGTTTTC CTGTTGCGAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
 51 TGCAGGTTTA CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
 101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
 151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
 201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
 251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
 301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
 351 TCCTTTCCGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACCGG
 401 CCTGTGCGGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC

```

451 CAACAAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGTTCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAAGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCAGGG
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTGTAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CCGCGCTGCG GTAAAAACAA AGACCATGTC TTACTGAAAA TCGACCATAT
951 CCGCGCAGAA AAAATTATGG AAAAAGTGGC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCGG
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTACC ACGGCGAAGT
1101 TGTGCTTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CCGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACCAACTCCC TGTGGACTT GGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCAAGTGA GTTACCCGCG CAACGTATCG AGCGTTTGGG CAACCAAACC
1351 GATGGTGAAG ACCTTGATGC ATTGCGTCCG GAACTGCAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTGATTGAA GTGCGGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCAGCGCG TCGCAGCGCT TCAGACGACC ATCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATATCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA

```

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pap..

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVFP PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGSDDLW GDQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIIYQRPFG GHTAHEGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENGDVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RCGGKKNKDHV LKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVPV QGEDYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFTDEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLE VAKATLVSAE ARKESRGAHA SDDHPRDDE
551 NWMKHTLYHS DINTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010-1 / g010-1 99.5% identity in 410 aa overlap

```

          10      20      30      40      50      60
m010-1.pap  MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV
|||||
g010-1      MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCVLSKVFPTRSHTVAAQGGISASLGNV
          10      20      30      40      50      60

          70      80      90     100     110     120
m010-1.pap  QEDRWDWHMYDTVKGSDWLGDDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
|||||
g010-1      QEDRWDWHMYDTVKGSDWLGDDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG
          70      80      90     100     110     120

          130     140     150     160     170     180
m010-1.pap  GHTAHEGKRAVERACAVADRGTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENGDVVG
|||||
g010-1      GHTAHEGKRAVERACAVADRGTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENGDVVG
          130     140     150     160     170     180

          190     200     210     220     230     240
m010-1.pap  TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDLGICARAGIPLEDMEFWQ
|||||
g010-1      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDLGICARAGIPLEDMEFWQ

```

190

	190	200	210	220	230	240
m010-1.pep	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVSRAAMEIYEG					
g010-1	250	260	270	280	290	300
	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVSRAAMEIYEG					
m010-1.pep	310	320	330	340	350	360
	RGCGRKNKHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIFVVPPTHYMMGGIP					
g010-1	310	320	330	340	350	360
	RGCGRKNKHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIFVVPPTHYMMGGIP					
m010-1.pep	370	380	390	400	410	420
	TNYHGEVVVPQGEDYEVPVKGLYAAGECACASVHGARNLGTNSLLDLVVFKAAGDSMIK					
g010-1	370	380	390	400	410	
	TNYHGEVVVPQGEDYEVPVKGLYAAGECACASVHGARNLGTNSLLDLVVFRTPRX					
m010-1.pep	430	440	450	460	470	480
	FIKEQSDWKPLPANAGELTRQIERLDNQTGDNVDALRRELQRSVQLHAGVFRTEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1.seq..

```

1  ATGGGCTTTC CTGTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTGTTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGATATTG CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGCG GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTGTGAT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGTTTGGT GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGCGGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGATATTC TGTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAT CTACGAAGGT
901 CGCGGCTCGG GTAAAAACAA AGACCATGTC TTAGTGAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTCCG GGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGTATTCCG ACCAACTACC ATGGCGAAGT
1101 TGTGTTCTCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCCTGT GCTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCTT TTGCCTGCTA
1301 ATGCCGCGCA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GGCATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1.pep..

```

1  MGFVPRKFDA VIVGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDDHMY DTVKGSWDLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY

```

151 QQNVRANTQF FVEWTAQDLI RDENGDVVG TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RCGGKNKDHV LLKIDHIGAE KIMEKLP GIR EISIQFAGID PIKDFIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWK L PANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVQLHA GVFRTEILS KGVREVMAIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY*

m010-1 / a010-1 99.3% identity in 587 aa overlap

	10	20	30	40	50	60
a010-1.pep	MGFPVRKFD	AVIVGGG	AGLRAXL	QLSKSGL	NCVLSKV	FPTRSH
a010-1	MGFPVRKFD	AVIVGGG	AGLRAXL	QLSKSGL	NCVLSKV	FPTRSH
	70	80	90	100	110	120
a010-1.pep	QEDRW	DWHMYD	TVKGS	DWLGDQ	DAIEF	MCRAA
m010-1	QEDRW	DWHMYD	TVKGS	DWLGDQ	DAIEF	MCRAA
	130	140	150	160	170	180
a010-1.pep	GHTAE	HGKRA	VERAC	AVADRT	GHAML	HTLYQ
m010-1	GHTAE	HGKRA	VERAC	AVADRT	GHAML	HTLYQ
	190	200	210	220	230	240
a010-1.pep	TAMEM	ETGEV	YIFHA	KAVMF	FATGG	GGRIY
m010-1	TAMEM	ETGEV	YIFHA	KAVMF	FATGG	GGRIY
	250	260	270	280	290	300
a010-1.pep	FHPTG	VAGAG	VLITE	GVRGE	GGILL	NADGE
m010-1	FHPTG	VAGAG	VLITE	GVRGE	GGILL	NADGE
	310	320	330	340	350	360
a010-1.pep	RCGGK	NKDHV	LLKID	HIGAE	KIMEK	LPGIR
m010-1	RCGGK	NKDHV	LLKID	HIGAE	KIMEK	LPGIR
	370	380	390	400	410	420
a010-1.pep	TNYHG	EVVVP	QGDEY	EVVK	GLYAA	GECAC
m010-1	TNYHG	EVVVP	QGDEY	EVVK	GLYAA	GECAC
	430	440	450	460	470	480
a010-1.pep	FIKEQ	SDWK	LPAN	AGELT	RQRIE	RDNQT
m010-1	FIKEQ	SDWK	LPAN	AGELT	RQRIE	RDNQT
	490	500	510	520	530	540
a010-1.pep	KGVRE	VMAIA	ERVKR	TEIKD	KSKVW	NTARI
m010-1	KGVRE	VMAIA	ERVKR	TEIKD	KSKVW	NTARI
	550	560	570	580		
a010-1.pep	SDDHP	ERDDE	NWMKH	TLYHS	DANTL	SYKPV

m010-1 SDDHPERDDENWMKHTLYHSDINTLSYKPVHTKPLSVEYIKPAKRVYX
550 560 570 580

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 73>:

g011.seq
1 ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAC CCGCCTTACC GAAGATATGA AAACCGCGAT GCGCGCCAAA
151 GATCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAATGCCG CCGTCAAACA
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGCGCGGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT
351 GCTGCACCGC TACCTGCCGC AAATGCTCTC CGCCGGCGAA ATCCGCACCG
401 CCGTCGAAGC AGCCGTGTCG GAAACCGCGC CGGCAGGTAT GCGCGATATG
451 GGCAAAGTGA TGGTCGTATT GAAAaccGC CTCGCCGCA AAGccgATAT
501 GGGCGAAGTC AACAAATCT TGAaaaaccGt aCTGACCGCC tga

This corresponds to the amino acid sequence <SEQ ID 74; ORF 011.ng>:

g011.pep
1 MKTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDGAKIYT
101 EAGRQDLADK ENAEIDVLHR YLPQMLSAGE IRTAVEAAVA ETGAAGMADM
151 GKVMVVLKTR LAGKADMGVEV NKILKTVLTA *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 75>:

m011.seq (partial)
1 ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTTG CTTTTCAGAC
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA
101 GCCTGAAAAT CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCCG CCGTCAAACA
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGAGGT
351 ACTGCACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG
401 AGGTCGAAGC TGCCGTGTCG GAAACCGCGC CGGCAGGTAT GCGCGATATG
451 GGTAAAGTCA TGGGGCTGCT GAAAACCCGC CTCGCAGGTA AAGCCGA...

This corresponds to the amino acid sequence <SEQ ID 76; ORF 011>:

m011.pep (partial)
1 MRTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKIRLT EDMKTAMRAK
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDSAKIYT
101 EAGRQDLADK ENAEIEVLHR YLPQMLSAGE IRTEVEAAVA ETGAAGMADM
151 GKVMGLLKTR LAGKA.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 011 shows 95.8% identity over a 165 aa overlap with a predicted ORF (ORF 011.ng) from *N. gonorrhoeae*:

m011/g011

	10	20	30	40	50	60
m011.pep	MRTHRKTCSAVCF	AFQTASKPAVS	IRHPSE	DIMSLKIRLT	EDMKTAMRAK	DQVSLGTIRL
	:	:	:	:	:	:
g011	MKTHRKTCSAVCF	AFQTASKPAVS	IRHPSE	DIMSLKTRLT	EDMKTAMRAK	DQVSLGTIRL
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m011.pep	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDSAKIY	TEAGRQDLADK	ENAEIEVLHR
	:	:	:	:	:	:
g011	INAAVKQFEV	DERTEADDAK	ITAILTKMVK	QRKDGAKIY	TEAGRQDLADK	ENAEIDVLHR
	:	:	:	:	:	:

193

	70	80	90	100	110	120
	130	140	150	160		
m011.pep	YLPQMLSAGEIRTEVEAAVAETGAAGMADMGKVMGLLKTRLAGKA					
					:	
g011	YLPQMLSAGEIRTAVEAAVAETGAAGMADMGKVMVVLKTRLAGKADMGVEVNKILKTVLTA					
	130	140	150	160	170	180
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

g012.seq

```

1  ATGCTCGCCC GTCGCTATTT TTTCAATATC CAACCCGGGG CGGTTTTCAC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGCCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACa
201 gGcggTGGAT ATTCGgcact tccgCcacca caccaccga accgatgacc
251 gcaaacggaG CGGAACAAT TTTATCCGcC acacacgcca tcatatagcc
301 gcCGCTTGCC GCGACCTTAT CGAcggcgac ggTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CGCCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATTT TTGCGTTTCG
551 GCAGATTCTT CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CTTTTTTTTC CTGATGTTT GTCTCTTCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

g012.pep

```

1  MLARRYFNI QPGAVFTDKL LEQLMRFLQF LPEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRFRHHHTHR TDDRKRSGNN FIRHTRHHIA
101 AACRDLIDGD QORNIAFAQT PKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPAL LQTLFLCFGF
201 RLFLFLFFFF LMFLFLA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

m012.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCGGTACT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCGCTCGCn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
351 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
401 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
451 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
501 nnnnnnnnnn nnnnnnnnnC AACACAAAAA GGCGTGATTT nTGCCTTTCG
551 GCAGATTCTT CCCCACCCTC CTTCAAACGT TTTTCcTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTGTG GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

m012.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRHHHTR TDNRKRSGSN FIRHTRHHIT
101 AARXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XXXXQHKKA*F XRFGRFLPTL LQTFFLCFGF
201 RLFLFLFLFF LMLCLFPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAACTG  CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTGCGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGGTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGTCGCC  GCCACCTTAT CGACGGCGAC GGTACGCGGA ATATTGCGTT
351 CCGCAAACG  CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TCGCGTTTCG
551 GAAGATTCT  CCCACCCCTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQA VD IRYFRYNTHR TDNRKRSGNN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKRRNLMTQ  GFYGVCIQIA VKIQHKKAGF LRFRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*
```

m012/a012 64.2% identity over a 218 aa overlap

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
a012	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m012.pep	NIMFFQQAVIDIRYFRHHTRTDNRKRSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXXXX					
a012	NIMFFQQAVIDIRYFRYNTHRTDNRKRSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m012.pep	XXQHKKAXF					
a012	PKLRSRQTVTVNHAARTFQSKQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
m012.pep	XRFRFLPTLLQTLFLCFGRFLFLFLFLFFLMLCLFPAX					
a012	LRFRFLPTLLQTLFLCFGRFLFLFLFLFFLMLCLFPAX					
	190	200	210			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

	10	20	30	40	50	60
m012.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					

		10	20	30	40	50	60
m012.pep		70	80	90	100	110	120
	NIMFFQQA	VDIRYFRHHTHR	TDNRKRS	GSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXXXXX			
g012	:	:	:	:		:	:
	NIMFFQQA	VDIRHFRHHTHR	TDDRKRSGNNFIRHTRHHIAAACRDLIDGGGQRNIAFAQT				
		70	80	90	100	110	120
m012.pep		130	140	150	160	170	180
	XX	XHKKAXF					
g012	: :	:	:	:	:		
	PKLRSRQTVTVNHAART	FQSEQNLIFRLGNQKHRRNLMTQGFGVCIQI	AVKIQHKKAGF				
		130	140	150	160	170	180
m012.pep		190	200	210	219		
	XRFGRLFPTLLQTFLCFGRFLFLFLFLFFLMLCLFPAX						
g012	:	:	:	:			
	LRFGRFLPALQLFLCFGRFLFLFLFFFLLMFCLFLAX						
		190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

```
m012-1.seq
1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CTCCGAGTTC CTGTCGGAAT
101 TTCTGTTTGC CTTTTCCTGT ATTTTCACCC ATAAAAGTAA CCGTGC GCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTTC AACA
201 GGCGGTGGAT ATTCCGTAAT TCCGCCACCA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCACT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CGCGCAAACG CyTAAGCTGC GAAGCCGCCA AACCGTAAAC GTGAACCACG
401 CCGCCCGGAG TTTCCAATCT GAGCAGAACC TCATCTTCAG CGTTGGCAAT
451 CAAAGACACC GCTCGTAATC CATGACGCAA GGATTTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT T TGC GTTTCG
551 GCAGATTTCT CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

```
m012-1.pep
1  MLARCHFLNI  QLRVLADKL  LEQLMRFLQF  LSEFLFALFR  IFTHSNRL
51  KFARRHHIHI  NIMFFQAVD  IRYFRHHTHR  TDNRKRSGSN  FIRHRRHIT
101 AARRHLIDGD  GQRNIAFAQT  XKLRSQTVT  VNHAARTFQS  EQNLIFRLGN
151 QKHRRLNMTQ  GFYGVCIQIA  VKIQHKKAGF  LRFGFRFLPTL  LQTLFLCFGF
201 RLFLFLFLFF  LMFCLFPA*
```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHF	LNIQLR	AVLADK	LEQLMR	FLQFLS	EF
g012	MLARRY	FFNIQ	PGAVFT	DKLLEQ	LMRFLQ	FLPEFL
	10	20	30	40	50	60
	70	80	90	100	110	120
m012-1.pep	NIMFFQ	QAVDIR	YFRHHT	HRTHRT	DNKRKS	GSNFI
g012	NIMFFQ	QAVDIR	YFRHHT	HRTHRT	DDKRKS	GSNNFI
	70	80	90	100	110	120
	130	140	150	160	170	180
m012-1.pep	XKLRSR	QTVT	VNHAAR	TFSQSE	QNLI	FRLGNQ
g012	PKLRSR	QTVT	VNHAAR	TFSQSE	QNLI	FRLGNQ

196

	130	140	150	160	170	180
	190	200	210	219		
m012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFFLMFCLFPAX					
	: : : :					
g012	LRFGRLPALQLTLFLCFGRFLFLFLFFLMFCLFLAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCCGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGTGGAT ATTGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAACAAT TTTATCCGCC ACACAGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGCGGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TCGGTTTCG
551 GAAGATTTCT CCCCACCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTTC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKRSNGN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60
a012-1.pep	MLARCHFLNIQLRAVLADKLL	EQLMRFLQFLSEFLFALFR	IFTHKSNRALKFARRHHIHI			
m012-1	MLARCHFLNIQLRAVLADKLL	EQLMRFLQFLSEFLFALFR	IFTHKSNRALKFARRHHIHI			
	10	20	30	40	50	60
	70	80	90	100	110	120
a012-1.pep	NIMFFQQAVDIRYFRYNTHR	TDNRKRSNGNFIRHTRHHIT	TARRHLIDGDGQRNIAFAQT			
m012-1	NIMFFQQAVDIRYFRHHTHR	TDNRKRSNGNFIRHTRHHIT	AARRHLIDGDGQRNIAFAQT			
	70	80	90	100	110	120
	130	140	150	160	170	180
a012-1.pep	PKLRSRQTVT VNHAARTFQSK	QNLIFRLGNQKHRRNLMTQ	GFYGVCIQIAVKIQHKKAGF			
m012-1	XKLRSRQTVT VNHAARTFQSE	QNLIFRLGNQKHRRNLMTQ	GFYGVCIQIAVKIQHKKAGF			
	130	140	150	160	170	180
	190	200	210	219		
a012-1.pep	LRFGRLPTLLQTLFLCFGRFL	FLFLFFLMFCLFPAX				
m012-1	LRFGRLPTLLQTLFLCFGRFL	FLFLFFLMFCLFPAX				
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1  aTgcctttga ccatgctgtg cagcaGGAcg tGCGGTTtgt tcataatata
51  gtCcgaccGG AAAagcggAG GAAaCGCAGT GCCGCGCCCT TCCCTTTTCT
101 TGCCGTGGCA GGCGATGCag tTgGATTCGT AACTTTTTTG CCCTTTtGtc

```

```

151 atgatGCTgt tgtcggCGGC AGAAGCgGCG GcgCAGAGGC AGCACAAGAT
201 GAAGGCGGTC GGCAGTCGGG TTGTGTtcat tGgcgTTTCC cctaattgtt
251 tgaaaccttg ttttttgatt Ttgctttac ggggtgaaaa gtttttTtgg
301 cccaaatccg gaatttag

```

This corresponds to the amino acid sequence <SEQ ID 88; ORF 013.ng>

g013.pep

```

1 MPLTMLCSRT CGLFIIQSDR KSGGNAVPRP SPFLPWQAMQ LDSYTFCPFV
51 MMLLSAAEAA AQRQHMKAV GSRVVFIGVS PNVLKPCFLI LPLRGEKFFV
101 PKSGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 89>:

m013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TGCGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCACGCAG TTGGATTTCG ACACTTTTTG CCCTTTTGTC
151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTCAT TGGTGTTCCT TTCATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT TTTGCCGAAT
301 CAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 90; ORF 013>:

m013.pep

```

1 MPLTMLCSST CGFFMMKSER XSGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQKQPKTRAV GSRVVFIGVS FMFETLLLLIL RSGXKIFLPN
101 Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 91>:

a013.seq

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TGCGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCACGCAG TTGGATTTCG ACACTTTTTG CCCTTTTGTC
151 ATGATGCTGT TGTCGGCGGC AGAAGCGGCG GCGCAGAGGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTCAT TGGTGTTCCT TTAATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT CTTGCCGAAT
301 CGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 92; ORF 013.a>:

a013.pep

```

1 MPLTMLCSST CGFFMMKSER *SGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIGVS LMFETLLLLIL RSG*KIFLPN
101 R*

```

m013/a013 97.0% identity over a 101 aa overlap

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
a013	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFIGVSFMFETLLLLILRSGXKIFLPNQX					
	:					
a013	AQKQPKTRAVGSRVVFIGVSLMFETLLLLILRSGXKIFLPNRX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m013.pep	MPLT	MLCSSTCGF	FMKSERXSGGN	MVPRSPFLPWQATQLD	SYTFCFPVM	MLLSAAEEAA
		: : :				
g013	MPLT	MLCSRTCGLF	IIQSDRKSGGN	AVPRSPFLPWQAMQLD	SYTFCFPVM	MLLSAAEEAA
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSR	VVFIGVSF-MFET	LLLILR-SGXX	KIFLPNQX		
	:	:	: : :	:		
g013	AQRQHKMAVGSR	VVFIGVSPNVLK	PCFLILPLRGEK	FFWPKSGIX		
	70	80	90	100		

```
g015.seq
  1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TCCAACATCC GTTTTTTCCT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGT CCGCTTTGG AAGCACTGC CCCACCTAA CGACACGATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAG ATTACCCATT TCTCCCGTT
201 CAACGCGCCT TGGCTCGGCA CAAAATCCT GCTCCTGTTT GCCTACATCG
251 CACTGGGCAT GGTAAATGAT GCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTGCCTAT GTGTTGCATC GCCTGCATCG TTTACCTTGC
351 CAAAACCAAA TGCCTGCCAT TCTGA
```

g015.pap

1 MQYLIVKYSH QIFVTITILV FNIRFFLLWK NPEKPLVGFW KALPHLNDTM

51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLF AYIALGMVMM RARPRSTKFY

101 TVYLLAMCCI ACIVYLAKTK VLPF*

```
m015.seq      (partial)
1  ..AAATACGAGAA AAGCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51 CGACACCATTG   CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101 TCTCCCCGTT    CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC
151 GCCTATATCG    CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC
201 CAAGTTCTAC    ACCGTTTACC TGCTCGCCAT GTGTTGCGCT GCCTGCATCG
251 TTACCTTGC     CAAACCAAAA GTCCTGCCTT TCTGA
```

```
m015.pep (partial)
      1  ..KIRKALAGFW KALPHLNDTM LLFTGLWLMK ITHFSPFNAP WLGTKILLLL
     51  AYIALGMMM RARPRSTKFY TVYLLAMCCV ACIVYLAKTK VLPF*
```

```

a015.seq
1  ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51  CATTTTGGTA TTCAACATCC GTGTTTTCTN ACTTTGGAAA AATCCAGAAA
101 AGCCTTGGC GTGCCTTTGG AAGGCATGCT CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAA ACCACCTATT TCTCCCGTT
201 CAACGCGCCT TGGCTCGGTA CAAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCCAT GTGTTGCCTC ACCTGCATCG TTTACCTTGC
351 CAAAACCAAA GTCTCGCCTT TCTGA

```

a015.pap

1 MQYLIVKYSH QIFVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM
 51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY
 101 TVYLLAMCCL TCIVYLAKTK VLPF*

m015/a015 96.7% identity over a 91 aa overlap

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
a015	LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep	40	50	60	70	80	90
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP					
a015	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCLTCIVYLAKTKVLP					
	70	80	90	100	110	120
m015.pep	FX					
a015	FX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng)

from *N. gonorrhoeae*:

m015/g015

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
g015	LIVKYSHQIFVTITILVFNIRFFLLWKNPEKPLVGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep	40	50	60	70	80	90
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP					
g015	FSPFNAPWLGTKILLLLFAYIALGMVMMRRARPRSTKFYTVYLLAMCCVACIVYLAKTKVLP					
	70	80	90	100	110	120
m015.pep	FX					
g015	FX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

g018.seq

1 atGCAGCAGG GGCagttggt tggacgcgtc gcccgcaata AAGATATGCG
 51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGGtac gccgcgcgcg
 101 tctttgTCGA TATTGATGTT TTCCAAACCG ATATgtCAA CGTTCTGGACG
 151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTTCGC
 201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC
 251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT
 301 CGCCTCGTCT GA

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

g018.pep

1 MQQGQLVGRV ARNKDMRNAG LHGQRIGNGY AARVFVDIDV FQTDIVNVRT
 51 ATYGCQHIFG NKYAFFAILL PMDFYIAVCV EFDLGFSIQM QFQFFSEHGF

101 RLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 101>:

m018.seq

```

1   ATGCAGCAGA GGCAGTTGGT TGGACGCATC GCCTGCGATG AAGATATGCG
51  GAATACTGGT CTGCATGGTC AGCGGGTCGG CAACAGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATATT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCACAG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCATC GAGTTTGACC
251 TCGGTTTtag CATCCAGATG CAGTTTCAAT TCTTCGCCGA ACACGGCGTT
301 CGCCTCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 102; ORF 018>:

m018.pep

```

1   MQQRQLVGRI ACDEDMRNTG LHGQRVGNRY AARIFFDIDI FQTDIVNVRT
51  AAHGCGHIFG NKYAFAILL PMDFYIAVCI EFDLGFSIQM QFQFFAEHGV
101 RLV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 103>:

a018.seq

```

1   ATGCAGCAGG GGCAGTTGGT TGGACGCGTC GCCCGCAATA AAGATATGCG
51  GAATACTGGT CTGCATAGTC AGCGGATCGG CAACGGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATGTT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCACAG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCGTC GAGTTTGCCG
251 TCGGTTTtag CATCCAAATG CAGTTTCAAT TCTTCACCGA ACACGGCTTT
301 CGCCTCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 104; ORF 018.a>:

a018.pep

```

1   MQQGQLVGRV ARNKDMRNTG LHSQRIGNGY AARIFFDIDV FQTDIVNVRT
51  AAYGCGHIFG NKYAFAILL PMDFYIAVCV EFGLGFSIQM QFQFFTEHGF
101 RLV*

```

m018/a018 86.4% identity over a 103 aa overlap

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG					
	10	20	30	40	50	60
a018	MQQGQLVGRVARNKDMRNTGLHSQRIGNGYAARIFFDIDVFQTDIVNVRTAAYGCGHIFG					
	70	80	90	100		
m018.pep	NKYAFAILLPMDFYIAVCIEFDLGFSIQMQFQFFAEHGVRLVX					
	70	80	90	100		
a018	NKYAFAILLPMDFYIAVCVEFGLGFSIQMQFQFFTEHGFRLVX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 018 shows 84.5% identity over a 103 aa overlap with a predicted ORF (ORF 018.ng) from *N. gonorrhoeae*:

m018/g018

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG					
	10	20	30	40	50	60
g018	MQQGQLVGRVARNKDMRNAGLHGQRIGNGYAARVFVDIDVFQTDIVNVRTATYGCQHIFG					

	70	80	90	100
m018.pep	NKYAFFAILLPMDFYIAVCIEFDLGFSIQMQQFFAEHGVRLVX			
	: : :			
g018	NKYAFFAILLPMDFYIAVCVEFDLGFSIQMQQFFSEHGFRLVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

g019.seq (partial)

```

1  ..ctgctggcgg ccctggtgct tgcgcgtgt tcttcgACAA ACacacTGCC
51  AGCCGGCAAG ACCCCGGCAG ACAATATAGA AActgcCgAC CTTTCGGCAA
101 GCGTTCCAC ccgcCCTGCC GAACCGGAAG GAAAAACGCT GGCAGATTAC
151 GGCGGCTACC CGTCCGCACT GGATGCAGTG AAACAGAACA ACGATGCGGC
201 AGCCGCCGCC TATTTGGAAÀ Acgcaggaga cagCGcgatg gcGGAAtg
251 tccgcaagga gtgGCTGa

```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

g019.pep (partial)

```

1  ..LLAALVLAAC SSTNTLPAGK TPAENIETAD LSASVPTRPA EPEGKTLADY
51  GGYPSALDAV KQNNDAÀAAA YLENAGDSAM AENVRKEWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

m019.seq (partial)

```

1  ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGCTGCTGG CGGCCCTGGT
51  GCTTGCCGCG TGTCTTCGA CAAACACACT GCCAGCCGGC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCCGCCCT
151 GCCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCACGCAG ACAGTGGACG CTGTTTGAC AGGAATACGC
351 CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451 AAAGTGCCTT CGGGCTGCAC CAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCAGCGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTAAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCCT TGGACTATTA
801 CGGCAAGGTT GCCGACCGCC GCCAAGTAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCCTTGCGC GCCGACGTT GGGACGAGCT GGCCTCCGTT
901 ATCTCGCATA TGCCGAAAA ACTGCAAAA AGCCCGACCT GGCTCTACTG
951 GCTGGCACGC AGCCGCGCCG CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GGCGGCAGCG ACGGCAGGA ATTTTATGC GGTGCTGGCA
1051 GGGGAAGAAT TGGTTCGGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAAACCGC
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG GCGTTTGGC ACACGCGGCT TTGACGAAGA
1251 CAAGCTGCTG ACCGCGCGC AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCAGC GCAAACTCAA CTACACCTTG
1351 CGCTATATTT CGCGTTTAA AGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGCG AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCCGACG GG...

```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

m019.pep (partial)

```

1  MYLPSMKHSL PLLAALVLAA CSSTNTLPAG KTPADNIETA DLSASVPTRP

```

```

51  AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARROWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYYGKV ADRRLTDDQ IEWYARAALR ARRWEDELASV
301 ISHMPEKLQK SPTWLYWLR SRAATGNTQE AEKLYKQAAA TGRNFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQV SQSAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

```

a019.seq
1  ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCCTGGT
51  GCTTGCCGCG TGTCTTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTCC CACCNCGCCT
151 GCCGAACCCG AANGAAAAAC GTNGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCCGCG AACTGGTCAA AAATACGGGC
451 AAACTGCCTT CGGGCTGCAC CAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGC CGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCC
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAGAA GACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTAAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCT TGGACTATTA
801 NGGCAAGGTT GCCGACCGCC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGC NNTNNGC NNNCGNNGT NGNANGANN TGGC NCCGN
901 ANCNCGNNN TGCNNGANAA ACNNNNNNAN AGNCNNANT NGNTNNANT
951 NNTGGCACGC AGCCGCGCGC CNACGGGCAA CACGCAANAN GCGGANAAC
1001 TNTACAAACA GCGGCGAGCA NCGGGCANGA ATTTTATGC NGTCTGN
1051 GGGGAAGAGT TGGGCGGCAN AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAANC AGCGTCTCTC GTATGGCGGA AGACGGCGCG ATTAAGCGCG
1151 CGCTGGTGCT GTTCCGAAAC AGCCGAACCG CCGCGATGC GAAATGCGC
1201 CGTCNNGGCTC AGCGGGAATG GCGTTTCGCC ACACGCGGCT TCGATGAAGA
1251 CAAGCTGCTG ACCGCGCGCG AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTT
1351 CGCTACATT CGNNNNNTNA NGACACGGTA ATCCGCCACG CGCAAAATG
1401 TAATGTCGAT CCGCGGTGGG TTTACGGGCT GATTCGTCAG GAAAGCCGCT
1451 TCGTTATGGG CCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCTGCCA CCGCGCGCGA AATCGCCGCG AAAATCGGTA TGGATGCCG
1551 ACAACTTTAC ACCGCCGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCCGCTG CAAAACAACG AAGTCTCGC CACCGCAGGC
1651 TATAACGCGG GTCCCGGCAG GCGCGCCGA TGGCAGGCGG ACACGCCCT
1701 CGAAGGCGCG GTATATGCCG AAACCATCCC GTTTCCGAA ACGCGGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCTC ACTACGCTC CCTCTCGGC
1801 GCGCCGCACA TCCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

```

a019.pep
1  MYPPSLKHSL PLLVXLVLA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51  AEPEKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARROWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYXGKV ADRRLTDDQ IEWYARAAXX XXXXXXXXXX
301 XXXXXXXXXX XXXXXXXXAR SRAATGNTQX AXKLYKQAAA XGNFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFN SRTAGDAKMR
401 RQAQAEWRFA TRGFDEDKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL

```

451 RYISXXXTV IRHAQNVNVD PAWVYGLIRQ ESRFVMGAQS RVGAQGLMQV
 501 MPATAREIAG KIGMDAAQLY TADGNIRMGW WYADTKRRL QNNEVLATAG
 551 YNAGPGRARR WQADTPLEGA VYAETIPFSE TRDYVKKVMA NAAYYASLFG
 601 APHILKQRM GIVPAR*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLPSMKHSLPLLAALVLAACSSNTNLPAGKTPADNIETADLSASVPTRPAPERKTLAD					
a019	10	20	30	40	50	60
	MYPPSLKHSLPLLVXLVLAACSXTNTLSADKTPADNIETADLSASVPTXPAEPEXKTXAD					
m019.pep	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSGLGARRQWTLFAQEYAKLE					
a019	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSGLGARRQWTLXAXEYAKLE					
m019.pep	130	140	150	160	170	180
	PAGRAQEVECYADSSRNDYTRAAELVKNTGKLPSCGCTKLLEQAAASGLLDGNDAWRRVRG					
a019	130	140	150	160	170	180
	PAXRAQEVECYADSSRNDYTRAAELVKNTGKLPSCGCTKLLEQAAASGLLDGNDAWRRVRG					
m019.pep	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
a019	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSPFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
m019.pep	250	260	270	280	290	300
	EQRSAFWGVLGHYQSQNLNVPAALDYXGKVADRRQLTDDQIEWYARAALRARRWDELASV					
a019	250	260	270	280	290	300
	EQRSAFWGVLGHYQSQNLNVPAALDYXGKVADRRQLTDDQIEWYARAAXXXXXXXXXXX					
m019.pep	310	320	330	340	350	360
	ISHMPEKLQKSPTWLYWLARSRAATGNTQEAELKLYKQAAATGRNFYAVLAGEELGRKIDT					
a019	310	320	330	340	350	360
	XXXXXXXXXXXXXXXXXARSRAATGNTQXAXKLYKQAAAXGXNFYAVLXGEELGRKIDT					
m019.pep	370	380	390	400	410	420
	RNNVPDAGKNSVRRMAEDGAVKRALVLFQNSQSAGDAKMRRQAQAEWRFRATRGFDEKLL					
a019	370	380	390	400	410	420
	RNNVPDAGKXSVLRMAEDGAIKRALVLFNRSRTAGDAKMRRXAQAEWRFRATRGFDEKLL					
m019.pep	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLNLYTLRYISPFKDTVIRHAQNVNVDPAWVYGLIRQ					
a019	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLNLYTLRYISXXXTVIRHAQNVNVDPAWVYGLIRQ					
m019.pep	490	500	510	520		
	ESRFVIGAQS RVGAQGLMQVMPATAREIAGKIGMDAAQLYTADG					
a019	490	500	510	520	530	540
	ESRFVIGAQS RVGAQGLMQVMPATAREIAGKIGMDAAQLYTADGNIRMGWYADTKRRL					
a019	550	560	570	580	590	600
	QNNEVLATAGYNAGPGRARRWQADTPLEGAVYAETIPFSETRDYVKKVMAAAYYASLFG					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

g019/m019

		10	20	30	40	49
g019.pep		LLAALVLAACSSNTLPAGKTPADNIETADLSASVPTRPAEPEGKTLAD				
m019	MYLPSMKHSLPLLAALVLAACSSNTLPAGKTPADNIETADLSASVPTRPAEPEKTLAD					
		10	20	30	40	50 60

	50	60	70	80	89
g019.pep	YGGYPSALDAVKQMNDAAYLENAGDSAMAENVRKEWL				
	: : : : : : : : :				
m019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARROWTLFAQEYAKLE				
	70	80	90	100	110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 111>:

g023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  AATGCAGCGT GCGACTGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATTT
151 TTTAGTCAAG CTTGGGTAAA AGTATTTACC CAAGTGAGCT TTATCGCCGT
201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCCTCGG CGTGC GTTTG TTTTGCAGG TTGCCACCAT TGtctGGCTG
301 GTCGGCTGCC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 023.ng>:

g023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVL FAL PKEYPAWQAF
51  FSQAWVKVFT QVSFIAVFLH AWVGIRDLWM DYIKPFGVRL FLOVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

m023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GCGATTGGGT
51  GATGCAACGT GCGACTGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTCCCTG CCTAAAGAAT ATTCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT
201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCCTCGG CGTGC GTTTG TTTTGCAGG TTGCCACCAT CGTTTGGCTG
301 GTCGGCTGTC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 023>:

m023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVL FSL PKEYSAWQAF
51  FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYIKPFGVRL FLOVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

a023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCAT TACGGTTTGC GGGATTGGGC
51  GATGCAACGT GCGACCGCGG TTATTATGTT GATTTATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCTCTG CCTAAAGAAT ATTCGGCATG GCAGGCATTT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT

```

201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA
 251 AACCTTCGG CGTGCCTTG TTTTTCAGG TTGCCACCAT CGTCTGGCTG
 301 GTCGGCTGCT TGGTGTATTC AATTAAAGTA ATTTGGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVLFL PKEYSAWQAF
 51 FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYXKPGVRL FLQVATIVWL
 101 VGCLVYSIKV IWG*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFLSLPKEYSAWQAFSSQTWVKVFT					
a023	MVERKLTGAHYGLRDWAMQRATAVIMLIYTVALLVVLFLALPKEYSAWQAFSSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
a023	QVSFIAVFLHAWVGIRDLWMDYXKPGVRLFLQVATIVWLVGCLVYSIKVIWGX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFLALPKEYPAWQAFSSQAWVKVFT					
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFLSLPKEYSAWQAFSSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
m023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq

1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TTGCCGCTCT
 51 GTTGGGCGGT TGcGCCACCC AACAGCCTGC TccTGTCATT GCAGGCAATT
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA
 151 ACGCCGTACA ATGCCGCTCC TGCCGCCAac gatgcGCCgT ATGTGCCGCC
 201 CGTGCAAact gcgcgggttT ATTGCGCTCC TGCTTATGTT CCGCcgTCTG
 251 CACCTGCCGT TTCGGgtaca tatgtTCCTT CTTACGCACC CgtcgACATC
 301 aacgCGCGCa cgCataCTAT TGTGCGTGGC GACACgGtgt acaACATTTC
 351 caaAcgCtAc CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
 401 CCGACAATAC GTTGAGCATC GGTcAGATTG TTAAAGTCAA ACCGGCaggA
 451 TATGCCGCAC CGAAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC
 501 TGCCCGCAA ACCCTGTGA AACCcGCCGC gcaACCGCCC GTTCAGTCCG
 551 CGCCGCAACC TGCCCGCCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC
 601 GCGCCCGCCC CGCAATCTCC TGCCGCTTCG CCTTCCGCA CGCGTTCGGT
 651 CGGCGGCATT GTTTGGCAGC GTCCGACCCA AGGTAAAGTG GTTGCCGATT

```

701 TCGGCGGCGG CAACAAGGGT GTCGATATTG CCGGCAATGC CCGACAACCC
751 GTTTTGGCGG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAA TTGCTGGTGC GCGAAGGTCA GCAGGTCAAA
901 CGCGGTCAGC AGGTGCTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTC GAGGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

```

g025.pep
1 MLKQTTLLAA CTAVAALLGG CATQQPAPVI AGNSGMQTVS SAPVYNPYGA
51 TPYNAAPAAAN DAPYVPPVQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHTIVRG DTVYNISKRY HISQDDFRW NGMTDNTLSI GQIVKVKPAG
151 YAAPKTAAVE SRPAVPAAQ TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQGV VADFGGNGK VDIAGNAGQP
251 VLAAADGKVV YAGSGLRGY NLVIIQHNS FLTAYGHNQK LLVGEGQQVK
301 RGQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

m025.seq (partial)
1 ..GTGCCGCGG TGCAAAGCGC GCCGGTTTAT ACGCCTCCTG CTTATGTTCC
51 GCCGTCTGCA CCTGCCGTTT CGGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGGCGACG CATACTATTG TCGCGGCGCA CACGGTGTAC
151 AACATTTCOA AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCCGCAACG AAAGCCGCG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CGCGCAACC GCCCGTACAG TCCGCACCCG TCGACATTAA
351 CGCGGCGACG CATACTATTG TCGCGGCGCA CACGGTGTAC AACATTTCOA
401 AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACCGCAG CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCCTGTGAAA CCGCGCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCGC TCGGAAAAAT AAAGCGGTTT CCGCGCCCGC
651 CCGCAATCT CCTGCCGCTT CGCCTTCCGG CACGCGTTCG GTCGGCGGCA
701 TTGTTTGGCA GCGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCGGCGGC
751 AACAACAAGG GTGTCGATAT TGCCGTAAT GCGGGACAGC CCGTTTGGC
801 GGCGGCTGAC GGCAAAGTGG TTTATGCCGG TTCAGTTTG AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCCTGAC CGCATACGGG
901 CACAACCAAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACCGCGTCA
951 GCAGGTTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGGTGCG TCAAACCGG AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

```

m025.pep (partial)
1 ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
51 NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNLSIGQIV KVKPAGYAAP KTAAVESRPA VPAAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRP QGKVVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVVYAGSGL RGYGNLVIIQ HNSSFLLTAYG
301 HNQKLLVGEG QQVKRGQOVA LMGNTDASRT QLHFVVRQNG KPVNPNSYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

a025.seq
1 ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACCGCCC TTGCCGCTCA
51 GTTGGGCGGA TGCCCCACCC AACACCCTTC TCCTGTCAAT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAAATC TTATGGCGCA

```

```
151 ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCGCC
201 GGTGCAAAGC GCGCCGGTTT ATANGCCTCC TGCTTATGTT CCGCCGTCTG
251 CACCTGCCGT TTCGGGTACA TACGTTCTT CTTACGCANC CGTCGACATC
301 AACGCGGCGA CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351 CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCGTGG AACGCGATGA
401 CCGACAATAC GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA
451 TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC
501 TGCCGCGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACGCGGCGA
551 CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601 CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA CCGACAATAC
651 GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701 CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC TGCCGTGCAA
751 ACCCCTGTGA AACCCGCCGC GCAACCGCCT GTGCAGTCCG CGCCGCAACC
801 TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCGCCC GCCCCGCAAT
851 CTCCTGCCGC TTCGCCTTCC GGCACGCGTT CCGTCGGCGG CATTGTTTGG
901 CAGCGTCCGA CGCAAGGTAA AGTGGTTGCC GATTTCGGCG GCAACAACAA
951 GGGTGTCGAT ATTGCAGGAA ATGCGGGACA GCCCGTTTGG GCGGCGGCTG
1001 ACGGCAAAGT GGTATTATGCA GGTTCGGTT TGAGGGGATA CGGCAATTTG
1051 GTCATCATCC AGCATAATTC TTCCTTCCTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGGCGAAG GCCAGCAGGT CAAACGCGGG CAGCAGGTCG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTGAGGTCG
1201 CGGCAAAACG GCAAACCGGT TAATCCGAAC AGCTATATCG CGTTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

a025.pep

```
1 MLTP TTL*VA CTALAAQLGG CPTQHSPVI AGNSGMQTVP SAPVYNPYGA
51 TPYNAAPAAN DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101 NAATH TIVRG DTVYKISKCY HISQDD FRAW NGMTDNTLSI QIVKVKPAG
151 YAAPKAAAVK SRPAVPAAQ PLVQSAPVDI NAATH TIVRG DTVYNISKRY
201 HISQDD FRAW NGMTDNTLSI QIVKVKPAG YAAPKAAAVK SRPAVPAAVQ
251 TPVKPAAQPP VQSAPQPAAP AAENKAVPAP APQSPAASPS GTRSVGGIVW
301 QRPTQ GKVVA DFGGNNKGVD IAGNAGQPV LAAADGKV VYA GSGLRGYGNL
351 VIIQH NSSF L TAYGHNQKLL VEGEQQVKRG QQVALMGNTE ASRTQLHFEV
401 RQNGKPVNPN SYIAF*
```

m025/a025 97.4% identity over a 351 aa overlap

```

                                     10      20      30
m025.pep                               VPPVQSAPVYTTPAYVPPSAPAVSGTYVPS
                                     |||:|||:|||:|||:|||:|||:|||
a025      GMQTVPSAPVYNPYGATPYNAAPAANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
               40      50      60      70      80      90

               40      50      60      70      80      90
m025.pep      YAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMTDNTLSI QIVKVKPAGYAAP
               || |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025      YAXVDINAATH TIVRGDTVYKISKCYHISQDD FRAWNGMTDNTLSI QIVKVKPAGYAAP
               100     110     120     130     140     150

               100     110     120     130     140     150
m025.pep      KAAAVKSRPAVPAAQPPVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
               |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025      KAAAVKSRPAVPAAQPLVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
               160     170     180     190     200     210

               160     170     180     190     200     210
m025.pep      DNMLSIGQIVKVKPAGYAAPKTA AVESRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
               || |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a025      DNTLSIGQIVKVKPAGYAAPKAAAVKSRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
               220     230     240     250     260     270

               220     230     240     250     260     270
m025.pep      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQ GKVVADFGGNNKGVDIAGNAGQPVLAAD
               |||||:|||:|||:|||:|||:|||:|||:|||:|||:|||
```

```

a025      KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLAAD
           280      290      300      310      320      330

m025.pep      280      290      300      310      320      330
GKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDASRT
|||||
a025      GKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTEASRT
           340      350      360      370      380      390

m025.pep      340      350
QLHFEVRQNGKPVNPNSYIAFX
|||||
a025      QLHFEVRQNGKPVNPNSYIAFX
           400      410

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 025 shows 75.6% identity over a 353 aa overlap with a predicted ORF (ORF 025.ng) from *N. gonorrhoeae*:

m025/g025

```

m025.pep      10      20      30
               VPPVQSAPVYTTPPAYVPPSAPAVSGTYVPS
               |||||:||||:|||||
g025      GMQTVSSAPVYNPYGATPYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
           40      50      60      70      80      90

m025.pep      40      50      60      70      80      90
YAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMTDNTLSIGQIVKVKPAGYAAP
|||||
g025      YAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMTDNTLSIGQIVKVKPAGYAAP
           100     110     120     130     140     150

m025.pep      100     110     120     130     140     150
KAAAVKSRPAVPAAPAAQPPVQSAPVDINAATHITVRGDTVYNISKRYHISQDDFAWNGMT
|
g025      K-----

m025.pep      160     170     180     190     200     210
DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
|||||
g025      -----TAAVESRPAPVPAAPAAQTPVKPAAQPPVQSAPQPAAPAAEN
               160     170     180     190

m025.pep      220     230     240     250     260
KAVPAPAP--QSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
|||||
g025      KAVPAPAPAPQSPAASPSGTRSVGGIVWQRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
           200     210     220     230     240     250

m025.pep      270     280     290     300     310     320
ADGKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDAS
|||||
g025      ADGKVVYAGSGLRGYGNLVIIQHNSFLTAYGHNQKLLVGEGQQVKRGQQVALMGNTDAS
           260     270     280     290     300     310

m025.pep      330     340     350
RTQLHFEVRQNGKPVNPNSYIAFX

```

g025 |||||
 RTQLHFEVRQNGKPVNPNSYIAFX
 320 330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 113>:

g031.seq
 1 ATGGTGTCCC TCCGCTTCAG ATTCGGCAAC CACTTTAAAC GCCGACATTC
 51 TGACAATTTC CTTTCCGCC AGCCAAATAT CATGCGTATC TTTTCGGTTTCG
 101 GGCTTGTGG GCATGGCAAC CTTCAACAGC CGCGCCATCA CAGGAATCGT
 151 CGTTCCCTGA ATCAGCAGCG ACAGCACCAC CACGGCAAAC GCCACATCAA
 201 ACAGCAGGTG CGAATTGGGA ACGCCCATCA CCAGCGGCAT CATCGCCAGC
 251 GAAATCGGTA CGGCTCCTCG CAAGCCCAAC CAACTGATAT ACGCCTTTTC
 301 ACGCAGGTG TAATTGAATT TCCACAAACC GCCGAACACT GCCAGCGGAC
 351 GCGCGACCAG CATCAGGAAC GCCGCAATCG CCAAGGCTTC CGCCGCCCTG
 401 TCCAACACGC CGCGGGGAGA AACCAGCAGA CCGAGCATGA CGAACAAAGT
 451 TGCCTGCGCC AGCCAAGCCA AACCGTCCAT CACACGCAA ACCTGTTCCG
 501 TgcACGTT GCGCTGGTTA CCGACAATGA TGCCGGCAAG GTAAACCGCC
 551 AAAAAGCCGC TGCCGCCTAT GGTATTGGTA AACGCAAACA CAAGCAGCCC
 601 GCCGACACA ATCATCAGCG CGTACAGACC TTCCGtacac acctccaatt
 651 cccaatcaac gtcatagtg tctcccggtg taaaatgttc ttcacttcag
 701 aatccccccc ttcttcccag cccgaaacct tcatgtgtta nacctgggg
 751 tgccccaacg gathtagtaa cctcccaatg actctgcttg tcgccccctt
 801 cgcccgcttt ctccttcggt gaaaacttgt tgtcccgctc ttacattaa

This corresponds to the amino acid sequence <SEQ ID 114; ORF 031.ng>:

g031.pep
 1 MVSLRFREGN HFKRRHSDNF LFRQPNIMRI FRFGLVGHGN LQQPRHHRNR
 51 RSLNQQRQHH HGKRHIKQV RIGNAHQHRH HRQRNRYGSS QAQPTDIRLF
 101 TQAVIEFPQT AEHCQRTRDQ HQERRNRQGF RRPVQHAGGR NQQTEDHEQS
 151 CLRQPSQTVH HTQNVFRRTV ALVTDNDAGK VNRQKAAAY GIGKRKHQKQ
 201 ARHNHQRVQT FRTHLQFPIN VIAVSRVKMF FTSESPPSSQ PETFMEXTLG
 251 CPNGFSNLPM TLVAPFARF LLPGKLVVPV LH*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

m031.seq (partial)
 1 ...CGCCTGAAGC ACGGTGTCGG ACTGCATTTT TATTCGGCTA TACGCCTTTT
 51 CACGCAGGCT GTAATTGAAT TTCCACAAAC CGCCGAACAC TGCCGACGGA
 101 CGCGCGACCA GCATCAGGAA CGCCGCAATC GCCAAGGCTT CCGCGCCCT
 151 GTCCAACACG TTGGCAGGAG AAACCAGCAG CAAAGGCATT CCCAAACGTG
 201 CGGACAAAGT GGTGCAAAAC ACGCTCAGAA ACAACAGTGC GCCACCCGGC
 251 AG....

This corresponds to the amino acid sequence <SEQ ID 116; ORF 031>:

m031.pep (partial)
 1 ...RLKHGVLHF YSAIRLFTQA VIEFPQTAEH CRRTRDQHQE RRRNRQGFRRP
 51 VQHVGRNRQQ QRHSQTCGQS GRNHAQKQOC ATRQ....

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

a031.seq
 1 ATACGCCTTT TCACGCAGGC TGTAATTGAA TTTCCACAAA CCGCCGAACA
 51 CTGCCGCGCG ACGCGCGACC AGCATCAGGA ACGCCGCAAT GCCAAGGCT
 101 TCCGCCGCCG CGTCCAACAC GTTGGCAGGA GAAACCAGCA GCAAAGGCAT
 151 TCCCAAACGT GCGGACAAAG TGCTCGAAAC CACGCTCAGA AACAACAGTG
 201 CGCCACCCGG CAG

This corresponds to the amino acid sequence <SEQ ID 118; ORF 031.a>:

a031.pep (partial)
 1 IRLFTQAVIE FPQTAEHCRN TRDQHQERRN RQGFRFPVQH VGRNRQQQRH
 51 SQTGQSGRN HAQKQCATR Q

m031/a031 100.0% identity over a 71 aa overlap

10 20 30 40 50 60
 m031.pep RLKHGVLGHFYSAIRLFTQAVIEFPQTAEHCRRTRDQHQERRNRQGFRRPVQHVGRNRQQ
 a031 IRLFTQAVIEFPQTAEHCRRTRDQHQERRNRQGFRRPVQHVGRNRQQ
 10 20 30 40
 70 80
 m031.pep QRHSQTCGQSGRNHAQKQQCATRQ
 a031 QRHSQTCGQSGRNHAQKQQCATRQ
 50 60 70

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032.seq

1	ATGCGCGCAA	ACGTGCCTGC	CGTCGCCGTA	TTGCGCCGCC	CACGATTCGA
51	GGCGTTT	GATTTGGCGT	TGGCTCAGGG	GCGTGCCGTT	CCTGCCGGTA
101	AACAGGGCTT	TGCCGTC	TCCGCTCTGA	CGCAGCGGCA	GATAGTTT
151	CAAGGCTTCC	ACGCTTTTGC	CGGTCTAGCG	AACCTGACGC	TGATTGCGCC
201	CTTTGCCGGT	AACGTGTACC	CACGCTTCGT	CCAAATATAC	ATCATCTGCA
251	TTCAAGCCGT	GTATCTCGT	CACCGCAAA	CCGCTGCCGT	ACATCAGCTC
301	GAACAGCGCG	TGGTCGCGCA	CCGCCAGCGG	GTCCGCCCGC	TCCACGGGCA
351	AATCCAACAT	CCGGTTCAGC	CATTCTGCG	GCAGGGCTTT	GGGTACGCGC
401	TCGGGCTGCT	TCGGCGGTTT	GATGTCGGCG	GTCCGGTTCGG	CGCGCATCAG
451	CCCGCGCTTG	ACCAGCCAGG	CGCAATACTG	CCGCCACGCC	CACAGCTTGC
501	GCGCCAGCGT	CCGACCGTCC	AAACCGCGCT	CGCAGACGCC	CGCACAACGCC
551	GcggTAAAAAT	CGCGCCGCGA	CAAGTCTGCG	GGCAGCGcgc	ctgcaTCTTC
601	AGACGGCATT	TGTGCCAACA	GTGCAAAACAG	TTCTTCCAAA	TGCGCGCGGT
651	ATGCCGCAAC	CGTGTGCTCG	GACTTGCCCT	CGCGCACGAT	GTTTTCCAAA
701	TAAGCGTCAA	AATAcgcgcC	AAACcgcTCC	AAAACCATAA	CCGTCCCCACA
751	CAAAATATCAA	AAAACACAGTG	A		

This corresponds to the amino acid sequence <SEQ ID 110; ORF 032.ng>:

g032.pap

1 MRRNVPAAVAV LRRPRFEAFI DLALAQARAV PAGKQGFVR CRLTQRQIVF
51 QGFHAFAGQR NLTLAPFAG NVYPRFVQIY IICIQAVYLA HAOTAAVHOL

101 EQRVVAHRQR VAAVHGQIQH PVQPFLRQGF GYALGLLRRF DVGGRVGAHQ
151 PAFDPQGAIL PPRRLARQR PTVQTALRQP PQRRLKIAPR QVLRHAACIF
201 RRHLCQCKQK FFQIAPVCRN RVLRLALAHQ VFQISVKIRR KPVQNHNRPT
251 QISKNQ*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```
m032.seq (partial)
1 ATGCGGCGAA AC GTG C m TGC mGTCCCGTT kTGCGCCGCC CATTGCGCCA
51 AACGTTTTTG GATTTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC GCACCAGCGG CACCTGCCGC TgTT.CGCGC
201 CTTTGCCGAT AAcGTGTACC CACGcyTCGT CCAAATAGAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAAcAGGGCG TGGTCGCGCA CCGCAGCGG GTCGCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTcAGC GATTCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGC GTCGGGTTCG CGTGcATCAG
451 GCCGCGCTTT ACCAGC AAA CGAATACTG CCGCAAGAC GAAAGCTTGC
501 GAGCCAGCGT CCGTTCCCC AAACGCG...
```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 032>:

```
m032.pep (partial)
1 MRRNVXAVAV XRRPLRQTFL DLALAQARAV PAGKQGFVR CRLTQRQIVF
51 QGFHAFADQR HLPLXAPFAD NVYPRXVQID IICIQAVYLA HAQTAAVHQF
101 EQGVVAHRQR VAAVHGQIQH VPQPFRLRQGF GYALGLLRRF DVGGRGVGHQ
151 AALYQPNAIL PPRRKLASQR PFPQTA...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

```
a032.seq
1  ATGCGGCGCAA  ACGTGCCCTGC  CGTCGCCGTT  TTGCGCCGCC  CATTGCGCCA
51  AACGTTTTTGT  GATTTGGCGTT  TGGCTCAGCG  GCGTGCCGTT  CCTGCGCGTA
101 AACAGGCGTTT  TGCCGTCCGA  TGCCGTCTGA  CGCAGCGCGA  GATAGTTTTT
151 CAGGGCTTCC  ACGCTTTTGC  CGGTACGCGG  AACCTGCCGC  TGCTTGCGTC
201 CTTTGCCGGT  AACGTGTACC  CACGCCTCGT  CCAATATAC  ATCATCTGCA
251 TTCAAGCCGT  GTATCTCGCT  CACGCGCAA  CCGTGCCGT  ACATCAGTTT
301 GAACAGCGCG  TGATCGCGCA  CGCCAGCGG  GTCGCGCCG  TCCACGGGCA
351 AATCCAGCAT  CCGGTTCAGC  CATTCTGCG  GCAGGGCTTT  GGGTACGGCG
401 TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  GTCGGGTCGG  TATGCAGCAG
451 ACCGCGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCCAAGAC  GACAGCTTGC
501 GCGCCACGT  CCGCGCATTC  AAACCGCGCT  CGCAGACGCG  CCGCAACGCC
551 GCCGTAAAT  CGCGCTCGCA  CAAGCCTGCG  GGCACGCGCG  CTGCATCTTC
601 AGACGGCATT  TGTGCCAACA  GCGCAAACAG  TTCTTCCAAA  TCGCGCCGGT
651 ATGCCGCCAC  CGTGTGCTCC  GACTTGCCCT  CGCGCACGAT  GTTTTCCAAA
701 TAAGCGTCAA  AATGCGCCGC  AAACCCGTCC  AAAACCATAA  CCGCCCCACA
751 CAAATATCAA  AAAAACAGTG  A
```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 032.a>:

```
a032.pep
1  MRRNPVAVV LRRPLRQTF L DLALAQARV PAGKGQFAVR CRLTQRQIVF
51  QGFHAFAGQR NLPLLHSFAG NVYPRLVQIY IICIQAVYLA HAQTAAVHVF
101 EQRVIAHRQR VAAVHGQIQH PVQPLRQGF GYALGLLRRF DVGGRVGMQQ
151 TAFDQPGARL PPRRQLARQR PRIQTALRQP PQRKRKIALR QALRHAACIF
201 RRHLCQQRKQ FFQIAPVCRH RVLRLALAH D VFQISVKMRR KPVQNHNRPT
251 QISKKO*
```

m032/a032 88.1% identity over a 176 aa overlap

```

              10      20      30      40      50      60
m032.pep  MRRNVXAVAVXRRPLRQTFDLALAQAARAVPAGKQGFAVRCRLTORQIVFQGFHAFADQR
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a032      MRRNVPAAVAVLRRPLRQTFDLALAQAARAVPAGKQGFAVRCRLTORQIVFQGFHAFAGQR
              10      20      30      40      50      60

```

	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIIICIQAVYLAAHQTAAVHQQFEQGVAHRQRVAAVHVGQIQH					
a032	: :					
	70	80	90	100	110	120
	NLPLLASFAGNVYPRLVQIYYIICIQAVYLAAHQTAAVHQQFEQRVIAHRQRVAAVHVGQIQH					
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFGYALGLLRFDVGGRGVGHQAALYQPNAILPPRRKLASQRPFPTA					
a032	: : :					
	PVQPFLLRQGFGYALGLLRFDVGGRGVMQQTAFDQPGAILPPRRQLARQRPRIQTALRQP					
	130	140	150	160	170	180
a032	PQRRRKIALRQALRHAACIFRRHLCQQRKQFFQIAPVCRHRVLRLALAHDFQISVKMR					
	190	200	210	220	230	240

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng) from *N. gonorrhoeae*:

m032/g032

	10	20	30	40	50	60
m032.pep	MRRNVXAVAVXRRPLRQTFDLALAQAARAVPAGKQGFAVRCRLTQRQIVFQGFHAFADQR					
	:					
g032	MRRNVPAVAVLRRPRFEAFDLALAQAARAVPAGKQGFAVRCRLTQRQIVFQGFHAFAGQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQRVAAVHGGQIQH					
	:					
g032	NLTLLAPFAGNVYPRFVQIYIICIQAVYLAHAQTAAVHQLEQRVVAHRQRVAAVHGGQIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFRLRQGFYALGLLRRFDVGGRGVGVHQAALYQPNAILPPRRKLASQRFPFQTA					
g032	PVQPFRLRQGFYALGLLRRFDVGGRGVGAHQPAFDQPGAILPPRRQLARQRPVQTALRQP					
	130	140	150	160	170	180
	190	200	210	220	230	240
g032	PQRRRKIAPRQVLRHAACIFRRHLCQCKQFFQIAPVCNRNVLRLALAHQVFIQSVKIRR					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

၄၀၃၃. နေရာ

1	ATGGCGGCGG	CGGACAAACT	CTTGGGCGGC	GACCGCCGCA	GGTTCGCCAT
51	CATCGGAGAC	GGCGCGATGA	CGGCGGGGCA	GGCGTTTGAA	GCCTTGAATT
101	GCGCGGGCGA	TATCGATGTG	GATTTGTCTG	TCGTCCTCAA	CGACAACGAA
151	ATGTCGATT	CTGGCAACGT	CGGCGGTGG	CCCAAATATC	TTGCCAGCAA
201	CGTCGTGCGC	GATATGCACG	GACTGTTGAG	TACCGTCAAA	CGCAAAACgg
251	GCAAGGTATT	AGACAAAATA	CCCGGCGCGA	TGGagtTTGC	CCAAAAAGTC
301	GAACAcaaa	TCAAAACCTT	TGCGGAAGAA	GCCGAACACG	CCAAACAGTC
351	GCTGTCGCTG	TTTGAATAAT	TCGGCTTCCG	CTACACCGGC	CCCGTGGACG
401	GACACACGT	CGAGAATCTG	GTGGACGTAT	TGAAAGACTT	GGCGACCGCG
451	AAAGGCCCTC	AGTTGCTGCA	CGTCATCACC	AAAAAGGCA	ACGGCTACAA
501	ACTCGCCGAA	AACGACAACTg	tcaAATACCA	CGCCGTGCGc	aACCTGccta
551	AAGAAGGCGG	GGGCGCAAATg	ccGTCTGAAA	AAGAACCCTA	GCCCGCCgCc
601	aaaccgACCT	ATACCAAAAT	ATTTCGAAA	TGGCTGTGCG	ACCGGGCGGC
651	GGCAGATTCC	CGACTGGTTG	CGATTATCCC	CGGCATCGCG	GAGGGCAGCg

```

701 GACTGGTGGG GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT tacCTTTGCC GCGGTTTGG CGTGCGAAGG
801 CATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTGCCCGT TTTGTTTGCC
901 GTCGACCGTG CGGGCATCGT CGGCGCGGAC GGTCCGACCC ATGCCGGCTT
951 GTACGATTTG AGCTTCTTGC GCTGTGTGCC GAACATGATT GTTGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCTGCTGC TTTCGACCTG CTATCAGGCG
1051 GATGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CCGGCGCGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCC TTcatTGCCT TCGGCAGTAT GGTGCCACCC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTt
1251 cgtcaaacCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCAcg
1301 accGCATCGT TACCCTTGAA GAAAACGCGG AACAGGGCGG CGCAGGCGGC
1351 GCGGTCTTGG AAGTGTGTGG GAAACACGGC ATCTGCAAAC CCGTTTGTCT
1401 TTTGGGCGTT GCCGATACCG TAACCGAACA CGGCGATCCG AAAAACTTT
1451 TGGACGATTT GGGTTTGAGT GCCGAAGCGG TGAACGCCG GGTGCGCGAG
1501 TGGCTGCCGG ACCGTGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

g033.pep

```

1 MAAADKLLGG DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDLKDLRSR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKEGGAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAT
401 ALAVAEKLNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLLG V ADTVTEHGD P KKLLDDLGLS AEAVERRVRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

m033.seq

```

1 ATGGCGCGCG CAGACAACT CTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGGCGAC GCGCGATGA CCGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCaG.CGA TATGGATGTr GATTTGCTrG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCACGCT CCGCGCGCTG CCGAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GCCTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGAGTTTGC CCAAAAAGTC
301 GAACACAAAA TCAAAACCTT TGCCGAAGAA GCCGAACACG CCAACAGTC
351 GCTGTCTTTG TTTGAAAAC TCGGCTTCG CTACACCGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCCG TCAAATACCA CGCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAAAATG CCGTCTGAAA AAGAACCCTA GCCCGCGGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAAA TGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTACCGT TTTGTTTGCC
901 GTCGACCGCG CGGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCCGGTCT
951 GTACGATTTG AGCTTTTTGC GCTGCGTGCC GAACATGATT GTCGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCTGTTGC TTTCGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CCGGCGCGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCGCCCC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTGCGCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG

```

```

1301 ACCGCATCGT TACCCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCGGC
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTGTCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATT GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

m033.pep

```

1  MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51  MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAE AEHAKQSLSL FENFGFRYT PVDGHNVENL VDVLDLRSR
151 KGPQLLHVIT KKGNGYKLA NDVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGK IIRREGKTA FIAFGSMVAP
401 ALAVAEKLNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

a033.seq

```

1  ATGGCGGCGG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51  CATCGGCGAC GGC CGGATGA CGGCGGGTCA GCGCTTTGAA GCCTTGAAC
101 GCGCGGGCGA TATGGATGTG GATTGCTGG TCGTCTCAA CGACAACGAA
151 ATGTCGATT CCCCAACGT CGGTGCGTTG CCCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAATA CCCGGCGCGA TGGAGTTTGC CCAAAAGTC
301 GAACATAAAA TCAAAACCTT TCGCGAAGAA GCCGAACAG CCAACAGTC
351 ACTGTCTTTG TTTGAAAAC TCGGCTTCCG CTATACCGGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTCGATGTAT TGGGAAGACCT GCGCGGACGC
451 AAAGGCCCGC AGCTTCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGATCCCG TCAAATACCA CGCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAAATG CCGTCTGAAA AAGAACCCAA GCCCGCGCGC
601 AAACCGACCT ATACCCAAGT GTTCGGCAA TGGCTGTGCG ACCGGGCGCG
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCG ACCGCTATT CGATGTCGGC
751 ATCGCCGAGC AGCAGCCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAA ACCTGCCCGT TTTGTTTGGC
901 GTCGACCGCG CGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCCGGTTT
951 GTACGATTTA AGCTTTTTC GCTGCATTCC GAATATGATT GTCGCCGCGC
1001 CGAGCGATGA AAATGAATGC CGCCTGTGTC TTTGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGTGCC
1101 GGTTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCCCCCT
1201 GCATTGGCGG TCGCCGAAA ACTGAACGCC ACCGTCGCCG ATATGCGCTT
1251 CGTCAAAACG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCACG
1301 ACCGCATCGT TACCCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTGGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATT GGGCTTGAGT GCCGAAGCGG TGGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

a033.pep

```

1  MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51  MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAE AEHAKQSLSL FENFGFRYT PVDGHNVENL VDVLEDLRGR
151 KGPQLLHVIT KKGNGYKLA NDVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRRAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA

```

301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA
 351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREG EKTA FIAFGSMVAP
 401 ALAVAGKLNA TVADMRFVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS
 451 AVLEVLAKHG ICKPVLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
 501 WLSDRDAAN*

m033/a033 98.4% identity over a 509 aa overlap

m033.pep	10	20	30	40	50	60
	MAAADKLLGSDRRSVAII GDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISP NVGAL					
a033	MAAADKQLGSDRRSVAII GDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISP NVGAL					
	10	20	30	40	50	60
m033.pep	70	80	90	100	110	120
	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL					
	70	80	90	100	110	120
m033.pep	130	140	150	160	170	180
	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKG PQLLVITKKGNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGPVDGHNVENLVDVLEDLRGRKG PQLLVITKKGNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
m033.pep	190	200	210	220	230	240
	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
m033.pep	250	260	270	280	290	300
	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA					
	250	260	270	280	290	300
m033.pep	310	320	330	340	350	360
	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENEC RLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENEC RLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
m033.pep	370	380	390	400	410	420
	GTGTGAPVSDGMETVEIGKGIIRREG EKTA FIAFGSMVAPALAVAEKLNATVADMRFVKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREG EKTA FIAFGSMVAPALAVAGKLNATVADMRFVKP					
	370	380	390	400	410	420
m033.pep	430	440	450	460	470	480
	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLG VADTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGS AVLEVLAKHGICKPVLLLG VADTVTGHGDP					
	430	440	450	460	470	480
m033.pep	490	500	510			
	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSDRDAANX					
	490	500	510			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng)

from *N. gonorrhoeae*:

m033/g033

m033 . pep	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISP NVGAL	60
	:	
g033	MAAADKLLGGDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISP NVGAL	60
m033 . pep	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDKIPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
m033 . pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKG PQLLHVITKKGNGYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKG PQLLHVITKKGNGYKLAENDPVKYHAVA	180
m033 . pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ	240
	:	
g033	NLPKEGGAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSR LVAITPAMREGSGLVEFEQ	240
m033 . pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNL PVLFA	300
m033 . pep	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRL LLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRL LLLSTCYQADAPAAVRYPR	360
m033 . pep	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGSMVAPAL AVEKLNATVADMR FVKP	420
g033	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGSMVATAL AVEKLNATVADMR FVKP	420
m033 . pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHG ICKPVLLLGVADTVTGHGDP	480
g033	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHG ICKPVLLLGVADTVTEHGDP	480
m033 . pep	KKLLDDLGLSAEAVERRVRWLSDRDAANX	510
g033	KKLLDDLGLSAEAVERRVREWL PDRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034 . seq

1	ATGAGCCGTT	TATGGTTTTT	TGCCGTAAAA	AACATTATAA	TCCGCCTTAT
51	TTACCTATTG	CCCAAGGAGA	CACAAATGGC	ACTCGTATCC	ATGCGCCAAC
101	TGCTTGACCA	CGCCGCCGAA	AACAGCTACG	GCCTGCCCGC	GTTCAACGTC
151	AACAACCTCG	AACAAATGCG	CGCCATTATG	GAAGCCGCCG	ACCAAGTCAA
201	CGCGCCCGTC	ATCGTACAGG	CGAGCGCAGG	TGCGCGCAAA	TACGcgGCG
251	CGCCGTTTTT	GCGCCACCTG	ATTCTGGCGG	CAGTCGAAGA	ATTTCCGCAC
301	ATCCCCGTCG	TGATGCACCA	AGACCACGGC	GCATCGCCCG	ACGTgtgCCA
351	ACGCTCCATC	CAACTGGGCT	TCTCCTCCGT	GATGATGGAC	GGCTCTTTGC
401	TCGAAGACGG	CAAAACCCCT	TCTTCTTACG	AATACAACGT	CAACGCCACC
451	CGTACCGTCG	TCAACTTCTC	CCACGCCTGC	GGCGTGTCG	TGAAGGCGA
501	AATCGGCGTA	TTGGGCAACC	TCGAAACCGG	CGAAGCAGGC	GAAGAAGACG
551	GAGTGGGCGC	GGCAGGCAAA	CTCTCACACG	ACCAAATGCT	CACCAGCGTT
601	GAAGATGCCG	TGCGTTTCGT	TAAAGATACC	GGCGTTGACG	CATTGGCGAT
651	TGCCGTCGGC	ACCAGCCACG	GCGCATACAA	ATTCAACCGT	CCGCCACAG

```

701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGGctCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CCGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GGCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTcAGG CAGGCAAAAT CAAACCTGTT TCGTTGGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

```

g034.pep
1 MSRLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKVI NEYGNIGET YGVPVEEIVE GIKHGVKRVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

```

m034.seq (partial)
1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA wACAGCTACG GCyTGCCGGC GTTCAACGTC
151 AACAACTCG wACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCCGTC ATCGTACAGG CGAGTGCCGG TGCGCGCAA TATGCGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGCGCG CTGTCGAAGT ATTTCCACAC
301 ATCCCCGTCG TCATGCACCA AGACCACGGC GCATCACCGG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAACCTCTC CCACGCTTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAA CTTTCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GCGTGTGACG CATTTGGCTAT
651 TGCCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCCACAG
701 GCGATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

```

m034.pep (partial)
1 MSCLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE XSYGLPAFNV
51 NNIXQMRAIM EAADQVDAPV IVQASAGARK YAGAPFLRHL ILAAVEVFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

```

a034.seq
1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCGCG GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCCG ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGCGCG CTGTCGAAGA ATTTCCGCAC
301 ATCCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TTTCTCCGT GATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

```

```

451 CGTACCGTGG TTAATTTCTC CCACGCCTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TGC GTTTCGT TAAAGATACC GCGGTTGACG CATTGGCGAT
651 TGCCGTCGCG ACCAGCCACG GCGCGTACAA ATTCACCCGT CCGCCACAG
701 GCGACGTGTT GCGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CCGCTCCAGC TCCGTTCCGC AAGAATGGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CCGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG TAAAGTCAAC
901 ATCGATACCG ACTTGCGCCT TGCTTCCACC GCGCGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TCGATCCGCG CAAATATTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCTCGACC GCTACCTCGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCGGTT TCCTTGAAA AAATGGCAAA
1101 CCGTTATGCC AAGGCGAAT TGAACCAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

```

a034.pep
1  MSRLWFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51  NNLEQMRAIM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVFNSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAI AVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVRKVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL SKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

```

          10      20      30      40      50      60
m034.pep  MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAIM
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a034      MSRLWFFAAKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAIM
          10      20      30      40      50      60

          70      80      90     100     110     120
m034.pep  EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a034      EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI
          70      80      90     100     110     120

          130     140     150     160     170     180
m034.pep  QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVFNSHACGVSVEGEIGVLGNLETGDAG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a034      QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVFNSHACGVSVEGEIGVLGNLETGEAG
          130     140     150     160     170     180

          190     200     210     220     230     240
m034.pep  EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a034      EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAI AVGTSHGAYKFTRPPTGDVLRID
          190     200     210     220     230     240

          250
m034.pep  RIKEIHQALPNTHIVMH
          |||:|||||:|||||
a034      RIKEIHQALPNTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN
          250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

m034/g034

m034 . pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNVLXQMRAIM	60
g034	MSRLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNLEQMRAIM	60
m034 . pep	EAADQVDAPVIVQASAGARKYAGAPFLRLHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRLHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI	120
m034 . pep	QLGFSSVMDGSLMEDGKTPSSYEYNVNATRTVNFSSHACGVSVEGEIGVLGNLETGDAG	180
g034	QLGFSSVMDGSLLEDGKTPSSYEYNVNATRTVNFSSHACGVSVEGEIGVLGNLETGEAG	180
m034 . pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID	240
m034 . pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSVPOEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

g036 . seq

```

1  ATGCTGAAGC CGTGTGTTGGT ATACAGTGCC TGTGCGGCGG cgttgCCTGC
51  GCGGACTTCG AGCAGCAGGC GTTGCCTGCC TTCGGGCAGA TGTGCGTACC
101 AATATTCGAG CAGGGCGGAC GCAACGCCCC GTCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCTGCCGT CTTTTCCTCG AAGGAAAACC TGTTCGGACG
251 GCGAAACAAG CGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGTAT CGAGCGCGGC CAGTGCAGGC CAGTCGGACG GTGAGGCTGG
351 GCGGATGTTC ATGTTCTGTC CTTCCGTTCC GCCTGTTCTT TGGCAGTCAG
401 GCGGATTTTG TTGCGGACGT AGAGCAGTTC GCGGTGTGCC GCGCCAGTTG
451 CCGGATAGCC GCCGCCGAGG GCGAGCGCGA GAAAATCGGC GCGGTCGGC
501 ATATCGGTTT TGCCTGAGAA GGGCGGACGG TTTTCCAGTG CGAACGCACT
551 GCCGATGCCG TCTGAAAAGA CGTACCCCTC GGGGAGGGCA ATGTCTGCCG
601 CCCTACCGAC TTGATAATCG CTCAAACGGC GCGGTTTCAG CGTGTGCAAC
651 CACGCATAAA AACTTTCGCC CATACGCGCG TCCGAGCGG CGAGTATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGTG GGGATGCCGA
751 TTAAAGGCGT GTCGAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

g036 . pep

```

1  MLKPCLVYSA CAAALPARTS SSRRCVPSGR CAYQYSSRAD ATPRRRHSGA
51  VAIRCSSDSS GRFCQTIKAA ILPSFSARKT CSDGETSADS NWRVCVHADGL
101 QTVSSAASAA QSDGEAGRMF MFVPSVPPVL WQSGRFCCGR RAVRRVPRQL
151 RDSRRRGRAR ENRRRSAYRV CLRRADGFPV RTHCRCLKR RTPRGGQCLP
201 PYRLDNRSNG GGSACRTTHK TLRPYARPQR RVCSFAAAAA RRRHRAWGCR
251 LKACRTALPN LAPRRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

m036 . seq

```

1  ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCCTGC
51  ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCCG . CGT CTTTTCCTCG AAGGAAAACC TGTTCGGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGCAGC CAGCTCCTCA CAATCGGCAC AAACGGCACG

```

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTCT GCCTGTTCTT TGGCAGTCAG
401 GGCGATTTTG TTGCGGACGT AGAGCAAACC GGCGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA AACTTTCGCC CATACGAGCG TCCGTAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGGT ATCAAACGGC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

m036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMR ESRRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

a036.seq

```

1 ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCTGTC
51 ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GGCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGCGCGCA ATCCCGCCGT CTTTTCGCGC AAGGAAAACC TGTTCCGACG
251 GCGAAACAGC TCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCAGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTT ACAGGCGCGC CCTCCGTTCC GCCTGTTCTT TGGCAGTCAA
401 GGCGATTTTG TTGCGGACGT AGAGCAGCTC GGCGTGTGCC GCAGCGACGG
451 CGGGAAAACC GCCTTCAGCC GCCAGATTGA GGAAGTCGCG GCGGTCGCGC
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGCG CGAACGCATT
551 GCCGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGTCTGCCG
601 CCCGACCGAC CTGATAATCG CTCAAACGGC GGCAGTTCAG CGTGTGCAAC
651 CATGCATAAA AACTTTCGCC CATACGTGCG TCCGAGCGCG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGAGT ATCAAACGGC GTTGCCAAAC CTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

a036.pep

```

1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRRFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFPA RTHCRCLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

m036/a036 85.6% identity over a 270 aa overlap

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRVCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS					
a036	MLKPCAVYSACAAVLPARTSSSRRCVSSGRVCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
m036.pep	GRFCQTIKAAIPXSFSAKRTCSNRCVHADGLQTASSAASSSQSAQTARRMF					
a036	GRFCQTIKAAIPPSFSAKRTCSNRCVHADGLQTASSAASAAQSAXTARRMF					
	70	80	90	100	110	120

	130	140	150	160	170	180
m036.pep	130	140	150	160	170	180
a036	130	140	150	160	170	180
m036.pep	190	200	210	220	230	240
a036	190	200	210	220	230	240
m036.pep	250	260	270			
a036	250	260	270			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 036 shows 74.9% identity over a 271 aa overlap with a predicted ORF (ORF 036.ng) from *N. gonorrhoeae*:

m036/g036

	10	20	30	40	50	60
m036.pep	10	20	30	40	50	60
g036	10	20	30	40	50	60
m036.pep	70	80	90	100	110	120
g036	70	80	90	100	110	120
m036.pep	130	140	150	160	170	180
g036	130	140	150	160	170	180
m036.pep	190	200	210	220	230	240
g036	190	200	210	220	230	240
m036.pep	250	260	270			
g036	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 133>:

m036-1.seq

```

1  ATGCTGAAGC CGTGC GCCGT GTACAGTGCC TGTGCGCGG TGTGCTGCTG
51  ACGGACTTCG AGCAGCAGGC GTTGC GTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GCGGCGCGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTCTT GCCAAACGAT
201 AAAGGCGGCA ATCCCGCCGT CTTTTCCTGC AAGGAAAACC TGTTCCGACG
251 GCGAAACCAG TCGGACTCA AATTGGCGTT GCGTCCATGC GGACGGGTTG
301 CAGACGGCAT CGAGTGGCGC CAGCTCCTCA CAATCGGCAC AAACGGCAGC

```

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTCC GCCTGTTCTT TGGCAGTCAG
401 GCGGATTTTG TTGCGGACGT AGAGCAAACC GCGGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCCA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA AACTTTCGCC CATACGAGCG TCCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

```

m036-1.pep
  1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
 51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMP ESRRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*

```

m036-1/g036 76.8% identity in 228 aa overlap

```

              10      20      30      40      50      60
m036-1.pep  MLKPCAVYSACAAVLPARTSSRRCVSSGRVCNQYSSRADAIIPWRRHSGAVAIRCSSDSS
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g036        MLKPCLVYSACAAALPARTSSRRCVPSGRCAQYSSRADATPRRRHSGAVAIRCSSDSS
              10      20      30      40      50      60

              70      80      90      100     110     120
m036-1.pep  GRFCQTIKAAIPPSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g036        GRFCQTIKAAILPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF
              70      80      90      100     110     120

              130     140     150     160     170     180
m036-1.pep  TGALSVRPVLWQSGRFCCGRANRRVRHGRQDNRPWLPMPRESRRQSAYPVCLRTAELLPA
              : || ||||| ||||| ||||| : ||| : ||| : ||| : ||| : |||
g036        MFPVSPVPVLWQSGRFCCGRRAVRVRPQLRDSRRRGRARENRRRSAYRVCLRRADGFPV
              130     140     150     160     170     180

              190     200     210     220     229
m036-1.pep  RTRCLCRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERPX
              ||| ||||| ||| : ||||| ||||| ||||| ||||| ||||| |||||
g036        RTHCRCLKRRTPRGQCLPPYRLDNRSNGGGSACRTHKTLRPYARPQRRVCSFAAAAA
              190     200     210     220     230     240

g036        RRRHRAWGCRLKACRTALPNLAPRRCRYAVRX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

```

g038.seq
  1 ATGACTGATT TCCGCCAAGA TTTCCTCAAA TTCTCCCTCG CCCAAATGT
 51 TTTGAAATTC GCGGAATTTA CCACCAAAGC CGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTC AACGACGGCG CGTCCACGCT GCAACTGGCA
151 AAATTCATAG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCCTACAAAG GCATTATTTT GGCGGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC GCGGCGAAGG CGGCGTGTG GTGCGGCGCG CGCTTAAAGG
351 GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACCGG
401 AATCAATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGCG CGGTGTCGCC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTAAATGTG CCGCCGTTCA
501 GGAAGTGGA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTGTG TATCCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCGTCC GCACCTACCG CCGGCAGTAC GCGGTAGAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
  1 MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
 51 KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101 AKDRGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151 IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201 EPVRTYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
  1 ATGACCGATT TCCGCCAAGA TTCTCTCAAA TTCTCCCTCG CCCAAAATGT
 51 TTTGAAATTC GCGCAATTTA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151 AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGTCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCCT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351 GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451 ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501 GGAAGTGGAA AAACAATACG GCTGCCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTGTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
  1 MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51 KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101 AKDHGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151 IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201 EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
  1 ATGACCGATT TCCGCCAAGA TTCTCTCAAA TTCTCCCTCG CCCAAAATGT
 51 TTTGAAATTC GCGCAATTTA CCACCAAGC CGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151 AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGCGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCCT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351 GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501 GGAAGTGGAA AAACAATACG GCTGCCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTGTGTT TATTCTGTTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601 GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
  1 MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51 KFYAQSIIES GIRFDMFLGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101 AKDHGEGGVL VGAPLKGRVL IIDDVISAGT SVRESIKLIE AEGATPAGVA
151 IALDRMEKGT GELSAVQEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201 EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```

      10      20      30      40      50      60
m038.pep MTDFRQDFLK FSLAQNVLFK GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA KFYAQSIIES
```

```

|||||
a038      MTDFRQDFLKFSLAQNVLKFGFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
           10      20      30      40      50      60

           70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           |||||||
a038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           70      80      90      100     110     120

           130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVKQYGLPVAPI
           |||||||
a038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVKQYGLPVAPI
           130     140     150     160     170     180

           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           |||||||
a038      ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng)

from *N. gonorrhoeae*:

m038/g038

```

           10      20      30      40      50      60
m038.pep  MTDFRQDFLKFSLAQNVLKFGFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
           |||||||
g038      MTDFRQDFLKFSLAQNVLKFGFTTKAGRRSPYFFNAGLFNDGASTLQLAKFYAQSIIES
           10      20      30      40      50      60

           70      80      90      100     110     120
m038.pep  GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           |||||||
g038      GIRFDMFLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
           70      80      90      100     110     120

           130     140     150     160     170     180
m038.pep  IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVKQYGLPVAPI
           |||||||
g038      IIDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQVEVKQYGLPVAPI
           130     140     150     160     170     180

           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           |||||||
g038      ASLNDLFILLQNNPEFGQFLEPVRTYRRQYGVEX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

g039.seq

```

1  ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51 CGAGAAAACA TCATGCCCGC CTGTTTCTGT CCGCACTGCA AAACCCGCCT
101 CTGGGTCAAA GAAAcccagC TCAAcgtCgC ccaagGCTTC GTCGTCTgcc
151 aaAAAtgcga agGGCTgttt aaAgccaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaaagt gtttcgggat gTcaaaCTCG

```

```

251 TCcaccgcaT cggcacgcac gccattagca aGAaacagat gtccccgcgac
301 gaaatCgccg atatacctcaa cggcgggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGCaggTT TCCGTACCGC
401 CCGCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCCT GTTCGCACTT
451 ATCGTCCTCA TTATGCAGCT TTCCTACCTC TTCATCCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

```

g039.pep
  1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSSA
 51 KNAKGCLPKP TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKKQMSRD
101 EIADILNGGT TLHDTTPATA AAAPAAAPQV SVPPARQEGF NWTIATLFAL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

```

m039.seq
  1 ATGCCGTCCG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCCTGCA AAACCCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CGnnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCT GTGACGAAAT CGCCGCGCAT CTCAACGGCG GTACAACCCA
351 GCCCGATATT CCGCCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCCCGCGCGC CCGCCCGGTC AGGATGGGTT CAACTGGACG
451 ATTGCAACCC TGTTTGCCCT TATCGTCCTC ATTATGCAGC TTCTCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

```

m039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPPXXXXXX
 51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LGGTTQPD I PPATAATPAA APQVTVPPAA PARQDGFNWT
151 IATLFLALIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

```

a039.seq
  1 ATGCCGTCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
 51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCCTGCA AAACCCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CCAAGGCTTC GTCGTCTGCC
151 AAAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCACGAAA
201 GAACCCATAT TCAACGATT. TGCCCCGAAGC TGTTTCGGAT GTCAAACCTCG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCCGCC
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGGTTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTCC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

```

a039.pep
  1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSSA
 51 KNAKECLPKP TIWQARKNLY STIXPEAVSD VKLVHRIGTS AIGKKQISR
101 EIAGILNGGT TQPDIPPATA ATPAAAPQVT VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLVIL*

```

m039/a039 79.4% identity over a 170 aa overlap

```

          10      20      30      40      50      60
m039.pep  MPSEPPYASDGIKPDTHEEIPCPPVSAPTA KPVSGSKKPN SMSPPXXXXXXXXXXXXXXXXX
          |||
a039      MPSEPPYASDGIKPDTHEEIPCPPVSAPTA KPVSGSKKPN SMSPKASSSAKNAKECLPKP

```

	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD				
a039	TIWQARKNPYSTIX----	PEAVSDVKLVHRIGTSAIGKKQISRDEIAGILNGGTTQPD				
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAATPAAAPQVTVP	PPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
a039	PPATAATPAAAPQVTVP	PPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
	120	130	140	150	160	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 039 shows 60.8% identity over a 171 aa overlap with a predicted ORF (ORF 039.ng) from *N. gonorrhoeae*:

m039/g039

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPD	THEEIPC	PPVSAPTAKPV	SGSKKPN	SMPXXXXXXXXXXXXXXXXX	
			:		:	
g039	MPSEPPAASDGIKPT	HTTEKTS	CPPVSVRTAK	PASGSKKPS	STSPKASSAKNAKGCLKPK	
	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD				
	:	:	:			
g039	TIWQARKNLYSTIG----	PKLFRDVKLVHRIGTHAISKQMSRDEIADILNGGTTLHDT				
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAAT-PAAAPQVTVP	PPAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
		:		:		
g039	PPATAAAAPAAAPQVSV	PPA---RQEGLNWTIATLFALIVLIMQLSYLFILX				
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 147>:

g040.seq

```

1  ATGAACGCGC CCGACAGCTT TGTCGCCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGGCA CGACACTGGT CGCCGGCATA GAcggCCGCC
101 TGCTCGAAGG CGGCACCTTA AATAAGCTCG CCGCCGACAT CGGGCTGTG
151 TCGCAACTGG GCATCCGACT CGTCCTCATC CACGGCGCGT ACCACTTCCT
201 GAcggCCTC GCGCGCCGCG AAGgccGCAC GCCGCATTAT TGCCGgggtt
251 tGCGCGTTAC CGACGaAACc tcGctcgGAC AGGCGCAGCA GtttGCCGGC
301 AccgTCCGCA GCCGTTTGA agcCGCATTG tgcggcagCG tttcaggatt
351 cgcgCGCGCG CCTTCCGTCC CGCTCGTAtc gggcaacttc ctgacCGCCC
401 GTCcgatggg cgtgattgac ggaACCGata tggaatacgc ggggggttatc
451 cgcaaaaccg ACACCGCCGC CCTCCGTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGATG CCGCCGCTCG GGCATTCTTA CCGCGGCAAA ACCTTCAATC
551 TCGATATGGT GCAGGCCGCC GCTTCCGTCT CCGTCTCGCT TCAGGCCGAA
601 AAACTCGTTT ACCTGACCTT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GTCGCGCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGCCAGCGA AACCCGACGA CTGATTTCGT CCGCCGTGTC CGCGCTCGAA
751 GCGCGCGTGC ATCGGTCCA AATCCTCAAC GGGGCCGCCG ACGGCAGCCT
801 GCTGCAAGAA CTCTTACCCG GCAACGGCAT CGGCACGTCC ATTGCCAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCGACAT CCCGCACATC
901 GCGGCCCTCA TCCGCCCGCT GGAAGAACAG GCGGTCTAT TGCACCGCAG
951 CCGGAATAC CTCGAAAACC ACATTTCGGA ATTTTCATC CTCGAACACG

```

```

1001 ACGGCGACCT GTACGGCTGT GCCGCACTCA AAACCTTTGC CGAAGCCGAT
1051 TCGGCGGAAA TGCCTGCTT TGCCTGCTCG CCGCAGGCAC AGGACGGCGG
1101 ctACGGCGGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151 GCATAAGCAG GCTGTTTCGA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGCTGCCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGAAACCC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

g040.pep

```

1 MNAPDSFVAH FREAAPYIRQ MRGTTLVAGI DGRLLGGTIL NKLAADIGLL
51 SQLGIRLVLI HGAYHFLDRL AAAQGRTPHY CRGLRVTDET SLGQAQQFAG
101 TVRSRFEAL CGSVSGFARA PSVPLVSGNF LTARPMGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWM PPLGHSYGGK TFNLDMVQAA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLSAQEAQSL AEHAASETRR LISSAVAALAE
251 GGVHRVQILN GAADGSLLEQ LFTRNGIGTS IAKEAFVSIR QAHSQDIPHI
301 AALIRPLEEQ GVLLHRSREY LENHISEFSI LEHGDGDLGC AALKTFAEAD
351 CGEIACLAVS PQAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNGRNPHIL VRRLLHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

m040.seq

```

1 ATGAGCGCGC CCGACCTCTT TGTGCGCCAC TTCCGCGAAG CCGTCCCCTA
51 CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAAGCTCG CCGCCGACAT CGGGCTGTTG
151 TCGCAACTGG GCATCAGGCT CGTCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCCGCTC AAGGCCGCGC GCCGCATTAT TGCCGGGGCT
251 TCGCGGTTAC CGACGAAACC TCGCTCGAAC AGGCGCAGCA GTTTGCCGGC
301 ACCGTCCGCA GCCGTTTGA AGCCGCATTG TGCGGCAGCG TTTCCGGGTT
351 CGCGCGCGCG CCTTCCGTCC CGCTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGAATACGC GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCCGCTCG GACATTCTTA CAGCGGCAAG ACCTTCTATC
551 TCGATATGCT TCAAACCGCC GCCTCCGCGC CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTT ACCTGACCTT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG CGGGAACACG
701 CCGGCGGGCA AACCGGACGG CTGATTTCGT CCGCCGAAC CTTCACCCGC
751 AACGGCATCG GCACGTCCAT TGCCAAAGAA GCCTTCGTCT CCATCCGGCA
801 rGCGCAywgG G.CGACATCC CGCACATCGC CGCCCTCATC CGCCCGCTGG
851 AAGAACAGGG CATCCTGCTG CACCGCAs.c GCGAATACCT CGAAAACCAC
901 ATTTCCGAAT TTCCATCCT CGAACACGAC GGCAACCTGT ACGGTTGCCG
951 CGCCCTGAAA ACCTTTGCCG AAGCCGATTG CGGCGAAATC GCCTGCCTTG
1001 CCGTCTCGCC GCag.cACAG GACGGCGGCT ACGGCGAACG CnTGCTTGCC
1051 CACATTATCG ATAAGGCGCG CGGCATAGGC ATAAGCAGCG TGTTGCGACT
1101 GTCCACAAAT ACCGGCGAAT GGTTCGCCGA ACGCGGCTTT CAGACGGCAT
1151 CGGAAGACGA GTTGCCCGAA ACGCGGCGCA AAGACTACCG CAGCAACGGA
1201 CGGAACTCGC ATATTCTGGT ACGTCGCTG CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

m040.pep

```

1 MSAPDLFVAH FREAVPYIRQ MRGKTLVAGI DDRLLEGDTL NKLAADIGLL
51 SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFYLDMLQTA ASAAVSLQAE
201 KLVYLTLSDG ISRPDGTAE TLSAQEAQSL AEHAGGQTRR LISSAEFLTR
251 NGIGTSIAKE AFSVIRQAHX XDIPHIAALI RPLEEQGILL HRXREYLENH
301 ISEFSILEHD GNLYGCAALK TFAEADCGEI ACLAVSPQXQ DGGYGERXLA
351 HIIDKARGIG ISRLFALSTN TGEWFAERGF QTASEDELPE TRRKDYRSNG
401 RNSHILVRRL HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

a040.seq

```

1  ATGATCGTGC CCGACCTCTT TGTGCCCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAAGTTCG CCGCCGACAT CCGGCTTTTG
151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCGCGC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TCGCGGTTAC CGACGAAACC TCGCTCGAAC AGGCGCAGCA GTTTGCCGGC
301 ACCGTCCGCA GCCGTTTTGA AGCCGCATTG TCGCGCAGCG TTTCCGGGTT
351 CGCGCGCGCG CCTTCCGTCC CGTCGTATC GGGCAACTTC CTGACCGCCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGGAAATACG GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTC CAACTCGACG CCGGCAATAT
501 CGTCTGGCTG CCGCCGCTCG GACATTCCTA CAGCGGCAAG ACCTTCCATC
551 TCGATATGCT TCAAACCGCC GCCTCCGTCG CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTT ACCTGACCCT TTCAGACGGC ATTTCCCGCC CCGACGGCAC
651 GCTCGCCGTA ACCCTCTCGG CACAGGAAGC GCAATCGCTG CGGGAACACG
701 CCGGCGGCGA AACGCGACGG CTGATTTCTG CCGCCGTTGC CGCGCTCGAA
751 GGCGGCGTGC ATCGCGTCCA AATCCTCAAC GGAGCCGCGG ACGGCAGCCT
801 GCTGCAAGAA CTCTTCAACC GCAACGGCAT CGGCACGTCC ATTGCCAAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCGACAT CCGGCACATT
901 GCGGCCCTCA TCCGCCCGCT GGAAGAACAG GGCATCCTGC TGCACCGCAG
951 CCGCGAATAC CTGAAAACC ACATTTCCGA ATTTTCCATC CTGAAACACG
1001 ACGGCAACCT GTACGGTTGC GCGGCCCTGA AAACCTTTGC CGAAGCCGAT
1051 TGCGGCGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGG
1101 CTACGGCGAA CGCTGCTTG CCCACATTAT CGATAAGCGG CGCGGCATAG
1151 GCATAAGCAG GCTGTTGCA CTGTCCACAA ATACCGGCGA ATGTTTGGCC
1201 GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGTTGCCCG AAACGCGGCG
1251 CAAAGACTAC CGCAGCAACG GACGGAATC GCATATTCTG GTGCGTCGCC
1301 TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 152; ORF 040.a>:

a040.pep

```

1  MIVPDLFVAH FREAAPYIRQ MRKTLVAGI DDRLLEGDTL NKFAADIGLL
51  SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFHLDMLQTA ASVAVSLQAE
201 KLVYLTSLDG ISRPDGTLAV TLSAQEAQSL AEHAGGETRR LISSAVAAL
251 GGVHRVQILN GAADGSLLOE LFTRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GILLHRSREY LENHISEFSI LEHDGNLYGC AALKTFEAD
351 CGEIACLAVS POAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNRNSHIL VRRLHR*

```

m040/a040 91.5% identity in 436 aa overlap

	10	20	30	40	50	60
m040.pep	MSAPDLFVAHFREAVPYIRQMRKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI					
a040	MIVPDLFVAHFREAAPYIRQMRKTLVAGIDDRLLEGDTLNKFAADIGLLSQLGIRLVLI					
	10	20	30	40	50	60
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
a040	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
	70	80	90	100	110	120
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
a040	HGARHFLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
	130	140	150	160	170	180
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPLGLHSYSGK					
a040	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPLGLHSYSGK					
	130	140	150	160	170	180
m040.pep	TFYLDMLQTAASAASVSLQAEKLVYLTSLDGISRDPDGTLAETLSAQEAQSLAEHAGGQTRR					
a040	TFHLDMLQTAASVAVSLQAEKLVYLTSLDGISRDPDGTAVTSLAQEAQSLAEHAGGETRR					
	190	200	210	220	230	240
m040.pep	TFYLDMLQTAASAASVSLQAEKLVYLTSLDGISRDPDGTLAETLSAQEAQSLAEHAGGQTRR					
a040	TFHLDMLQTAASVAVSLQAEKLVYLTSLDGISRDPDGTAVTSLAQEAQSLAEHAGGETRR					

		190	200	210	220	230	240
m040.pep		<div> <div>250260270</div> <div>LISSA-----ELFTRNGIGTSlAKEAFVSIRQAHXXDIPHI</div> <div> </div> </div>					
a040		<div> <div>250260270280290300</div> <div>LISSAVAALEGGVHRVQILNGAADGSLQLFTRNGIGTSlAKEAFVSIRQAHSGDIPHI</div> <div> </div> </div>					
m040.pep		<div> <div>280290300310320330</div> <div>AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS</div> <div> </div> </div>					
a040		<div> <div>310320330340350360</div> <div>AALIRPLEEQGILLHRSREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS</div> <div> </div> </div>					
m040.pep		<div> <div>340350360370380390</div> <div>PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY</div> <div> </div> </div>					
a040		<div> <div>370380390400410420</div> <div>PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY</div> <div> </div> </div>					
m040.pep		<div> <div>400410</div> <div>RSNGRNSHILVRRLHRX</div> <div> </div> </div>					
a040		<div> <div>430</div> <div>RSNGRNSHILVRRLHRX</div> <div> </div> </div>					

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 040 shows 88.3% identity over a 436 aa overlap with a predicted ORF (ORF 040.ng) from *N. gonorrhoeae*:

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIQMRGKTLVAGIDRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
g040	MNAPDSFVAHFREAAAPYIQMRGTTLVAGIDGRLLLEGDTLNKLAADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAAQGRTPHYCRGLRVTDDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA	120
g040	HGAYHFLDRLAAAQGRTPHYCRGLRVTDDETSLGQAQQFAGTVRSRFEAALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPLGHSYSGK	180
g040	PSVPLVSGNFLTARPMGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYSGK	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRDPDGLAETLSAQEAQSLAEHAGGQTRR	240
g040	TFNLDMVQAAASVAVSLQAEKLVYLTLSDGISRDPDGLAETLSAQEAQSLAEHAASETRR	240
m040.pep	LISSA-----ELFTRNGIGTSLIAKEAFVSIRQAHXXDIPHI	276
g040	LISSAVAALEGGVHRVQILNGAADGSLQLQELFTRNGIGTSLIAKEAFVSIRQAHSGDIPHI	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS	336
g040	AALIRPLEEQGVLLHRSREYLENHISEFSILEHDGDLYGCAALKTFAEADCGEIACLAVS	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRKKDY	396
g040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRKKDY	420
m040.pep	RSNGRNSHILVRRLHRX 413	
g040	RSNGRNPHILVRRLHRX 437	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
1  ATGAGTTCGC CCAAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGCCT
51  GATTACCGCC GCCGCTTCG TGCGCGAACC GCAAAGCATC GGTGCGCTGG
101 TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151 GGTTCAGT  GGACGGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201 CAAACGCCGG CTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCACTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301 CATCCCGCCC ACGCGCTCAA ATTCTACGCC AACTGCGCG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCCGAC AACTCGCCT GCGTGTGCT GTTTTGTAAA
451 GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
1  MSSPKHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQRESAD KLACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGACT
51  GATTACTGCC GCCGCTTCG TGCGCGAACC GCAAAGCATC GGC GCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGT  GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AACTGCGCG AAACCTCCGC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCCAACGCGA ATCCGCCGAC GAACTCGCCT GCGTCTTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
1  ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCRRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYSPDGGGHT GNGTQRESAD ELACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
1  ATCAGTTCGC CCGAACACAT CGGCTTGCAG GCGGCAGCA ACGGCGGACT
51  GATTACTGCC GCCGCTTCG TGCGCGAACC GCAAAGCATA GGC GCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGT  GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCGG TTGGGCGAAT TGTGCGCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AACTGCGCG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CGCAGCGCGA AGCCGCCGAC GAACTCGCCT GCGTGTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
1  ISSPEHIGLQ GGSNGGLITA AAFVREPQSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCRRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSPQSW LYSPDGGGHT GNGTQREAAD ELACVLLFLK
```

151 EFLG*

m041/a041 98.7% identity over a 154 aa overlap

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
a041	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSW					
a041	PQKYEVCKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAPQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
a041	LYSPDGGGHTGNGTQREAADELACVLLFLKEFLGX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 041 shows 96.8% identity over a 154 aa overlap with a predicted ORF (ORF 041.ng) from *N. gonorrhoeae*:

m041/g041

	10	20	30	40	50	60
m041.pep	ISSPEHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
g041	MSSPKHIGLQGGSNGLITAAAFVREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041.pep	PQKYEVCKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAQSW					
g041	PQKYEACKRRLGELSPYHNLSGDIDYPPALITTSLSDDRVPAPAHALKFYAKLRETSAPQSW					
	70	80	90	100	110	120
	130	140	150			
m041.pep	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
g041	LYSPDGGGHTGNGTQRESADKLACVLLFLKEFLGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 159>:

g041-1.seq

```

1  ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCG CGCGCACTTT CAGACGGCAT TTTGAATCAA
151 ATGCAGGACA CGCGGCAGAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAGAAATG CGGAATATCC GAAGGGCGTG TACCGCATGT
251 GTACGGCGGC GACCTACCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTCGATGA GTTGCTCGGC GACGATGTGT ATTTGGGCGG
351 CGTGTCGCAC TTGGTGGAGC AGCCCAACCG CGCGCTGCTG ACTTTGAACA
401 AATCGGGCGG CGATACGGCG TATACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAATTGGTAG AGGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAAG TGTGGCTGGT GGAACGCGGC

```

```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCG
751 TCCGAAGGCG GGGCGAAACC GTTGAACCTG CCTAATGATT GCGATGTGGT
801 CGGCTATCTG GCGGGACATC TTTTGCTGAC GCTGCGCAAG GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CCGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAATGT ACAAGGCCGT CTGAAAGCGT GCGGTTTTCG CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACCTGGTTTA TCTTGCCGCC AGCGATTTC A
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAC TGACC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGTT TCAGACGGCA TCGAAGTGC
1251 GCAGTTTGGG GCGGTGTCGT CCGACGGCGA ACGATTTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACACGCCGA CCTAGTCTA TGCTTACGGA
1351 GGTTCGCGCA TTCCTGAATT GCCGATTAT CTGGGCAGCG TCGGCAAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTGTATT GGCAACATC CGCGGCGGCG
1451 GAGAATTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAAACAC
1501 AAAAGCGTTG ATGATTTGTT GGCAGTCGTG CGTGATTTGT CCGAACGCGG
1551 CATGAGTTCG CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGCGGCGC
1601 TGATTACCGC CGCCGCTTTC GTGCGCGAAC CGCAAAGCAT CGGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGATC CGTTATCCCG TGCTGTCCCG
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGCAGAAA TACGAAGCCT
1751 GCAAACGCGG GCTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCACT CATTACCACC AGCCTCAGCG ACGACCGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CAACTCGCC TCGGTGTTGC TGTTTTGTAA
2001 AGAATTTTTC GGATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1 MKSYDPYRHH FENLDSAEQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51 MQDTRQIPFC QEHRARMYHF HQNAEYPKGV YRMCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLNKSGGDTA YTLEVDLEAG
151 ELVEGGFHFH AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 SEGGAAPLNL PNDCDVVGYL AGHLLLTLRK DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADSK
351 WQEAELPHLP SGALEMTDQF WGGDVVYLA SDFTTPLTLF ALDLNVMELT
401 VMRLQPQQFV SDGIEVRQFW AVSSDGERIP YFHVGNNAAP DTPTLVYAYG
451 GFGIPELPHY LGSVGKYWLE EGNFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV RDLSEGRMSS PKHIGLQGG NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPALITT SLSDDRVHPA HALKFYAKLR ETSFQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1 ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGGCG CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTGACGCA ATTGCTTGGC GACGATGTGT ATTTGGGCGG
351 CGTGTGCGAC TTGGTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATTGGGCAG CGATACGGCG TACACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAGTTGGTCG AAGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCTGTGTAT CAAATCGGCG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ATCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AAACCTATTT GCGGGTCTCA

```

```

751  GCCGAAGGCG AGGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTGGT
801  CCGCTATCTG GCGGGGCATC TTTTGCTGAC GCTGCGCAAG GACTGGAACC
851  GCGCGAACCA AAGCTATCCG AGCGGCGCGC TGGTGGCGGT GAAGCTGAAT
901  CCGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951  GGCATTGGAA AGCGTGGAAG CGACCAAGCG TTTTGTGGTG GCGAGCCTGT
1001 TGGAGAACGT ACAAGGCCGT CTGAAAGCAT GCGGTTTGC CGACGGCAAA
1051 TGGCAGGAAG TCGAATTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCT TGGGGCGGCG ACGTGGTTTA CCTTGCCGCC AGCGATTTCa
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAGTGAAC
1201 GTCATGCGCC GCCAGCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCGAATT GCCGATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAAG GAGGCAATG CCTTTGTATT GGCGAACATC CGCGCGCGCG
1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAACAT
1501 AAAAGCGTTG ATGATTATT GGCAGTCGTG CGCGATTGT CCGAACGCGG
1551 TATCAGTTCC CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCTTC GTGCGCGAAC CGCAAAGCAT CGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCGG GTTGGGCGAA TTGTCGCGCT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCAATCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCCG
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CGAACTCGCC TGCGTCTTGC TGTTTTGA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 162; ORF 041-1>:

m041-1.pep

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLENDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKG VYRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSLKLGSDTA YTLEVDLEAG
151 ELVEGGFHP AGKNHVSWRD ENSVWVCPAW NERQLTQSGY PREVWLVERG
201 KSFEESLPVY QIGEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLRVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRK DWNRRANQSY SGALVAVKLN
301 RGELGAAQLL FAPDETQALE SVETTKRFV ASLLENVQGR LKAWRFADGK
351 WQEVLPRLP SGALEMTDQP WGGDVVYLAA SDFTPPLTLF ALDLNVMELT
401 VMRRQPQFD SDGINVQFW TTSADGERIP YFHVGNKNAAP DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGFEFPRW HQAAQGISKH
501 KSVDDLLAVV RDLSEGISS PEHIGLQGS NGGLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDRVHPA HALKFYAKLR ETSAQSWLYS PDGGGHTGNG
651 TQRESADELA CVLLFLKEFL G*

```

m041-1/g041-1 94.6% identity in 671 aa overlap

	10	20	30	40	50	60
m041-1.pep	MKSYPDPYRHFENLDSAETQNFAAEANAETRARFLENDKARALSDGILAQ					
	: : : : :					
g041-1	MKSYPDPYRHFENLDSAETQNFAAEANAETRARFLNNDKARALSDGILNQMQDTRQIPFC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m041-1.pep	QEHRARMYHFHQDAEYPKG VYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
	: : : : :					
g041-1	QEHRARMYHFHQNAEYPKG VYRMCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m041-1.pep	LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHPAGKNHVSWRDENS VWVCPAW					
	: : : : :					
g041-1	LVEQPNRALLTLNKGSDTAYTLEVDLEAGELVEGGFHPAGKNHVSWRDENS VWVCPAW					
	130	140	150	160	170	180
	190	200	210	220	230	240
m041-1.pep	NERQLTQSGYPREVWLVERGKSFEESLPVYQIGEDGMMVN AWRYLDPQGS PIDLIEASDG					
	: : : : : :					

```

g041-1      DERQLTESGYPREVWLVERGKSFEESLPAYQIDKGAMMVNAWRYLDPQGSPIDLIEASDG
              190      200      210      220      230      240

              250      260      270      280      290      300
m041-1.pep  FYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLLTLRKDWNRANQSYPSGALVAVKLN
              |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|
g041-1      FYTKTYLQVSSEGGAKPLNLPNDCDVVGYLAGHLLLTLRKDWNRANQSYPSGALVAVKLN
              250      260      270      280      290      300

              310      320      330      340      350      360
m041-1.pep  RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADGKWQEVELPRLP
              |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|
g041-1      RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGRKAWRFADSKWQEAELPHLP
              310      320      330      340      350      360

              370      380      390      400      410      420
m041-1.pep  SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTVMRRQFQQFSDGINVQQFW
              |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|
g041-1      SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTVMRLQFQQFVSDGIEVRQFW
              370      380      390      400      410      420

              430      440      450      460      470      480
m041-1.pep  TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI
              :|:|:|:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|
g041-1      AVSSDGERIPYFHVGNKNAAPDPTPLVYAYGGFGIPELPHYLGSVGKYWLEEGNAFVLANI
              430      440      450      460      470      480

              490      500      510      520      530      540
m041-1.pep  RGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF
              |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|
g041-1      RGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSESGMSSPKHIGLQGGSNGLITAAAF
              490      500      510      520      530      540

              550      560      570      580      590      600
m041-1.pep  VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG
              |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|
g041-1      VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYACKRRLGELSPYHNLSDG
              550      560      570      580      590      600

              610      620      630      640      650      660
m041-1.pep  IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADELA
              |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:| |||||:|:|:|
g041-1      IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADKLA
              610      620      630      640      650      660

              670
m041-1.pep  CVLLFLKEFLGX
              |||||:|:|:|
g041-1      CVLLFLKEFLGX
              670

```

m041-1/P55577

sp|P55577|Y4NA_RHISN PROBABLE PEPTIDASE Y4NA >gi|2182536 (AE000086) Y4na [Rhizobium sp. NGR234] Length = 726

Score = 370 bits (940), Expect = e-101

Identities = 217/682 (31%), Positives = 331/682 (47%), Gaps = 22/682 (3%)

Query: 2 KSYDPYRHFENLDSAETQNFAAEANAETRARFLENDKARALSDGILAQDTRQIPFCQ 61
 K DP + +D + + N T + ++ + L LQ T +I
 Sbjct: 42 KDASDPRAYLNEIDGDKAMTWVEAHNLSTVDKLSKDPYSEYQADALTILQATDRIASPS 101

Query: 62 EHRARMY-HFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH 120
 R M +F QD + +G++R T +YRSG P+W+ + V + G G
 Sbjct: 102 FARDGMIDNFWQDGHVQGLWRRTTWESYRSGNPQWRTILDVDALSKAEGKTWVFEGGDC 161

Query: 121 LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHPAGKNHVSWRDENSVVWCPAW 180
 L N L+ LS G D E D+ GE V+ GF P GK V+W DEN++V W

Sbjct: 162 LPPTSNLCLIRLSDGGKDADVVREFDIAKGEFVKEGFVLPEGKQSVTVVDENTIIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNAWRYLDPOGSPI 232
 ++T SGY +V+RG+S ++++ +++ E G++ ++ +D +

Sbjct: 222 TPGEVTS SGYAYVTKVVRKQSLDQAVEIFRGQKKDVS AERGLRDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDNWRANQS-YPS 291
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFFNTELA FYPNGH---PDTRKVVLP LPTTAVFSGYKQQA IYWLKSDWTS AKGT V FHN 337

Query: 292 GALVAVKLN R GELGAAQL----LFAPDETQALESVETTKRFVVASLLENVQGR LKAWRFA 347
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAIIAFDLKAALADPARVEPLVLFMPNEHQSVAGTTQTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKWQVEVLPRLPSGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQ 407
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KGGWSSFKLALPENSTLSLTSSDDESQ L FVSEGFLEPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFDS DGINVQQFWTTSADGERIPYFHVGNKNAAP---DMPTLVYAYGGFGIPELPHYL GSI 464
 +FD+ G+ QQFW TS DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGTKVPYFLVARKDV KLDGNTPTILYAYGGFQIPMQPSYSAVL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAQGISKHKSVDDLAVVRDLSERGISSPEHI 524
 GK WLE+G A+ LANIRGGGEFGP+WH A ++ + DD AV +DL + ++S H+

Sbjct: 518 GKLWLEKGGAYALANIRGGGEFGPKWH DAGLKTNRQRYDDFQAVAQDLIAKKVTSTPHL 577

Query: 525 GLQGSNGGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEV C 584
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGGSNGGLLMGVQMIQRPD LWNNAVVIQVPLLDVNFTRMSAGASWQAEYGS PDD-PVE 636

Query: 585 KRRLGELSPYHNLS D GIDYPPALITTSLSDDR VHPAHALKFYAKLRETS AQSWLYSPDGG 644
 L +SPYHN+ G+ YP TS DDRV P HA K A + + Y G

Sbjct: 637 GAFLRSISPYHNKAGVAYPEFFETSTKDDR VGPVHARKMAALFEDMGLPFYYENIEG 696

Query: 645 GHTGNGTQRESADELACVLLFL 666
 GH +E A A +++

Sbjct: 697 GHAAAANLQEHARRYALEYIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1 ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAAAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAAGATG CGGAATATCC GAAAGGCGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTTTCGACGA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 CGTGTCGCAC CTGGTGGAA CAGCCCAACCG CGCGTTGTTA ACACTGAGCA
401 AATCGGGCGG CGATACCGCG TACACGCTGG AAGTGGATTT GGAAGCAGGG
451 GAGTTGGTAG AAGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCGGTGAT CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 GCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CGGCTATCTG GCCGGACATC TTTTGTGAC CTTGCGTAAA GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGGC GCAGCTTTTG TTTGCGCCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGCTG GCGAGCCTGC
1001 TGGAAAACGT ACAGGGTCGT CTGAAAGCGT GCGCTTTTAC TGATGGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CCTTGCGGCC AGCGATTTC A
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAAGTACC
1201 GTCATGCGCC GCCAGCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TTCCCGAATT GCCGCATTAT CTGGGCAGCA TTGGCAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GCGCAACATC CGCGGCGGCG

```

```

1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTATT GGCAGTCGTG AGCGATTTGT CCGAACGCGG
1551 TATCAGTTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCGG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGCTT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TGCGTGTTCG TGTTTTGTAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

```

1  MKSYDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLSKSGGDTA YTLEVDLEAG
151 ELVEGGFHFH AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRK DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPNETQALE SVETTKRFVV ASLLENVQGR LKAWRFTDGR
351 WQETELPRLP SGALEMTDQP WGGDVVYLA SDFTPLTLF ALDLNVMELT
401 VMRRQPQFD SDGINVQQFW TTSADGERIP YFHVGNKNA DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV SDSLSEGISS PEHIGLQGS NGGLITAAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQREAADELA CVLLFLKEFL G*

```

a041-1/m041-1 97.9% identity in 671 aa overlap

	10	20	30	40	50	60
a041-1.pep	MKSYPDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKARALSDGILAQ LQDTRQIPFC					
m041-1	MKSYPDPYRHFENLDSAETQ NFAAEANAET RARFLNNDKARALSDGILAQ LQDTRQIPFC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a041-1.pep	QEHRARMYHFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
m041-1	QEHRARMYHFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH					
	70	80	90	100	110	120
	130	140	150	160	170	180
a041-1.pep	LVEQPNRALLTLSKSGGDTAYTLEVDLEAGELVEGGFHFAPAGKNHVSWRDENSVMVCPAW					
m041-1	LVEQPNRALLTLSKSGGDTAYTLEVDLEAGELVEGGFHFAPAGKNHVSWRDENSVMVCPAW					
	130	140	150	160	170	180
	190	200	210	220	230	240
a041-1.pep	DERQLTESGYPREVWLVERGKSFEEESLPVYQIAEDGMMVNARWRYLDPQGS PIDLIEASDG					
m041-1	NERQLTQSGYPREVWLVERGKSFEEESLPVYQIGEDGMMVNARWRYLDPQGS PIDLIEASDG					
	190	200	210	220	230	240
	250	260	270	280	290	300
a041-1.pep	FYTKTYLQVSAEAGEAKPLNLPNDCDVVGYLAGHLLTLRKDWHRANQSYRSGALVAVKLN					
m041-1	FYTKTYLQVSAEAGEAKPLNLPNDCDVVGYLAGHLLTLRKDWHRANQSYRSGALVAVKLN					
	250	260	270	280	290	300
	310	320	330	340	350	360
a041-1.pep	RGELGAAQLLFAPNETQALESVETTKRFVVASLLENVQGR LKAWRFTDGRWQETELPRLP					
m041-1	RGELGAAQLLFAPNETQALESVETTKRFVVASLLENVQGR LKAWRFTDGRWQETELPRLP					
	310	320	330	340	350	360

	370	380	390	400	410	420
a041-1.pep	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
m041-1	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQQFSDGINVQQFW					
	370	380	390	400	410	420
	430	440	450	460	470	480
a041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
	430	440	450	460	470	480
	490	500	510	520	530	540
a041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDLLAVVSDLSESGISSPEHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSESGISSPEHIGLQGGSNGLITAAAF					
	490	500	510	520	530	540
	550	560	570	580	590	600
a041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG					
	550	560	570	580	590	600
	610	620	630	640	650	660
a041-1.pep	IDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSWLYSPDGGGHTGNGTQREAADELA					
m041-1	IDYPPALITTSLSDDRVPAPAHALKFYAKLRETSQSWLYSPDGGGHTGNGTQRESADELA					
	610	620	630	640	650	660
	670					
a041-1.pep	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					
	670					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

g042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAagcG TTCGTGCCGC ATACCAGCGC
51  GTTATCCAAC ACTTCCACGG CAGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TCGGTCGAT  GATGAAATC CAGCCGGGGT TTTTCTCTTT GATGTATTCT
151 AAGGAAACGG GCTGCCCGTG CCCTTCGTTG CGTAAAGATT CGTCCACGGG
201 CGGCAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GATTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCTGTAACCG ACAGCACCAG CCCGCGTCTC
301 TTGCCTTTGG cggCTTCGCG CTTTGGGGCG AACAGCGCGT CAATCTGCCG
351 ATTCAATTCC GCCACGCGCG CTTCTTACC GAAAATCCGC GACAGGGTCT
401 CCATCTGCTT CTCGCCGCTG GTGCGGATAT TGCGGTTGTC CACCGTCAAA
451 TCTATGgtgG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCACCCGG
501 CCGCCCGGTA ATGACAAACT GCGGATTGTG GCGGTGCAGG GATTGCGAAT
551 CGGGCTCAAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

g042.pep

```

1  MTMICLRFQA FVPHTSALSN TSTAAGPSCP MAAVRSMMKI QPGFFSLMYS
51  KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASREFA NSASICAFNS ATRASLPKIR DRVSICFSPL VRILPLSTVK
151 SMVVAFFANC SYASAGPPV MTNCGLWRCR DSQSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

m042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCGCTG GTGCGGATAT TGCCGTGTGC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CTTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

m042.pep

```

1 MTMICLRFOA FVPRTSALSX TSTAAGXSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRCR ASXSGSNSVP TVAALSNAGC
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

a042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCGGCGCC TTCCTGCCCC ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCGCTG GTGCGGATAT TGCCGTGTGC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CTTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

a042.pep

```

1 MTMICLRFOA FVPRTSALSX TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAGC
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFOAFVPRTSALSXTSTAAGXSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR					
	130	140	150	160	170	180

```

a042      |||||
          AARASLPKIRAKVSICFSPVLRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          130      140      150      160      170      180

          190      200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          |||||
a042      ASXSGSNSVPTVAALSNAGCKX
          190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

          10      20      30      40      50      60
m042.pep  MTMICLRFAQFVPRTSALSXTSTAAGXSCPMMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
          |||||:|||||
g042      MTMICLRFAQFVPHTSALSNTSTAAGPSCPMMAAVRSMMKIQPGFFSLMYSKETGCPCPSL
          10      20      30      40      50      60

          70      80      90      100     110     120
m042.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRVWANSASICAFNS
          |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDSTSPRPLPLAASRFWANSASICAFNS
          70      80      90      100     110     120

          130     140     150     160     170     180
m042.pep  AARASLPKIRAKVSICFSPVLRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          |:|||||:|||||:|||||:|||||:|||||: |||||
g042      ATRASLPKIRDVSICFSPVLRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR
          130     140     150     160     170     180

          190     200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          | |||||
g042      DSQSGSNSVPTVAALSNAGCKX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTC CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1   MTMICLRFAQ FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51  KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVTDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPV VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap

240

```

              10      20      30      40      50      60
m042-1.pep  MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
              |||||:|||||:|||||:|||||:|||||:|||||
g042         MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQPGFFSLMYSKETGCPCPSL
              10      20      30      40      50      60

              70      80      90     100     110     120
m042-1.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS
              |||||:|||||:|||||:|||||:|||||:|||||
g042         RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS
              70      80      90     100     110     120

              130     140     150     160     170
m042-1.pep  AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX
              |:|||||:|||||:|||||:|||||:|||||:
g042         ATRASLPKIRDRVSICFSPLVRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR
              130     140     150     160     170     180

g042         DSQSGSNSVPTVAALSNAGCKX
              190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

```

a042-1.seq
1  ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCC
151 AAGGAAACAG GCTGCCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCCGTAACG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGTA A

```

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

```

a042-1.pep
1  MTMICLRFOA FVPRTSALSN TSTAAGPSCP MAAVRSMMKI QSGFFSLMY
51 KETGCPCPSL RKDSSTGGRP MSPCIQLANR DCPKADTLL PVT DSTSPR
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/a042-1 100.0% identity in 173 aa overlap

```

              10      20      30      40      50      60
m042-1.pep  MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
              |||||:|||||:|||||:|||||:|||||:|||||
a042-1       MTMICLRFQAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL
              10      20      30      40      50      60

              70      80      90     100     110     120
m042-1.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS
              |||||:|||||:|||||:|||||:|||||:|||||
a042-1       RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVT DSTSPRPLPLAASRVWANSASICAFNS
              70      80      90     100     110     120

              130     140     150     160     170
m042-1.pep  AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX
              |||||:|||||:|||||:|||||:|||||:
a042-1       AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX
              130     140     150     160     170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:

```

g043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GTCGGCCCAT CAGCACTTTT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GCCTGAACGC TTCgttgaAC
101 CGTCCCGCGT ggcggtagcc gcAAAAGTGC ATcGCGGCTT GGATGGTGCT
151 GCCCGATTTCG ATGAGGGcga gcGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 GTCCGGCGAC GGTTCGCGG GTTTGCCTT TGAATAGCG TTTCAGGTAG
251 CATTCGTTCA GCCCACGCG GCGGGCGATT TCGGCGATGG TCAGCGGGCG
301 GGCGAATTCG CTGTTCAAAA TATCGGCGGC TTCGTCTATG CGCCGGCGGC
351 GGTAGCCGTT GTCGTGGCGG CGGAAGGTGA AGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

```

g043.pep
1  MVVSNQNIYA VGPSALFHIR RQKSVMPER FVEPSRVAVA AKVHRGLDGA
51  ARFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQPD AAGDFGDGQRA
101 GEFVQNIIGG FVYAPAAVAV VVAEAGEA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 177>:

```

m043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCCT CAGCACTTCT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT
151 GCCGATTTCG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAgGC
201 ATCCGGCGAC GGTTCGCGG GTTTGCCTT TGAATAGCG TTTCAGGTAG
251 CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCG TGTTCAGGA TGTGCGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

```

m043.pep
1  MVVSNQNIYA AGPSALLHIR RQKSVMPSE FVEPSRVAVA AKVHGGLDGA
51  AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AAGDFGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAEAGEAQ*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

m043/g043

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
g043	MVVSNQNIYAVGPSALFHIRRQKSVMPSEFVEPSRVAVAAKVHRLDGAARFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
g043	QPQAAQASGDGFAGLRFEIAFQVAFVQPDAGDFGDGQRAGEFAVQNIIGGFVYAPAAVAV					
	70	80	90	100	110	120
	130					
m043.pep	VVAEAGEAQX					
g043	VVAEAGEAAX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

```

a043.seq
1  ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCCT CAGCACTTCT
51  TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

```

```

151 GCCGGATTCTG ATGAGGGCGA GCGCGTGTTC CAGCCGCAGG CCGCGCAGGC
201 ATCCGGCGAC GGTTCGCGG GTTTCGCGTT TGAATAGCG TTTCAGGTAG
251 CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTCTG TGTTCAGGA TGTGCGCGG TCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
  1 MVVSNQNIYA AGPSALLHIR RQKSVMPSER FVEPSRVAVA AKVHGGLDGA
  51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
 101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
a043	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	70	80	90	100	110	120
	130					
m043.pep	VVAAEGEAQX					
a043	VVAAEGEAQX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
  1 ATGCTGCCCG ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGCGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTCAGCCC TCGATAACG GCGGTCAGCT
 201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTTCG
 251 CGGCTGCCGT AGCGCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
  1 MLPDQSVEFL PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
  51 GAAAFERFQP FDNGGQLHAV VGGLRFAAEK FFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
  1 ATGCCGTCCG ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
  51 CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
 101 CAGTTTTTCCA TGCCATTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
 151 GGTGCAGCGG CGTTTGAGCG ATTTCAGTCC TCGATGACG GCAGTCAGTT
 201 CCATGCGGTT GTTGGTGGTT TCGCTTCGC CGCCGAAAAG TTCTTTTTTCG
 251 TGGCTACCGT AGCGCAyTaa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
  1 MPSDXSVEFF PEVVVFDGLF GGGFPAVALP TVYPVFHAIF DVLRVGADDD
  51 GAAAFERFQS FDDGSQFHAV VGGLRFAAEK FFFVATVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 185>:

```
a044.seq
  1 GTGCCGTCGG ACCAGCGCGT CGAGTTCTTT CCACAAGTCG TCGTTTTTGA
 51 CGGGCTGTTT GGCAGCGGTT TTCCAGCCGT TGCCTTCCA ACCGTGTATC
101 CAGTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTGAGCG ATTTCAGTCC TTCGATGACG GCGGTCAGTT
201 CCATACGGTT GTTGGTGGTT TGCCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGCTGCCGT AGCGATTAA
```

This corresponds to the amino acid sequence <SEQ ID 186; ORF 044.a>:

```
a044.pep
  1 VPSDQRVEFF PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
 51 GAAAFERFQS FDDGGQFHTV VGGLRFAAEK FFFVAVAH*
```

m044/a044 91.0% identity over a 89 aa overlap

	10	20	30	40	50	60
m044.pep	MPSDXSVEFFPEVVVFDGLFGGGFPVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS					
a044	VPSDQRVEFFPQVVVFDGLFGGGFPVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS					
	10	20	30	40	50	60
	70	80	90			
m044.pep	FDDGSQFHAVVGGLRFAAEKFFVATVAHX					
a044	FDDGGQFHTVVGGLRFAAEKFFVAVAHX					
	70	80	90			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 044 shows 86.5% identity over a 89 aa overlap with a predicted ORF (ORF 044.ng) from *N. gonorrhoeae*:

m044/g044

	10	20	30	40	50	60
m044.pep	MPSDXSVEFFPEVVVFDGLFGGGFPVALPTVYPVFHAFDVLRVGADDDGAAAFERFQS					
g044	MLPDQSVEFLPQVVVFDGLFGGGFPVALPTVYPVFHAFDVLRVGADDDGAAAFERFQP					
	10	20	30	40	50	60
	70	80	90			
m044.pep	FDDGSQFHAVVGGLRFAAEKFFVATVAHX					
g044	FDNGGQLHAVVGGLRFAAEKFFFAA VAHX					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 187>:

```
g046.seq
  1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGC CCGCCGCGcc gCGCCTGTAT
 51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC gaATATGGAA AGGCTGCCGt TTTcGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TtcgctGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGTCGCG GGagaGCGCG AGcagcaagt cggcatcttC
351 CgcgccggcG Cgttataatg tgAAGGGGGA TGCgcgctg ccgaAAACGG
401 TTTGGacatc gaggcggctg CCTGTTTCCT GCAATGCTTT TTCGTCGATG
451 TCGATAAcg TTACGTCGTT GTTGGTGATG GCGGCAAGGT TTTGCGCGAC
```

501 GGTAGAACCT ACCTGCCCCG TGCCTAAAAT GAGGATTTTC ACGGTATGGG
551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAaT CCGC.r.sGC gCGcCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep

1 MSAMLRPTSX PXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTTGTT
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCCCGTTG CCGAAAACGG
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTGATG
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC
501 GGTAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSLE RTRAMRPGML NRSAATLQAT
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM
151 SITVTSLLMV AARFCATVEP TCPLPKMRIF TVWVAE*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSGLMVSVMPNME					
a046	MSAMLRPTSSPPRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSGLMVSVMPNME					

245

	10	20	30	40	50	60
	70	80	90	100	110	120
m046.pep	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
a046	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m046.pep	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
a046	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTIRTRSSAKRKTCNAPGQSIRPASC SVTSCSGLMVSVMPNME					
g046	MSAMLRPTSPPPRRACMMTIRTRSSAKRKTCNAPGQSIRPASC SVTSCSGLMVSVMPNME					
	10	20	30	40	50	60
	70	80	90	100	110	120
m046.pep	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
g046	RLPFSLFSSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m046.pep	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
g046	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

1	ATGGTCATCA	TACAGGCGcg	gcGCGGCGGG	CTGCTTGTCG	GACGCAGCAT
51	TGCCGACATC	GCCCAAGATT	TGCCCGACGG	GGCCGACTGC	CAAATCTGCG
101	CCGTTTACCG	CAACAACCGC	CTCATCGTCC	CCGCGCCGCA	AACCGTCATC
151	ATCGAAGGCG	ACGAAATCCT	GTTTGCCGCC	GCCGCCGAAA	ACATCGGGGC
201	GGTCATACCc	gaATTGCGCC	CCAAAGAAAC	CAGCACCCGC	CGCATCATGA
251	TTGCCGCGCG	CGGCAACATc	tgctACCGCC	TCGCCAAGCA	GCTCGAACAC

```

301 GCATAcaacG TCAAAATCAT CGAATGCCGG CCGCGCcggtg ccgaATGGAT
351 AGCCGAAAAC ctcgAcaaCA CCCTCGTCCT GCAAGGTTTCG Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTAtg tCCGCCCTTT TGGCGAAAAA
501 CCTcggcgCG AAGCgcgtca teggCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCACG
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGCGCA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAAC TGAAGAACTC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

g047.pep

```

1 MVIIQARRGG LLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGNI CYRLAKQLEH
101 AYNVKIIIECR PRRAEWIAEN LDNTLVLQGS ATDETLLDNE YIDEIDVFCA
151 LTNDDESIM SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS AIIIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

m047.seq

```

1 ATGGTCATCA TACAGCGCG C...syGCGGA sTGCTTGTCG GACGCAGCAT
51 TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCGTCATC
151 ATCGAAGGCG ACGAAATCCT ATTGCGCCG CCGCGCGAAA ACATCGGCGC
201 GGTCATACCC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCGGCGGCG GCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTCGAACACG CATACAACGT yAAAATCATC GAATGCCGCG CGCGCCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTCyTG CAAGGTTCCG
401 CAACCGACGA AACCTGTGTC GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GGCGAAaAAC CTCGGCGCGA AGCGCGTCAT CGGCATCGTC AACCGCTCAA
551 GCTACGTCGA TTTGCTCGAA GGCAACAAAA TCGACATCGT CGTCTCCCCC
601 CACCTCATCA CCATCGGCTC GATACTCGCC CACATCCGGC GCGGCGACAT
651 CGTTGCCGTC CACCCATCC GCGCGGCGAC GGCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAA ACTTCCGCA TCATCGGCAG GCGCATCAGC
751 GGCATCAAAT GGCCCGAAGG CTGCCACATT GCCGCGTCG TCCGCGCCGG
801 AACC GGCGAA ACCATTATGG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCAT CATCTTTTTC GTCTCGCGCC GCGCATCCT GAACGAACG
901 GAAAAACTCA TCCAGGTCAA AATGGGCTTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

m047.pep

```

1 MVIIQARXXG XLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETQRN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLV LQGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSYVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAEA IEVVAHGD KTS AIIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRLILNEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

a047.seq

```

1 ATGGTCATCA TACAGGCGCG GCGCGGCGGA CTGCTTGTCG GACGCAGCAT

```

```

51  TGCCGACATC  GCCAAGATT  TGCCCGACGG  GGCCGACTGC  CAAATCTGCG
101 CCGTTTACCG  CAACAACCGC  CTCATCGTCC  CCGCGCCGCA  AACCGTCATC
151 ATCGAAGGCG  ACGAAATCCT  ATTTGCCGCC  GCCGCCGAAA  ACATCGGCGC
201 GGTCAATCCC  GAATTGCGCC  CCAAAGAAAC  CAGCACCCGC  CGCATCATGA
251 TTGCCGCGCG  CGGCAACATC  GGCTACCGTC  TCGCCAAGCA  GCTCGAACAC
301 GCATACAACG  TCAAAATCAT  CGAATGCCGG  CCGCGCCGTG  CCGAATGGAT
351 AGCCGAAAAC  CTCGACAACA  CCCTCGTCCT  GCAAGGTTCT  GCAACCGACG
401 AAACCCCTGCT  CGACAACGAA  TACATCGACG  AAATCGACGT  ATTCTGCGCC
451 CTGACCAACG  ACGACGAAAG  CAACATTATG  TCCGCCCTTT  TGCGCAAAAA
501 CCTCGGCGCG  AAGCGCGTCA  TCGGCATCGT  CAACCGCTCA  AGCTACGTCG
551 ATTTGCTCGA  AGGCAACAAA  ATCGACATCG  TCGTCTCCCC  CCACCTCATC
601 ACCATCGGCT  CGATACTCGC  CCACATCCGG  CGCGGCGACA  TCGTTGCCGT
651 CCACCCCATC  CGGCGCGGCA  CGCGGAAGC  CATCGAAGTC  GTCGCACACG
701 GCGACAAAAA  AACTTCCGCC  ATCATCGGCA  GCGCATCAG  CGGCATCAAA
751 TGGCCCGAAG  GCTGCCACAT  TGCCGCGGTC  GTCCGCGCCG  GAACCGGCGA
801 AACCATTATG  GGACACCATA  CCGAAACCGT  CATCCAAGAC  GCGGACCACA
851 TCATCTTTT  CGTCTCGGCG  CGGCGCATCC  TGAACGAACT  GGAAAACTC
901 ATCCAAGTCA  AAATGGGCTT  TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 198; ORF 047.a>:

```

a047.pep
1  MVIIQARRGG  LLVGRSIADI  AQDLDPGADC  QICAVYRNNR  LIVPAPQTVI
51  IEGDEILFAA  AAENIGAVIP  ELRPKETSTR  RIMIAGGNI  GYRLAKQLEH
101 AYNVKIIECR  PRRAEWIAEN  LDNTLVLQGS  ATDETLLDNE  YIDEIDVFCA
151 LTNDDESIM  SALLAKNLGA  KRVIGIVNRS  SYVDLLEGNK  IDIVVSPHLI
201 TIGSILAHIR  RGDIVAVHPI  RRGTAEAIEV  VAHGDKKTS  IIGRRISGK
251 WPEGCHIAAV  VRAGTGETIM  GHHTETVIQD  GDHIIFFVSR  RRIILNELEK
301 IQVKMGFFG*

```

m047/a047 96.5% identity over a 312 aa overlap

```

              10      20      30      40      50      60
m047.pep      MVIIQARXXGLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIEGDEILFAA
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a047           MVIIQARRGGLLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIEGDEILFAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m047.pep      AAENIGAVIPELRPKETQRNPXXIMIXGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a047           AAENIGAVIPELRPKETSTR---IMIAGGNGYRLAKQLEHAYNVKIIIECRPRRAEWI
              70      80      90      100     110

              130     140     150     160     170     180
m047.pep      AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESIMISALLAKNLGAKRVIGIV
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a047           AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESIMISALLAKNLGAKRVIGIV
              120     130     140     150     160     170

              190     200     210     220     230     240
m047.pep      NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a047           NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK
              180     190     200     210     220     230

              250     260     270     280     290     300
m047.pep      TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a047           TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL
              240     250     260     270     280     290

              310
m047.pep      EKLIQVKMGFFGX
              | | | | | | | |

```

a047 EKLIQVKMGFFGX
 300 310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGXLVGRSIADIAQDLPDGADCQICAVYRNRLIVPAPQTVIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLPDGADCQICAVYRNRLIVPAPQTVIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNQPPXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI	120
g047	AAENIGAVIPELRPKETSTR---IMIAGGNICYRLAKQLEHAYNVKIIIECRPRRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLDDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLDDNEYIDEIDVFCALTNDDES NIMSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEVVAHGDKK	237
m047.pep	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL	300
g047	TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQGDHIIFFVSRRIILNEL	297
m047.pep	EKLIQVKMGFFGX 313	
g047	EKLIQVKMGFFGX 310	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

```

1  ATGCTCGACA AAGGCGAGGA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTA CTACGTC ggcCCcgTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG
101 CAGGTCCGAC CACAGCCACC CGCATGGACA AATTTACCCG CCAAATGCTC
151 AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201 cacctGCGAA GCcatCGCCG ACAACAAGGC CGTGACCTC ATGGCAGTCG
251 GCGGCGCGGC ATACCTCGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCGG AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351 TATGCCCCTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401 CCGCCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451 TGA

```

This corresponds to the amino acid sequence <SEQ ID 200; ORF 048.ng>:

g048.pep

```

1  MLDKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51  KQTGLLMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAV YEFVKKMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

```

1  ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTA CTACGTC GGCCCCGTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCGG

```

101	CAGGTC	CCGAC	CACAGCCACC	CGCATGGACA	AATTCACCCG	CCAAATGCTC
151	GAACAAACCG	ACCTCTTGGG	CATGATCGGC	AAATCCGAGC	GCGGCGTGGC	
201	CACCTGCGAA	GCCATCGCCG	ACAACAAAGC	CGTGACCTC	ATGGCAGTCG	
251	GCGGCGCGGC	GTATCTCGTG	GCAAAAGCCA	TCAAATCTTC	CAAAGTCTTG	
301	GCGTTCCCGG	AATTGGGCAT	GGAAGCCATT	TACGAATTTG	AAGTCAAAGA	
351	CATGCCCGTA	ACCGTCGCCG	TAGATAGCAA	AGGCGAATCC	ATCCACGCCA	
401	CGCCCGCCG	CAAATGGCAG	GCGAAATATG	GCATCATCCC	CGTCGAATCT	
451	TTGA					

This corresponds to the amino acid sequence <SEQ ID 202; ORF 048>:

```
m048.pep
  1 MLNKGEELPV DFTNRLIIYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51 EQTDLLGMIG KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 APFELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 203>:

```
a048.seq
  1  ATGCTCGACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51  TTACTACGTC GGCCCCGTCG ATCCGGTCGG CGACGAAATC GTCGGCCCCAG
101 CAGGTCCGAC CACCGCCACC CGCATGGACA AATTCACCCG CCAAATGCTC
151 GAACAAACCG ACCTCTTTGG CATGATCGCG AAATCCGAGC CGGGCGCGGC
201 CACCTGCGAA GCCATCGCCG ACAACAAAGC CGTGACCTC ATCGGCAATCG
251 GCGGCGCGGC GTATCTCGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301 GCGTTCCCCG AATTGGGCAT GGAAGCCATT TACGAATTTC AAGTCAAAGA
351 CATGCCCGTA ACCGTCGCCG TAGACAGCAA AGGCGAATCC ATCCACGCCA
401 CGGCCCCGCC CCAATGGCAG GCGAAAATCG GCATCATCCC CGTCAAATCT
451 TGA
```

This corresponds to the amino acid sequence <SEQ ID 204; ORF 048.a>:

```
a048.pep
  1  MLDKGEELPV DFTNRLIYYV GPVDPVGDEI VGPAGPTTAT RMDKFTRQML
51  EQTDLIGMIG KSERGAATCE AIAADNAVYL MAVGGAAAYLV AKAIKSSKVL
101 AFPELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPPQWQ AKIGIIPVKS
151 *
```

m048/a048 96.0% identity over a 150 aa overlap

	10	20	30	40	50	60
m048.pep	MLNKGELPVDFTNRLIYYGVPDVGDEVGFPAGPTTATRMDKFTRQMLEQTDLGMIG					
a048	MLDKGEELPVDFTNRLIYYGVPDVGDEIVGFAGPTTATRMDKFTRQMLEQTDLGMIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFEVKDMPV					
a048	KSEGAATCEAIADNKAVYLMVGGAAAYLVAKAIKSSKVLAFPELGMEAIYEFEVKDMPV					
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
a048	TVAVDSKGESIHATAPPQWQAKIGIIPVKSX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:

m048/g048

	10	20	30	40	50	60
m048.pep	MLNKGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIG					
	:					
g048	MLDKGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLKQTGLLGMIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGVATCEAIADNKAVYILMAVGGAAYLVAKAIKSSKVLAFPELGMIAIYEFVKDMPV					
	:					
g048	KSERGAATCEAIADNKAVYILMAVGGAAYLVAKAIKSSKVLAFPELGMIAVYEFVKDMPV					
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
g048	TVAVDSKGESIHATAPRKWQAKIGIIPVESX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 205>:

```
g049.seq
  1  ATGCGGGGCGC AGGCGGTTGA TCAACCGTTC GGTCAGCTCC TGTTCCGACA
51  GGCAGAACAC  TTCGCGCCGC  TTGACGGGTT TCGGGTTCAG GATATTGATT
101 TGGACGGGCA TCAACGCCTC TTCGCAACCG CTTTCGCCGT TTTCCGCAAT
151 CCCGCTGTGC GCCGTACCGG ATTCTGCCGC ATCGGCGTTT TCCCCGCCCT
201 CAATCTGTGC GGTTTCAAAT TCGGCACTGT CTTTTTTGGC ATCGAACCGG
251 ATTCTCGGCC GCGATTTCGAT GTGTTTTTCC GAAAccggca tTTGCAGGGA
301 AGCCTgcgcg TTGAGCCAGT TTTCTGAAG  GACGATCATC GGGTCGGTTT
351 CGACTTCTCT GCCGCAATCG GCAACGGCgc tGTTGTGTTC TTCCTGCCAT
401 TTCTTCACG  AGCCCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 206; ORF 049.ng>:

g049.pep
1 MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ DIDLDGHQRL FRTAFAVFRN
51 PVCRRTGFCR IGVFPALNLC GFKFGTVFFG IEPDSPPRFD VFFRNRLHQ
101 SLRVEPVFLK DDHRVGFDL AAIGNGAVVF FLPLQIRL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 207>:

```
m049.seq (partial)
      1 ATGCGGGGCGC AGGCGTTTGA TCAGCCGTTC GGTCAGCTCC TGTTCCGGACA
     51 GGCAGAACAC TTCGCGCCGG TTGACGGCTT TCGGGTTTCAG GATATTGATT
    101 TGGACGGGCA TCAACGTTTC TTCGCCATCG TTTTCCCCGT TTTCCGAAAC
    151 CGCCGGCTCA TTCGTGCCGG ATTCGTGCCT GTCCGGCGTT TCCCCGCTTT
    201 CAATCTGTCC GGTTTTCAAAT TCGACACTGT CTTTTTTGGT ATCAAACCGG
    251 ATTCTCCGCC GCGATTTCGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
    301 AGCCTGCGCG TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
    351 CGACTTCCTC GCCGC AATCG GCAACGGCGG CATTGTGTTC CTCCTGCCAT
    401 TTTTTCAGT ACGCCTT...
```

This corresponds to the amino acid sequence <SEQ ID 208; ORF 049>:

```
m049.pep      (partial)
1  MRAQAFDQPF  GQLLFGQAEH  FAPVDGFRVQ  DIDLDGHQRF  FRIVFPVFRN
51  RRLIRAGFCL  VGVFPAFNLS  GFKFDTVFFG  IKPDSPPRFD  VFFRNRHLQG
101 SLRVEPVFLK  DDHRVGFDFL  AAIGNGGIVF  LLPFFQIRL...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 209>:

a049.seq

```

1 ATGCGGGCGC AGGCGTTTGA TCAGCCGTTT GGTGAGCTCC TGTTGGGACA
51 GGCAGAACAC TTCGCGCCCG TTGACGGCTT TCGGGTTCAG AATATTGATT
101 TGGACGGGCA TCAACGCTTC TTCCGCACCG CCTTCGCCGT TTCCCGCAAC
151 CCCGTCTGCC GCCGTACCCG ATTCTGCCGC ATCGGCGTTT TCCCGCCTT
201 CAATCTGTCC GGTTTCAAAT TCGGCACTGT CTTTTTGGC ATCAAACCGG
251 ATTCTCCGCC GCGATTCGAT GTGTTTTTCC GAAACCGACA TTTGCAGGGA
301 AGCCTGCGCG TTGAGCCAGT TTTCTGAAG GACGATCATC GGGTCGGTTT
351 CGACTTCCTC GCCGCAATCG GCAACGGCGG CATTGTGTTC CTCCTGCCAT
401 TTTTTCAGAT ACGCCTT

```

This corresponds to the amino acid sequence <SEQ ID 210; ORF 049.a>:

```

a049.pep
1  MRAQAFDQPF GQLLFGQAEH FAPVDGFRVQ NIDLDGHQRF FRTAFVFRN
51  PFCRRTRFCR IGVFPAFNLS GFKFGTVFFG IKPDSPPRF VFFRNRLQG
101 SLRVEPVFLK DDHRVGFDL AAIGNGGIVF LLPFFQIRL

```

m049/a049 90.6% identity over a 139 aa overlap

```

m049.pep      10      20      30      40      50      60
MRAQAFDQPFGLLFGQAEHFAPVDGFRVQDIDLGHQRFRRIVFPVFRNRRLIRAGFCL
|||||
a049           10      20      30      40      50      60
MRAQAFDQPFGLLFGQAEHFAPVDGFRVQDIDLGHQRFRRIVFPVFRNRRLIRAGFCL
|||||

m049.pep      70      80      90     100     110     120
VGVPFPAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLQGSLRVEPVFLKDDHRVGFDL
:|||||
a049           70      80      90     100     110     120
IGVPFPAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLQGSLRVEPVFLKDDHRVGFDL
|||||

m049.pep      130     139
AAIGNGGIVFLLPFFQIRL
|||||
a049           130
AAIGNGGIVFLLPFFQIRL

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 049 shows 86.3% identity over a 139 aa overlap with a predicted ORF (ORF 049.ng) from *N. gonorrhoeae*:

m049/g049

```

m049.pep      10      20      30      40      50      60
MRAQAFDQPFGLLFGQAEHFAPVDGFRVQDIDLGHQRFRRIVFPVFRNRRLIRAGFCL
|||||
g049           10      20      30      40      50      60
MRAQAFDQPFGLLFGQAEHFAPVDGFRVQDIDLGHQRFRRIVFPVFRNRRLIRAGFCL
|||||

m049.pep      70      80      90     100     110     120
VGVPFPAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLQGSLRVEPVFLKDDHRVGFDL
:|||||
g049           70      80      90     100     110     120
IGVPFPAFNLSGFKFDTVFFGIKPDSPPRFDVFFRNRLQGSLRVEPVFLKDDHRVGFDL
|||||

m049.pep      130     139
AAIGNGGIVFLLPFFQIRL
|||||
g049           130     140
AAIGNGAVVFLPFLQIRLX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

g050.seq

```

1   atgggcgcgg GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51  caccgccgaa AAAGccgtgt TGATGGcaaa AGAATCCCTG ATGAGCCACA
101 TCGACatCca aGaATTGCAG GAAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGgtcc
351 TGTCGAactc acgccGCcgc gtgtCGAAGA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

g050.pep

```

1   MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVED*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

m050.seq

```

1   ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGTATCG GCATCGGCGG
51  C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GgAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCC
351 TGTCGAACTC ACGCCGCCG GCGTCGAAGA TGGCCCGATT TGA

```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

m050.pep

```

1   MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDGPI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

a050.seq

```

1   ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51  TACGCCCCGAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GGAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCC
351 TGTCGAACTC ACGCCGCCG GCGTCGAAGA CTGGCCC

```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

a050.pep

```

1   MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51  TTEALRLELF EKVNALGIGA QGLGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATRHVEF ELDGSGPVEL TPRVEDWP

```

m050/a050 97.7% identity over a 129 aa overlap

```

              10      20      30      40      50      60
m050.pep      MGAGWCPPGILGIGIGGXAEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF
              |||||:|||||
a050           MGAGWCPPGILGIGIGGTPEKAVLMAKESLSMSHIDIQELQEKAASGAELSTTEALRLELF

```

253

	10	20	30	40	50	60
m050.pep	70	80	90	100	110	120
	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
a050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
m050.pep	130					
	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLELF					
g050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLSHIDIQELQEKAASGAELSTTEALRLELF					
	10	20	30	40	50	60
m050.pep	70	80	90	100	110	120
	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
g050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
m050.pep	130					
	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```

1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACACCGGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCGGA CATGAGCGTG GAAAAGATGG TTAACGAAGG CGTACGCCGC
301 GCCTACACTT GGAAGGCAA CACCCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCATCCACA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGGGCTCTG AAAACAAATC CAAACTCGCT ATGCTCAACC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACGATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTTGGGC ATCGGCATCG GCGGCACgcc CGAAAAAGCC
601 GTGTTGATGG cgaAAGAATC CCTGATGAGC CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAG GTCAACGCGC TGGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTACCCGAC
801 CCATGCCGCC TCCAAACCGA TTGCCATGAT TCCCAACTGT GCCGCCACCC
851 GCCACGTCGA ATTGAATTG GACGGCTCAG GTCCTGTCGA ACTCACGCCG
901 CCGCGCGTCG AAGACTGACC CGATCTGACT TACAGCCCGC ACAACGGCAA
951 ACGCGTCGAT GTCGATAAGC TGACCAAAGA AGAAGTGGCA AGCTGGAAAA
1001 CCGGGCAGCT ATTGCTGTTG AACGGCAAAA TCCTCACCGG CCGCGATGCC
1051 GCGCACAAAC GCCTCGTCAA TATGCTCGAC AAAGGCGAGG AGTTGCCCGT
1101 CGATTTACAC AACCGCCTGA TTTACTACGT CGGCCCCGTC GATCCGGTCG
1151 GCGATGAAGT CGTCGGTCCC GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTTACCC GCCAAATGCT CAAACAAACC GGCCTCTTGG GCATGATCGG

```

```

1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGACCT CATGGCAGTC GCGGCGCGG CATACCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCG GAATTGGGTA TGAAGCCGT
1401 TTACGAATTT GAAGTCAAAG ATATGCCCCG AACCGTCGCC GTGGACAGCA
1451 AAGGCGAATC CATCCAGGCC ACCGCCCCGC GCAAATGGCA GCGGAAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pap

```

1  MTVIKQEDFI QSICDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVGM DVQWDADMSV EKMVNEGVR
101 AYTWEENTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSSENKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLLEFEK VNALGIGAOG
251 LGGLTTVLVDV KILDYPHAA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVED*PDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLL NGKILTGRDA
351 AHKRLVNMLD KGEELPVDFN NRIYVVGVP DPVGEDEVGP AGPTTATRMD
401 KFTRQMLKQT GLLGMIGKSE RGAATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFV ELGMEAVYEF EVKDMPTVTA VDSKGESHA TAPRKWQAKI
501 GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir|B44511 fumarate hydratase (EC 4.2.1.2) fumb, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11  QSICDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAENNRPICQDTG 70
          Q+  DA  +  H K  L+      E +  K  Q L NS + A+  P CQDTG
Sbjct: 53  QAFHDASFMLRPAHQKQVAAILHDPEASEND---KYVALQFLRNSEIAAKGVLPCTCQDTG 109

```

```

Query: 71  IATVFLKVGMVDVQWDADMSVEKMVNEGVRRAAYTWEENTLRASVLADPAGKRQNTKDNTPA 130
          A + K G V W  E+ +++GV Y E N  +  A  K NT N PA
Sbjct: 110 TAIIVGKKGQRV-WTGGGD-EETLSKGVYNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131 VIHMSIVPGGKVEVTCAAKGGGSENKSKL-----AMNPSDNIVDWVLKTIPTMGAGWCP 185
          I + V G + + C AKGGGS NK+ L  A+L P  + +++++ + T+G  CP
Sbjct: 167 QIDLYAVDGDDEYKFLCVARGGGSANKTYLYQETKALLTPG-KLKNFLVEKMRTLGTAAAC 225

```

```

Query: 186 PXXXXXXXXTPEKAVLMAKESLMSHIDIQELQEKAAASGAELSTTEALRLLEFEKVNNXX 245
          P          T + L  +  +H  EL  +  +  L  EL E+
Sbjct: 226 PYHIAFVIGGTSAETNLKTVKLASAHY-YDELPTEGNEHGQAFRDVQLEQELLEEAQKLG 284

```

```

Query: 246 XXXXXXXXXXTTVDVKILDYPHAAASKPIAMIPNCAATRHVEFELDGS---PVELTPP 301
          D++++ P H AS P+ M  +C+A R+++ +++ G  +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSCADRNIAKINREGIWIKEHNP 343

```

```

Query: 302 RVEDXPDLTYSPDNGKRVDVDKLTKE---EVASWKTGDVLLNGKILTGRDAAHKRLVNM 358
          +          +VD+++ KE  +++ +  L L G I+ GRD AH +L  +
Sbjct: 344 QYIPQELRQAGEGEAVKVDLNRPMKEILAQLSQYPVSTRLSLTGTIIVGRDIAHAKL 403

```

```

Query: 359 LDKGEELPVDFNRIYXXXXXXXXXXXXXXXXXXXXTTATRMDKFTRQMLKQTGLLGMIGK 418
          +D G+ELP  + IYY          TTA RMD +  +  G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPYIYAGPAKTPAGYPSGSLGPTTAGRMDSYVDLLQSHGGSMIMLAK 463

```

```

Query: 419 SERGAATCEAIADNKAVYLMVGG-AAYLVAKAIKSSKVLAFPELGMEAVYEFVVKDMPV 477
          R  +A  +  YL ++GG AA L  ++IK  + +A+PELGMEA+++ EV+D P
Sbjct: 464 GNRSQQVTDACHKHGGFYLGSIIGGPAVLAQQSIKHLECVAYPELGMEAIWKIEVEDFPA 523

```

```

Query: 478 TVAVDSKG 485
          + VD KG

```

```

Sbjct: 524 FILVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATAGCCGTCA TCAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCTT
51  CCAATTCATC AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCTGCGC CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCGGAA AACAACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG AACGTCCAAT
251 GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCGC

```

```
301 GCCTACACTT GGAAGGCAA TACGCTGCGC GCTTCGCTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGGCC GTCCATCCATA
401 TGAGCATCTG GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAAAATC CAAACTCGCC ATGCTCAATC CTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACCATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTTGGGT ATCGGCATCG GCGGCACGCC CGAAAAAGCC
601 GTGCTGATGG CAAAAGAGTC CCTGATGAGC CACATCGACA TTCAAGAATT
651 GCAGGAAAAG GCGCGCTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAA GTCAACGCGC TGGGCATCGG CGCACAAAGG
751 TTGGGCGGAC TGACCACCGT GTTGACGTG AAAATCCTCG ATTATCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAATGC GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTCGA ACTCAGCCCG
901 CCGCGCGTCG AAGACTGGCC CGATTTGACT TACAGCCCCG ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAAGA AGAAGTGGCA AGCTGGAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCCG CCGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCAAC AAAGGCGAAG AATTGCCCCT
1101 CGATTTCACC AACCGCCTGA TTTACTACGT CGGCCCGCTC GATCCGGTCG
1151 GCGATGAACT CGTCGGTCCG GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGTGG CCACCTGCGA AGCCATCGCC GACAAACAAAG
1301 CCGTGATACCT CATGGCAGTC GCGGCGCGCG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCC GAATTGGGCA TGGAGCCAT
1401 TTACGAATTG GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGATAGCA
1451 AAGGCGAATC CATCCAGGCC ACCGCCCCGC GCAAATGGCA GCGGAAAATC
1501 GGCATCATCC CCGTCGAATC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pep

```
1 MTVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51 ILVNSRMCAE NNRPICQDTG IATVFLKVG M NVQWDADMSV EEMVNEGVRR
101 AYTWEQNTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSSENKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMKESLMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQQ
251 LGGLTTVL DV KILDYPTHA A SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVEDWPDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLLL NGKILTRDA
351 AHKRLVMDLN KGEELPVDFE NRLIYYVGPV DPVGDEVVGP AGPTTATRMD
401 KFTROMLEQT DLLGMIGKSE RGVATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKDMPTVTA VDSKGESIHA TAPRKWQAKI
501 GIIPVES*
```

m050-1/g050-1 98.2% identity in 507 aa overlap

```
10 20 30 40 50 60
m050-1.pep MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE
g050-1 MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE
10 20 30 40 50 60
70 80 90 100 110 120
m050-1.pep NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNTRLASVLADPAGK
g050-1 NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNTRLASVLADPAGK
70 80 90 100 110 120
130 140 150 160 170 180
m050-1.pep RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
g050-1 RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGSENKSKLAMLNPSDNIVDWVLKTIPTMG
130 140 150 160 170 180
190 200 210 220 230 240
m050-1.pep AGWCPPGILGIGIGGTPEKAVLMKESLMSHIDIQELQEKAAASGAELSTTEALRLELFEK
g050-1 AGWCPPGILGIGIGGTPEKAVLMKESLMSHIDIQELQEKAAASGAELSTTEALRLELFEK
190 200 210 220 230 240
250 260 270 280 290 300
m050-1.pep VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSVPVELTP
g050-1 VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSVPVELTP
250 260 270 280 290 300
```

	310	320	330	340	350	360
m050-1.pep	PRVEDWPDLTYS	PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVMDLN				
g050-1	PRVEDXPDLTYS	PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVNMLD				
	310	320	330	340	350	360
	370	380	390	400	410	420
m050-1.pep	KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE					
g050-1	KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTRQMLKQTGLLMIGKSE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m050-1.pep	RGVATCEAIADNKAVYLMVAVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA					
g050-1	RGAATCEAIADNKAVYLMVAVGGAAYLVAKAIKSSKVLAFPELGMEAVYEFVVKDMPVTVA					
	430	440	450	460	470	480
	490	500				
m050-1.pep	VDSKGESIHATAPRKWQAKIGIIPVESX					
g050-1	VDSKGESIHATAPRKWQAKIGIIPVESX					
	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

a050-1.seq

```

1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AACCCCGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCGCAT GTGTGCCGAA AACAAACGCC CCATCTGCCA
201 AGATACCGGT ATCGCGACCG TGTTTTGAAG AGTCGGTATG GATGTGCAAT
251 GGGATGCAGA CATGAGCGTC GAAGAGATGG TTAACGAAGG CGTGCGCCGC
301 GCCTACACTT GGGAAAGCAA TACGCTGCGC GCTTCCGTC TCGCCGACCC
351 CGCCGGCAAA CGCCAAAATA CCAAGACAA CACGCCGCCG GTCATCCATA
401 TGAGCATCGT GCCGGGCGAC AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGGGTTCTG AAAACAAATC CAACTCGCC ATGCTCAACC CTTCGACAA
501 CATCGTCCAT TGGGTATTGA AAACCAATCC GACCATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTGGGC ATCGGCATCG GCGGTACGCC CGAAAAGCC
601 GTGTTGATGG CGAAAGAATC CCTGATGAGC CACATCGACA TCCAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAA GTCAACGCGC TAGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGACGTG AAAATCCTCG ATTACCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAATGCG GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTGCG ACTCACGCCG
901 CCGCGCGTCG AAGACTGGCC CGATTGACT TACAGCCCGG ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAAGA AGAAGTGCGA AGCTGGAATA
1001 CCGCGACGAT ATTGCTGTTG AACGGCAAAA TCCTACCCGG CCGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCGAC AAAGCGGAAG AATTGCCCGT
1101 CGATTTACAC AACCGCCTGA TTTACTACGT CGGCCCGGTC GATCCGGTCG
1151 GCGACGAAAT CGTCGGCCCA GCAGGTCCGA CCACGCCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAAACAAG
1301 CCGTGTAACC CATGGCAGTC GCGGCGCGCG CGTATCTCGT GGCAAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCC GAATTGGGCA TGGAAAGCCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGCG CCCAATGGCA GCGGAAAAATC
1501 GGCATCATCC CCGTCAAATC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

a050-1.pep

```

1  MTVIKQEDFI QSIDAFQFI SYHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVG M DVOWDADMSV EEMVNEGVR
101 AYTWEGNLRL ASVLADPAGK RQNTKDNTFA VIHMSIVPGD KVEVTCAAKG
151 GGSNKSRLA MLNPSDNIVD WVLKTIPTMG AGWCPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELQEK AASGAELSTT EALRLELFEK VNALGIGAQG
251 LGGLTTVLVD KILDYPHTAA SKPIAMIPNC AATRHVEFEL DGSGPVELTP
301 PRVEDWPDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVMDLD KGEELPVDFN NRLIYYVGPV DPGDEIVGP AGPTTATRMD
401 KFTRQMLEQT DLLGMIGKSE RGAATCEAIA DNKAVYLMVAV GGAAYLVAKA
451 IKSSKVLAF ELMGEAIYEF EVKDMPTVTA VDSKGESIHA TAPPQWQAKI
501 GIIPVKS*

```

a050-1/m050-1 98.4% identity in 507 aa overlap

```

      10      20      30      40      50      60
a050-1.pep MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE
|||||
m050-1      MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE
      10      20      30      40      50      60

      70      80      90     100     110     120
a050-1.pep NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNTLRASVLADPAGK
|||||:|||||
m050-1      NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAYTWEGNTLRASVLADPAGK
      70      80      90     100     110     120

      130     140     150     160     170     180
a050-1.pep RQNTKDNTPAVIHMSIVPGDKVEVTC AAKGGSENKSKLAMLNPSDNIVDWLKTIP TMG
|||||
m050-1      RQNTKDNTPAVIHMSIVPGDKVEVTC AAKGGSENKSKLAMLNPSDNIVDWLKTIP TMG
      130     140     150     160     170     180

      190     200     210     220     230     240
a050-1.pep AGWCPPGILGIGIGGTPEKAVLMAKESLM SHIDIQELQEKAASGAELSTTEALRLELFEK
|||||
m050-1      AGWCPPGILGIGIGGTPEKAVLMAKESLM SHIDIQELQEKAASGAELSTTEALRLELFEK
      190     200     210     220     230     240

      250     260     270     280     290     300
a050-1.pep VNALGIGAQQGLGGLTTVL DVKILDYP THAASKPIAMIPNCAATRHVEFELDGSGPVELTP
|||||
m050-1      VNALGIGAQQGLGGLTTVL DVKILDYP THAASKPIAMIPNCAATRHVEFELDGSGPVELTP
      250     260     270     280     290     300

      310     320     330     340     350     360
a050-1.pep PRVEDWPDLTYS PDNGKRV DDKLTKEEVASWKTGDVLLNGKIL TGRDAAHKRLV DMLD
|||||
m050-1      PRVEDWPDLTYS PDNGKRV DDKLTKEEVASWKTGDVLLNGKIL TGRDAAHKRLV DMLN
      310     320     330     340     350     360

      370     380     390     400     410     420
a050-1.pep KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE
|||||
m050-1      KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDKFTRQMLEQTDLLGMIGKSE
      370     380     390     400     410     420

      430     440     450     460     470     480
a050-1.pep RGAATCEAIADNKAVYLM AVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFV KDMPTVTA
||:|||||
m050-1      RGVATCEAIADNKAVYLM AVGGAAYLVAKAIKSSKVLAFPELGMEAIYEFV KDMPTVTA
      430     440     450     460     470     480

      490     500
a050-1.pep VDSKGESIHATAPPQWQAKIGIIPVKSX
|||||:|||||
m050-1      VDSKGESIHATAPRKWQAKIGIIPVESX
      490     500

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

g052.seq

```

1  ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG
51  CTGCGAGCCG ACGGCGGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GCGGCTTTC CATTATTTA TATCAGTCGG CGACACGGG CTCACTCCGA
251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 224; ORF 052.ng>:

g052.pep

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

m052.seq
 1 ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTCAAAGG
 51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
 151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

m052.pep
 1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN
 101 RLRLETTWSP ACRKVKNA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

a052.seq
 1 ATGGCTTTGG TCGCGGAGGA AACGGAAATA TCCGCGCCGT GTTCAAAGG
 51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC
 151 AAGGGATTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
 201 GGCGGCTTTC CATTGCTTTA TATCAGTCGG CGACACGTGA CTCACTTCGA
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
 301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCC GCCTGCAAAA AGGTGAAAAA
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

a052.pep
 1 MALVAEETEI SAPCFKG*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP
 51 KGLDGVSKNS SLVLALTAAF HSFISVGD* LTSMPNLVTM LLIKPTVVPN
 101 RLRLEITWSP ACKKVKNA*

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
a052	MALVAEETEI SAPCFKGXEP TGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m052.pep	SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKVKNAAX					
a052	SLVLALTAAFHSFISVGDXTLTSMPNLVTMLLIKPTVVPNRLRLEITWSPACKKVKNAAX					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

m052/g052

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					

```

g052      MALVAEETEISAPCFKGCEPTGDSRLSTTKSAPMPCANSASAKSKSATSPKGLDGVSKNS
           10      20      30      40      50      60

           70      80      90      100     110     120
m052.pep  SLVLALTAAFHSFISVGDTWLTSMPLATMLLIKPTVVPNRLRLLEITWSPACKKVNAAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g052      SLVLALTAAFHSFISVGDTRLTLPMPNLVTMLLIKPTVVPNRLRLLETTWSPACRKVKNAAX
           70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073.seq
1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
51  TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AGTCCGGGGC GGatacCGGC GCGAGTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAAAAGAGT TCCACGACTT TCCACGCGGC TGCTTGGTCG
301 GCGACTTCAA AACCGATGAC GATGCCGCGC CCGTTTTGCT GTTTCGGGAT
351 AAGCTCCGCC TGCGGATGGT CGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073.pep
1  MCMPIAIRVS DGICRIFPPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
51  SPGRIPAASF SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAAWS
101 ATSKPMTMPP PFCCLRISSA CGWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073.seq
1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
51  GCCGTCTGAA ACACGCAATC AGCGTGCGAG TGCCTGTTTC AAATCGTCAA
101 TCAAATCGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151 CGGATGTTGG CCGCGAGTTT TTCTTCGGGC TGCATCCTGC CGTGCGTGGT
201 TGTCCACGGG TGGGTAATGG TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251 GGGAAAAGAG TTCCACGCCG TCCACAACCT TCCACGCCGC TTCTTGATCG
301 GCAACTTCAA AGCCGATGAC GATGCCGCGC CCGTTTTGCT GTTTCGGGAT
351 AAGCGCCGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073.pep
1  MCMPIKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
51  RMLAASFSSG CILPCVVVHG WVMVERTSPR LAVREKSSTP STTFHAASKS
101 ATSKPMTMPP PFCCLRISSA XGWSNPNV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073.seq
1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
51  TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AATCCGGGGC GGATGTTGGC GCGAGTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301 GCTTGGTTCG GACTTCAAA GCCGATGACG ATGCCGCCGC CGTTTTGCTG
351 TTTGCGGATA AGCTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073.pep
1  TCMSYKIRVS DGICGVFPPM PSEXNRQRAS ACFKSSIKSP TYSKPTDRRT
51  NPGRMLAASF SSGCILPCVV VHGWVMVERT SPRLAVREKS STPSTTFHAA
101 AWSATSKPMT MPPFPCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSEXRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVHGWVMVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCCLRI				
a073	SSGCILPCVVHGWVMVERTSPRLAVREKSSTPSTTFHAAAWSATSKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDNPVX				
a073	SSAXGWSGNPVX				
		130			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICCC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
g073	MCMPIKIRVSDGICRIFPMPSETRNQRASACFKSSIKSPTYSKPTDRRTSPGRIPAAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVHGWVMVERTSPRLAVREKSSTPSTTFHAASXSATSKPMTMPPPFCCCLRI				
g073	SSGCILPCVVHGLVMVERTSPRLAVREKSST---TFHAAAWSATSKPMTMPPPFCCCLRI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDNPVX				
g073	SSACGWSGNPVX				
		120			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCCTT ACTTCATCAC CCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GGCAGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCCGTTCGG GCAACGCTGC GTTTCCTGT
151 GCCGCCAAAG CCAGCGGGGC GGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTT ACGAAATTTT
251 TAAAAAATG TGTTCGCGG CTTTGTGAAG GTTTAGAGA CCGCTGCCG
301 GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAAA ATTACAAATT
351 CCCCCTAT CTCTCCAAT GCCGAGCTAA AAGCGTCTTC ATAGCTGTCA
401 TATTTACCGG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFILLT MENTKSAKT PTTIQPASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAAVT TASFAPYLQ VLINFMIFS TKFLKKCVCG LCEGFRDLRP
101 GLLNLIFFV ESENYKFPAY LFQCRKSVF IAVIFTG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 237>:

```
m075.seq
1  ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GCGGAAAATG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 GCGCTTCCAA AGCGTTTTTT GCCGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTC AAAAAAGTGT
251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TGCCTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 238; ORF 075>:

```
m075.pep
1  MPSYFITLLT MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51  AAKARGAAVT TASFAPYLQ VLINFMIFSF KKCLAVMDGA FFRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 075 shows 65.7% identity over a 137 aa overlap with a predicted ORF (ORF 075.ng) from *N. gonorrhoeae*:

```
m075/g075

      10      20      30      40      50      60
m075.pep  MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
          |||||||||||||||||||||||||||||||||||||||||:|||||||
g075      MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAKASGAVT
          10      20      30      40      50      60

      70      80      90      100     110
m075.pep  TASFAPYLQVVLINFMIFSF---KKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVAD
          |||||||||||||||||  |||:  :  :|  |::  :  :|  |::  :  :|
g075      TASFAPYLQVVLINFMIFSFTKFLKKVCVGLCEGFRDRLPGLLNLIFFVESENYKFPAY
          70      80      90      100     110     120

      120     130
m075.pep  FFQTCVNRFFEVEIIGIGDX
          :||  ::  |  :|  :|
g075      LFQCRAKSVFIIVFTGX
          130
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 239>:

```
a075.seq
1  ATGCCGTCTT ACTTCATCAC TCTCTTAACG ATGGAAAAGA CAAAAAGCGC
51  GCGGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCTGTATCGG GCAACGTTGC ATTTGCATGT
151 GCGGCCAAAG CCAGGGGAGC AGCTGTACA ACAGCCAGTT TTGCGCCGTA
201 TTTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTC AAAAAAGTGT
251 TGGCGGTAAT GGATGGAGCG TTTTTCAGAC GACCGCCGAA CATCCGAAAA
301 TCAGTCTTTC AAAAATCCGA ATACGACAAA TTCGTATTGG TTGCCGATTT
351 CTTCCAAACC TGCCTTAATC GCTTCTTCGA AGTCGTAGAA ATAATCGGCA
401 TTGGTGATTA A
```

This corresponds to the amino acid sequence <SEQ ID 240; ORF 075.a>:

```
a075.pep
1  MPSYFITLLT MEKTKSAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC
51  AAKARGAAVT TASFAPYLQ VLINFMIFSF KKCLAVMDGA FFRPPNIRK
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD*
```

m075/a075 98.5% identity over a 136 aa overlap

	10	20	30	40	50	60
m075.pep	MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
a075	MPSYFITLLTMEKTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	10	20	30	40	50	60
m075.pep	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
m075.pep	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLRQVLINFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
m075.pep	CVNRFFEVEIIGIGDX					
a075	CVNRFFEVEIIGIGDX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

g080.seq

1	ATGTGGGATA	ATGCCGAAGC	GATGGAACGG	CTGACGCGCT	GGCTGCTTGT
51	CATGATGGCG	ATGCTGCTTG	CTGCGTCCGG	GCTGGTTTGG	TTTTACAATT
101	CGAATCATCT	GCCCGTCAAG	CAGGTGTCGC	TGAAGGGCAA	CCTGGTTTAT
151	TCCGATAAGA	AGGCATTGGG	CAGTTTGGCG	AAAGAATACA	TCCATGGGAA
201	TATTTTGAGG	ACGGACATCA	ATGGCGCACA	GGAAGCCTAC	CGCCGGTATC
251	CGTGGATTGC	GTCGGTCATG	GTGCGCCGCC	GTTTTCCCGA	TACGGTTGAG
301	GTCGTCCTGA	CCGAGCGCAA	GCCGGTTGCA	CGTTGGGGCG	ACCATGCCTT
351	GGTGGACGGC	GAAGCAATG	TTTTTGAAGC	CCGCTTGGAC	AGACCCGGAA
401	TGCCGGTATT	CAGAGGCGCG	GAAGGAACGT	CTGCCGAAAT	GCTCCGCCGT
451	TATGACGAAT	TTTCGACTGT	TTTGGCAAAA	CAGGGTTTGG	GCATCAAAGA
501	GATGACCTAT	ACGGCACGTT	CGGCGTGGAA	TGTCGTTTTG	GACAACGGCA
551	TCACCGTCAG	GCTCGGACGG	GAAAACgaGA	TGAAACGCCT	CCgGCTTTTT
601	ACcgAAGCGT	GGCAGCATCT	gttgcGTAAG	AATAAAAATC	GGTTATCCTA
651	TGTGGATATG	Aggtataagg	acggatttTC	agtcccccat	gctCCCGACG
701	GTTTACCCGA	AAAAGAATcc	gAAGAAATatt	gggaacaggt	ttgggacata
751	ttacggcctg	gcgtcggaaa	cggttcgacg	caaatttcaa	tcagttataAA
801	GGGCAGacga	acaatggaac	AGcagtaa		

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

g080.pep

1	MWDNAEAMER	LTRWLLVMMMA	MLLAASGLVW	FYNSNHLPVK	QVSLKGNLVY
51	SDKKALGSLA	KEYIHGNILR	TDINGAQEAY	RRYPWIASVM	VRRRFPDIVE
101	VVLTERKPVA	RWGDHALVDG	EGNVFEARLD	RPMPVFRGA	EGTSAEMLRR
151	YDEFSTVLAK	QGLGIKEMTY	TARSAWNVVL	DNGITVRLGR	ENEMKRLRLF
201	TEAWQHLLRK	NKNRLSYVDM	RYKDGFSVPH	APDGLPEKES	EEYWEQVWDI
251	LRPGVNGGST	QISISYKGRR	TMEQQ*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

m080.seq

1	ATGTGGGATA	ATGCCGAAGC	GATGGAACGG	CTGACGCGCT	GGCTGCTTGT
51	CATGATGGCG	ATGCTGCTTG	CTGCGTCCGG	GCTGGTTTGG	TTTTACAATT
101	CGAATCATCT	GCCCGTCAAG	CAGGTGTCGC	TGAAGGGCAA	CCTGGTTTAT
151	TCCGATAAGA	AGACATTGGG	CAGTTTGGCG	AAAGAATACA	TCCATGGGAA
201	TATTTTGAGG	ACGGACATCA	ATGGCGCACA	GGAGCCTAC	CGCCGGTATC
251	CGTGGATTGC	GTCGGTCATG	GTGCGCCGCC	GTTTTCCCGA	CACGGTTGAG
301	GTCGTCCTGA	CCGAGCGCAA	GCCGGTCGCG	CGTTGGGGCG	ACCATGCCTT
351	GGTGGACGGC	GAAGGCAATG	TTTTTGAAGC	CCGCTTGGAC	AGACCCGGAA
401	TGCCGGTATT	CAGAGGCGCG	GAAGGAACGT	CTGCCGAAAT	GCTCCGCCGT
451	TATGACGAAT	TTTCGACTGT	TTTGGCAAAA	CAGGGTTTGG	GCATCAAAGA
501	GATGACCTAT	ACGGCACGTT	CGGCGTGGAT	TGTCGTTTTG	GACAACGGCA
551	TCACCGTCAG	GCTCGGACGG	GAAAACGAGA	TGAAACGCCT	CCGGCTTTTT

601 ACCGAAGCGT GGCAGCATCT GTTGCCTAAA AATAAAATC GGTTATCCTA
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTTCCGACG
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep
 1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNSNHLVPK QVSLKGNLVY
 51 SDKKTLGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES EE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng) from *N. gonorrhoeae*:

m080/g080

	10	20	30	40	50	60
m080.pep	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKTLGSLA					
080	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m080.pep	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVLTERRKPVARWGDHALVDG					
080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVLTERRKPVARWGDHALVDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m080.pep	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWNVVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m080.pep	DNGITVRLGRENMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYASDGLPEKES					
080	DNGITVRLGRENMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVPHAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
080	EEYWEQVWDILRPGVNGSTQISISYKGRRTMEQQX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq

1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT
 51 CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT
 101 CGAATCATCT GCGGCTCAAG CAGGTGTCGC TGAAGGGCAA CCTAGTTTAT
 151 TCCGATAAGA AAGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA
 201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC
 251 CGTGGATTGC GTCGTCATG GTGCGCCGCC GTTTTCCCGA CACGGTTGAG
 301 GTCGTCCTGA CCGAGCGCAA GCCGGTCGCG CGTTGGGGCG ACCATGCCTT
 351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGTTTGAC AGACCCGGAA
 401 TGCCGGTATT CAGAGCGCGG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT
 451 TATGACGAAT TTTGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTGG GACAACGGCA

```

551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT
601 ACCGAAGCGT GGCAACATCT GTTGCCTAAA AATAAAAAATC GGTATCCTA
651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTCCCGACG
701 GTTTACCGA AAAAGATCC GAAGAATAG

```

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep

```

1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNSNHLVK QVSLKGNLVY
51 SDKKALGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE
101 VVLTERRKPA RWGDHALVDG EGNVFEARLD RGPMPVFRGA EGTSAEMLRR
151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF
201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY APDGLPEKES EE*

```

m080/a080 99.2% identity over a 242 aa overlap

	10	20	30	40	50	60
m080.pep	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKTLGSLA					
a080	MWDNAEAMERLTRWLLVMMAMLLAASGLVWFYNSNHLVPKQVSLKGNLVYSDKKALGSLA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m080.pep	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVLTERRKPVARWGDHALVDG					
a080	KEYIHGNILRTDINGAQEAYRRYPWIASVMVRRRFPDTEVVLTERRKPVARWGDHALVDG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m080.pep	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
a080	EGNVFEARLDRPGMPVFRGAEGTSAEMLRRYDEFSTVLAKQGLGIKEMTYTARSAWIVVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m080.pep	DNGITVRLGRENNEMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYASDGLPEKES					
a080	DNGITVRLGRENNEMKRLRLFTEAWQHLLRKNKNRLSYVDMRYKDGFSVRYAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA
101 TTCGGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG
151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GGCGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGCGG CTTTGGGCGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC
301 CCGTTTGTGT TCGGCATTAC CGGTTGCGGC GGCAAGACGA CGGTGAAGGA
351 GATGCTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATGAT GCCGTTTCGG
401 CGACGGCAGG CAACTTCAAC AACCACatcg gaTTGCCGCT GACTTTATTG
451 AAATtaaaAcg aAAAAACCCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTTGGcgaa ctggcggtTt taacgcaaat CGCCAAACCC GATGCCGCTT
551 TGGtcaACAA CGCCTGCGC GCCCATGTCG GATGCGGTTt cgacggagtg
601 GGCATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTCAAG
651 CGGCATGGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGTT TAATTTGAAT ACGTGCACCT TCGGCGTCGA TAGCGCGGAT
751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTGATTT

```

265

```

801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAATCCC GACAGTATGA AAGCCGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG CATTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagtcgGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTTGGCGC GGACGGTTTG TGGTTCGCGC CCAAAGACCC
1251 GTTGATTCAA GTGTTGAGCC ACGATTGCC CGAACGCCGC ACCGTGTTGG
1301 TGAAAGGTTT CCGCTTTATG CAGAtggAAG AAGTGTCTGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

g081.pep

```

1 MKPLDLNFIC QALKLPMPSE NKPVSRIVTD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNALR AHVGCDFDGV
201 GDIKAKSEI YAGLCS DGMA LIPQEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFDLVCG DERTAVVLPV PGRHNVHNAA AAAALALAAG
301 LSLNDVAEGL QGFSNIKGR L NVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMMGELGED EAAAMHAEVG AYARDQGIEA AYFVGDNVSVE
401 AAEKFGADGL WFAAKDPLIQ VLSHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

m081.seq

```

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCT GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGTGCTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGGCAAAGG CGTGGCGTGA AAATGTGAAT
301 CCGTTTGTGT TCGGCATTAC CGGTTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGCTGGCT GCGGTATTGC GCCgCCGTTT CGGCGATGAT GCCGTGTTGG
401 CGACGGCAGG CAACTTCAAC AACCATATCG GATTGCCGCT GACTTGTGTT
451 AAGTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTGCGCGAA CTGGCGGTTT TAACGCAMAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GGCATATTG CCAAAGCGAA AAGCGAGATT TACCAAGGTT TATGTTTCTAGA
651 CGGCATTGCA CTGATTCTTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTTCACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTGATTT
801 GGTGTGCGGC GATGAGCGCG CCGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAACTG GCGGAGGACG AAGCCGCCGC TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCC CGACCAAGGC ATCGAAGCGG CTTATTTTGT CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGGCGCG GACGGTTTGT GGTTCGCGCG
1251 CAAAGACCCG TTGATTCAAG TGTTGCGCCA CGATTGCCC GAACGCGCCA
1301 CCGTGTGGT GAAAGGTTTC CGCTTTATGC AGATGGAAGA AGTGTGCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

m081.pep

```

1 MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLAA GAAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTXIAKP NAALVNNAMR AHVGCDFDGV

```

```

201  GDIAKAKSEI  YQGLCSDBGIA  LIPQEDANMA  VFKTATLNLN  TRTFGIDSGD
251  VHAENIVLKP  LSCEFDLVCG  DERAADVLPV  PGRHNVHNAA  AAAALALAAG
301  LSLNDVAEGL  KGFSNIKGRL  NVKSGIKGAT  LIDDTYNANP  DSMKAAIDVL
351  ARMPAPRIFV  MGDMMGELGEL  GEDEAAAMHA  EVGAYARDQG  IEAAYFVGDN
401  SVEAAEKFGA  DGLWFAAKDP  LIQVLRHDLF  ERATVLVKGS  RFMQMEEVVE
451  ALEDK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 081 shows 94.1% identity over a 455 aa overlap with a predicted ORF (ORF 081.ng) from *N. gonorrhoeae*:

m081/g081

		10	20	30	40	50	60
m081.pep		MKPLDLNFI	CQALKLPMPSESKPVSRI	VTDSRDIRAGDVFF	FALAGERF	DAHDFVED	VLAA
							:
g081		MKPLDLNFI	CQALKLPMPSENKPVSRIV	VTDSRDIREGDVFF	FALAGGRF	DAHDFVGG	VLSA
		10	20	30	40	50	60
		70	80	90	100	110	120
m081.pep		GAAAVVVS	REDCAAMD	GALKVDDT	LAALQTLAKA	WRNVNPFV	FGITGSGGKTTVKEMLA
							:
g081		GAAAVVVS	REDCAALGG	ALKVDDT	LAALQTLAKA	WRNVNPFV	FGITGSGGKTTVKEMLA
		70	80	90	100	110	120
		130	140	150	160	170	180
m081.pep		AVLRRR	FGDDAV	LATAGNF	NNHIGLPL	TLLKLNEKH	RYAVIEMGMNHF
							:
g081		AVLRRR	FGDDAV	SATAGNF	NNHIGLPL	TLLKLNEKH	RYAVIEMGMNHF
		130	140	150	160	170	180
		190	200	210	220	230	240
m081.pep		NAALVNN	AMRAHVG	CGFDG	VGDI	AKAKSEI	YQGLCSDG
							:
g081		DAALVNN	ALRAHVG	CGFDG	VGDI	AKAKSEI	YAGLCSDG
		190	200	210	220	230	240
		250	260	270	280	290	300
m081.pep		TRTFGID	SGDVHA	ENIVL	KPLSCE	FDLVCGD	ERA
		:	:				:
g081		TCTFGVD	SGDVRA	ENIVL	KPLSCE	FDLVCGD	ERT
		250	260	270	280	290	300
		310	320	330	340	350	360
m081.pep		LSLNDV	AEGLK	GF	SNIKGR	LVN	KG
							:
g081		LSLNDV	AEGLQ	GF	SNIKGR	LVN	K
		310	320	330	340	350	360
		370	380	390	400	410	420
m081.pep		MGDMG	ELGEL	GEDEA	AMHAE	V	GAYARD
							:
g081		MGDMG	ELGE	--DEA	AMHAE	V	GAYARD
		370	380	390	400	410	
		430	440	450			
m081.pep		LIQVLR	HD	LP	ERAT	VLVKG	S
							:
g081		LIQVLS	HD	LP	ERAT	VLVKG	S
		420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

```
a081.seq
1   ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGTTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTGG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAAACG AAAAAACCCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GCGCATATTG CCAAAGCGAA AAGCGAGATT TATCAAGGCT TATGTTCAGA
651 CGGCATGGCG CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCCACGCGG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC AACGAGTGCG CAGCCGTGGT TCTGCCCGTT CCCGCCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCCT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCCG CCATGCACGC CGAAGTCGGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTTGGCGC GGACGTTTGT TGGTTCGCGC CCAAAGACCC
1251 GTTGATTCAA GTGTTGCGCC ACGATTGGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAGGTTT CCGCTTTATG CAGATGGAAG AAGTGGTCTG GGCATTGGAG
1351 GATAAGTGA
```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

```
a081.pep
1   MKPLDLNFIC QALKLMPSE SKPVSRIVTD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLAA GAAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNFN NHIGLPLTLL
151 KLNKHHRYAV IEMGMNHFG E LAVLTQIAKP DAALVNNAMR AHVCGFDGV
201 GDIKAKSEI YQGLCSGDMA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFDLVCG NECAAVVLPV PGRHNVHNA AAAAAAALAA
301 LSLNDVAEGL KGFSNIKGR L NVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMLGELG E EAAAMHAEVG AYARDQGIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLI Q VLRHDLPERA TVLVKGSRFM QMEEVVEALE
451 DK*
```

m081/a081 96.7% identity over a 455 aa overlap

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLMPSESKPVSRIVTDSDRDIRAGDVFFALAGERFDAHDFVEDVLAA					
a081	MKPLDLNFICQALKLMPSESKPVSRIVTDSDRDIRAGDVFFALAGGRFDAHDFVEDVLAA					
	10	20	30	40	50	60
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNKHHRYAVIEMGMNHFGELAVLTXIAKP					
a081	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNKHHRYAVIEMGMNHFGELAVLTQIAKP					

268

	130	140	150	160	170	180
m081.pep	190	200	210	220	230	240
a081	190	200	210	220	230	240
m081.pep	250	260	270	280	290	300
a081	250	260	270	280	290	300
m081.pep	310	320	330	340	350	360
a081	310	320	330	340	350	360
m081.pep	370	380	390	400	410	420
a081	370	380	390	400	410	
m081.pep	430	440	450			
a081	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

g082.seq

```

1  aTGTGGTTGT TGAAGTTGCC TGCCGTCGCC GAAACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATCTC CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGGT TCACATTATC GCGCCACGCC
151 TTCGCCAAGC TTTGCAACGC GGCAAGCGTG TCATCGACTT TCAACGCGCC
201 GCCCAAAGCC GCGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCGCCCG
251 CAGACAATAC GCCTCCAACA AAATCATGCG CGTCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC TTCCCGAATA TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTTGT TTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTCATAT TTGCTTTCGT TAATATTCGG
451 CGGCGGACAC CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGTCTGT
501 GGTAAACAC AGATTATTTT CCCATTCTCA TTCGGCATTT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGCCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGACT GTCTGTGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCGGCAC ATCGGGGACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

g082.pep

```

1  MWLLKLPAVA ETASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTLSRHA
51  FANVCNAASV SSTFNAPPKA AQSSRETTTA AAPADNTPPT KSCASNRPAA
101 NAKNTSPSRI SRLSVTMRDT GLFSDGIGSL RAWQMKFRSS GFIFAFVNIR
151 AADTSVAADF FIACFAVVKH RLFSSHSAF FLYVSFFERRI FSRFAFSRIP
201 RRGVVGLSVD KGKVIARH IGDIPPKIIA VIGQLVGFD TPTAESA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

m082.seq

```

1  ATGnnGTTGT TGAAGTTGCC TGCCGTCGCC AACACGGCAT CATCGCCGAA
51  ACGGcGGCGC AATACCGCAG CCAGCATTTT CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAAACGGAT TCACATTTTC ACGCCACGCC
151 TTTGCCAGCG TTTGCAATGC GGCAAGCGTG TCATCGACTT TCAACGCGCC

```

```

201 ATCCATTGCA GCACAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCAG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CGTCAAACCG CTCGCCCCGC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CCGTTACGAT
351 CGCGGACACG GGTTTGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGCG
401 AGATGAAATT TAGGTCCAGT GGTTCATAT TTACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAACAC AGATTATTTT CCCATTCTCA TTCGGAATT TTTCTGTACG
551 TATCATTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 256; ORF 082>:

```

m082.pep
  1 MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTFSRHA
 51 FASVCNAASV SSTFNAPSIA AQSSRETTA AAPAANTSST KSCASNRSAP
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSXF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGQSDV KGKVIAFALH IGNIPPKIIA VIGQLVGFD TPTAESAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 082 shows 92.7% identity over a 247 aa overlap with a predicted ORF (ORF 082.ng) from *N. gonorrhoeae*:

m082/g082

	10	20	30	40	50	60
m082.pep	MXLLKLPVAVANTASSPKRRRNTAASISFTVVLPPEPVMPNTNGFTFSRHAFASVCNAASV					
g082	MWLLKLPVAETASSPKRRRNTAASISFTVVLPPEPVMPNTNGFTLSRHAFANVCNAASV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m082.pep	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRSAPANAKNTSPARMSRLSVTMRDT					
g082	SSTFNAPPKAAQSSRETTTAAAPADNTPPTKSCASNRPAPANAKNTSPSRISRLSVTMRDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m082.pep	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF					
g082	GLFSDGIGSLRAWQMKFRSSGFIFAFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m082.pep	FLYVSFFRRIFSRFAFSRIPRRGVVGQSDVKGKVIAFALHIGNIPPKIIAVIGQLVGFD					
g082	FLYVSFFRRIFSRFAFSRIPRRGVVGLSVDKGKVIAFARHIGDIPPKIIAVIGQLVGFD					
	190	200	210	220	230	240
m082.pep	RPTAESAX					
g082	RPTAESAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 257>:

a082.seq

```

  1 ATGTGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA
 51 ACGGCGGGCG AATACCGCAG CCAACATTTC CTTCACCGTC GTCTTGCCGC

```

270

```

101 CCGAGCCGGT AATACCGAAC ACAAACGGGT TCACATTCTC GCGCCACGCC
151 TTCGCCAACA TTGCAACGC GGTAAAGCGTG TCATCGACTT TCAACGCGCC
201 ATCCATTGCA ACGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCCG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CATCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTCGCTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTCATAT TACTTTCGT TAATATTCGG
451 GCGCGGACAC CATCGGTAGC GGCTGATTT TTTATCGCCT GTTTGCTGT
501 GGTAAAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCGTCGAT AAAGGCAAGG TTATGTCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
201 AACTCGTCGG TTCGATACC CGTCCAACG CCGAATCCG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

a082.pep

```

1 MWLLKLPAVA KTALSPKRRR NTAANISFTV VLPPEVPVNP TNGFTFSRHA
51 FANICNAVSV SSTFNAPSIA TQSSRETTA AAPAANTSST KSCASNPPA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFITFVNIR
151 AADTSVAADF FIACFAVKH RLFSSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVVQSV D KGVIAFALH IGNIPPKIIA VIGQLVGFDT RPTAESAX*

```

m082/a082 95.5% identity over a 247 aa overlap

	10	20	30	40	50	60
m082.pep	MXLLKLPAVANTASSPKRRRNTAASISFTVVLPPEVPMPNTNGFTFSRHA	FASVCNAASV				
a082	MWLLKLPAVAKTALSPKRRRNTAANISFTVVLPPEVPVNPNTNGFTFSRHA	FANICNAVSV				
	70	80	90	100	110	120
m082.pep	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRS	PANAKNTSPARMSRLSVTMRDT				
a082	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRP	PANAKNTSPARMSRLSVTMRDT				
	130	140	150	160	170	180
m082.pep	GLLSDGIGSLRAWQMKFRSSGFITFVNIRAADTSVAADFFIACFAVKH	RLFSSHSAF				
a082	GLLSDGIGSLRAWQMKFRSSGFITFVNIRAADTSVAADFFIACFAVKH	RLFSSHSAF				
	190	200	210	220	230	240
m082.pep	FLYVSFFRRIFSRFAFSRIPRRGVVQSV D KGVIAFALHIGNIPPKIIA	VIGQLVGFDT				
a082	FLYVSFFRRIFSRFAFSRIPRRGVVQSV D KGVIAFALHIGNIPPKIIA	VIGQLVGFDT				
	190	200	210	220	230	240
m082.pep	RPTAESAX					
a082	RPTAESAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

g084.seq

```

1 ATGAAacaAT CCGcccgaat aAAAAATATG GATCAGACAT TAAAAAATAC
51 attgggcatt tGCGCGcttt tagcctTTTG TTTTggcgcG gccatCGCAT
101 CAGGTATCA CTGGAATAT GAATACGGCT ACCGTATTTC TGCCGTGGGC
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GCTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCCTT CTTATCAGAT AGTCGGTTTCG
301 ATATTGAAA GCAATCCTGC CGAGGCGCGT GAATTGTTCG GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTTATTTT GGCTTGACAG

```

271

401 TTTGGAAATA TTGTGTATCT GTGGGGGTAT TTGCTGACGT AAAAACTAT
 451 AAACGTCGCA GCAAAATATG GCTGACCATA TTATTGACTT TGATTTTGTG
 501 CTGCGCGGTG ATGGAGAAAA TCGccggcga taaAGATTGG CGAGaacctg
 551 atgccggcct gttgttgaat ATTTTcgacc tgtattaCga cttggctttc
 601 cgcgccggca cAATATGCCG CCAAGCGCGC CCACattttg gaagCagcaa
 651 aaaaagcgtC AACATGGCAt atccgccaac ttgcgcccaa gTataa

This corresponds to the amino acid sequence <SEQ ID 260; ORF 084.ng>:

g084.pep

1 MKQSARIKNM DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
 51 ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS
 101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS VGVFADVKNY
 151 KRRSKIWLTI LLTLILSCAV MEKIDGDKDW REPDAGLLLN IFDLYYDLAF
 201 RAGTICRQAR PHFGSSKKSVMAYPPTCAQ V*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 261>:

m084.seq

1 ATGAAACAAT CCGCCcGAAT AAAa.ATATG AATCAGACAT TACTTTATAC
 51 ATTGGGCATT TGCGCGCTTT TAACCTTTnn nnnnnnnnnnn nnnnnnnnnnn
 101 nnnnnTATCA CCCnGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT
 151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG
 201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
 251 TGCCGCTCGG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGCTTCG
 301 ATATTGGAAA GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC
 351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTT GGCTTGACAG
 401 TTTGGAAATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAACTAT
 451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTG
 501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
 551 ATGCCGCGCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTGGCT.TC
 601 CGCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTG GAAGCAGCAA
 651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

This corresponds to the amino acid sequence <SEQ ID 262; ORF 084>:

m084.pep

1 MKQSARIKXM NQTLTYTLGI CALLTFXXXX XXXXXYHPEY EYGYRYSAVG
 51 ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS
 101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS GGVFADVKNY
 151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLLN IFDLYYDLAX
 201 RAGTICRQAR PHFGSSKKSVMAYPSCCAQ V*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/g084

	10	20	30	40	50
m084.pep	MKQSARIKXMNQTLTYTLGICALLTF-----YHPEYEGYRYSAVGALASVVFLLL				
	: :				
g084	MKQSARIKNMDQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVGALASVVFLLL				
	10	20	30	40	50
	60	70	80	90	100
m084.pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILESNPAEAREFVGNLPGSL				
g084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILESNPAEAREFVGNLPGSL				
	70	80	90	100	110
	120	130	140	150	160
m084.pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL				
g084	YFVQALFFIFGLTVWKYCVSVGVFADVKNYKRRSKIWLTI LLTLILSCAVMEKIDGDKDW				
	130	140	150	160	170
	130	140	150	160	170

	180	190	200	210	220
m084 . pep	REPDAGLLLNIFDLYDLAXRAGTICRQARPHFGSSKKSVNMAYPSCCAQVX				
g084	REPDAGLLLNIFDLYDLAFRAGTICRQARPHFGSSKKSVNMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

a084 . seq

```

1  ATGAAACAAT CCGCCCGAAT AAAAAATATG GATCAGACAT TAAAAAATAC
51  ATTGGGCATT TCGCGCTTT TAGCCTTTG TTTTGGCGCG GCCATCGCAT
101 CAGGTATCA CTTGGAATAT GAATACGGCT ACCGTATTTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCGG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTCG
301 ATATTGGAAT GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC
351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTT GGCTTGACAG
401 TTTGGAGATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAAACTAT
451 AAACGCCGCA GCAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCTTCC
601 .GCGCCGCA CAATATGCCG CCAAGCGCGC CCACATTTG GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

a084 . pep

```

1  MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG
51  ALASVVFLLL LARGFPRVSS VLLLIYVGT ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFVGNLPGSL YFVQALFFIF GLTVWRYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYDLAS
201 XAGTICRQAR PHFGSSKKSV NMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKXMQNTLLTYTLGICALLTFXXXXXXHPEYGYRYSAVGALASVVFLLL					
a084	MKQSARIKMDQTLKNTLGIALLAFCFGAAIASGYHLEYEYGYRYSAVGALASVVFLLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILESNPAEAREFVGNLPGSL					
a084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILESNPAEAREFVGNLPGSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
	190	200	210	220	230	
m084 . pep	REPDAGLLLNIFDLYDLAXRAGTICRQARPHFGSSKKSVNMAYPSCCAQVX					
a084	REPDAGLLLNIFDLYDLASXAGTICRQARPHFGSSKKSVNMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGCGACGCGT TGAAAGATAA

```

```

51  GGCAAAGGC GTGTCCTGA TCGGCGTCGA TCGCGCCGAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151 GCGGTTTCAGA CGGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201 CAGCCCCGCC TCGCGAGTT TCGATATGTT TAAAGGCTAC GCGCACC GTT
251 CGGAAGTGT tatCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

g085.pep

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGGL NLTDCVTLEE
51 AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

m085.seq

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCCTG CGCGATGCAC TGGTAGGCAA
51  GGCAAAGGC GTGTCCTGA TTGGTGTCGA TCGCGCCGAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151 GCCGTTTCAGA CGGCATATGC CCAAGCCGAA GCAGGCGATA TTGTGTTGCT
201 CAGCCCCGCC TCGCGAGCT TTGATATGTT CAAAGGCTAC GCGCACC GTT
251 CGGAAGTGT TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

m085.pep

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGGL NMTDCATLGE
51 AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

m085/g085

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGGLNMTDCATLGEAVQTAYAQA E					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGGLNLTDCVTLEEA VQTAYAQA E					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

a085.seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCCTG CGGACGCGC TTGCCGGCAA
51  GGCAAAGGC GTGTCCTGA TCGGTGTCGA TCGCGCCGAA ATCCGCCGCG
101 ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151 GCGGTTTCAGA AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTCTGCT
201 CAGCCCCGCC TCGCGAGTT TCGATATGTT TAAAGGCTAC GCGCACC GTT
251 CGGAAGTGT TATCGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

a085.pep

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATLEE
51 AVQKAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

m085/a085 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGGLNMTDCATLGEAVQTAYAQA E					

274

```

|||||
a085  MGKGQDFTPLRDALAGKAKGVFLIGVDAPQIRRDLDGCDLNMTDCATLEEAVQKAYAQAE
      10      20      30      40      50      60
      70      80      90
m085.ppep AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX
|||||
a085  AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX
      70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 271>:

```

g086.seq
1  ATGGTGGTGC TGATGACGGC GTTCGGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCGAAGG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GGCAGGCGGG GTTCGTCGTT GCCGGCCTTA TAGCGAGCGG TTTTGTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CTTATCCGGC CTGTGCTGG TAGCCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCa AGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTGCGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GGCAGGGGAC GGCCAACCTG ATTATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAAACAT TAGAAATGTA CGgcCGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTTCG
551 GTTCGTTTGT CGTCATTACC GTCATTACCG TTGGAATGCT GTTCTGCGCA
601 GGATTGCCGT GGAATATTT TTTTGTCTCG GTAGGCAGCG TCTTGGGTGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CCGGTAGTGG
701 CATTTTGGGA CCCGTGGAAA GACCCGACAG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TGCGAGTTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGTCCAT CATCGCTGAA GAATTCGGCT TCTTCGGGAT GTCGGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGtttgA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGctgCcg tTGATGTCCT ATGGcggTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATCGATT
1151 ATGAAAACCG CCAGAAAATG CGCGGTTACC GGGTGGAGTA AA

```

This corresponds to the amino acid sequence <SEQ ID 272; ORF 086.ng>:

```

g086.ppep
1  MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGFLW
51  FLCRMRTWRR LVPWIFALSG LLLVAVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VITVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFLDPWK DPQAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGWLVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGNVIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLLL RIDYENRQKM RGYRVE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 273>:

```

m086.seq
1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCAAAAG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCCTTA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CCTATCCGGC CTGTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCa AGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTGcGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GGCAGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGrCACGT
451 CGTGAAaACAT TAGAAATGTA CGGCCGTWTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTTCG

```

275

```

551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCGTCCTG GTAGGCAGCG TCTTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTTGA CCCGTGGAAA GACCCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTGGG
801 TGCGAGTTTG AGCAAACGCG GCTTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTGGAT CGGkrTCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA mCAAAGyCT GACGCGGCCG Tg.AtGTCCw ATGGCGGTTT
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTkG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGTTATC GGGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 274; ORF 086>:

m086.pep

```

1  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTRREE VLRSMESLGW QSIWRGTANL IMSATNPQXR
151 RETLEMYGRX RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFLDPWK DPQAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGLVVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGXQ SFFNIGVNIG
351 ALPXKGLTXP XMSXGGSSVF FMLISMMLLX RIDYENRRKM RGYRVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 086 shows 96.7% identity over a 396 aa overlap with a predicted ORF (ORF 086.ng)

from *N. gonorrhoeae*:

m086/g086

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	: : : : :					
g086	MVVLMTAFGLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLWFLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTRREE					
	: : : : :					
g086	LVPWIFALSGLLLVAVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTRREE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESLGWQSIWRGTANLIMSATNPQXRRETLEMYGRXRRAILPIMLVAFGLVLIMVQ					
	: : : : :					
g086	VLRSMESLGWQSIWRGTANLIMSATNPQARRETLEMYGRFRAILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQVVAFLDPWK					
	: : : : :					
g086	PDFGSFVVITVITVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQVVAFLDPWK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m086.pep	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
	: : : : :					
g086	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360

276

```

m086.pep      IPCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFNIGVNIGALPKKGLTXP
               |||||||||||||||||||||||||||||||||||||||||:|||||
g086          IPCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFNIGVNIGALPTKGLTLP
               310      320      330      340      350      360

               370      380      390
m086.pep      XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX
               |||||||||||||||||||:|||||||
g086          LMSYGGSSVFFMLISMMLLLRIDYENRQKMRGYRVEX
               370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 275>:

```

a086.seq
1  ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCCGGCTTC
51  TGTGTATTGG GCATCAAAAG AAGCGGGCGA TCAGTTTTTC TATTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTGC
201 CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCGGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GGCGGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAACAT TAGAAATGTA CGGCCGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTTC
551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCTCCTG GTAGGCAGCG TCTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTGGGA CCCGTGGAAA GACCCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TCGGAGTTTG AGCAAACGCG GCTTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGTCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTCAACGCG CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CCGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGCTGCCG TTGATGTCTT ATGGCGGTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGGTTACC GGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 276; ORF 086.a>:

```

a086.pep
1  MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTRREE VLRSMESLGW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK DPQGAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGWLVVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGVNIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLLL RIDYENRRKM RGYRVE*

```

m086/a086 98.0% identity over a 396 aa overlap

```

               10      20      30      40      50      60
m086.pep      MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW FLCRMRTWRR
               |||||||||||||||||||||||||||||||||||||||||
a086          MVVLMTAFSL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGLLW FLCRMRTWRR
               10      20      30      40      50      60

               70      80      90      100     110     120
m086.pep      LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTRREE
               |||||||||||||||||||||||||||||||||||||||||
a086          LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT ELFKLAVILY LASLFTRREE

```

277

	70	80	90	100	110	120
m086.pep	130	140	150	160	170	180
	VLRSMESLQWSIWRGTANLIMSATNPQXRRETLEMYGRXRAIILPIMLVAFGLVLMVQ					
a086	VLRSMESLQWSIWRGTANLIMSATNPQARRETLEMYGRFRAIILPIMLVAFGLVLMVQ					
	130	140	150	160	170	180
m086.pep	190	200	210	220	230	240
	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
a086	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	190	200	210	220	230	240
m086.pep	250	260	270	280	290	300
	DPQGAGYQLTHSLMAIGRGWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
a086	DPQGAGYQLTHSLMAIGRGWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
	250	260	270	280	290	300
m086.pep	310	320	330	340	350	360
	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFNIGVNIGALPKXGLTXP					
a086	IFCYGWLVVRAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFNIGVNIGALPTKGLTLP					
	310	320	330	340	350	360
m086.pep	370	380	390			
	XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX					
a086	LMSYGGSSVFFMLISMMLLLRIDYENRRKMRGYRVEX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

g087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GGCGGAACGG GCGGACACAT
51  TTTCCAGCT CTGGCTGTGG CGGATTCAAT GCGCGTGCGC GGTCAATCATG
101 TAATTGGCT GGGCAGCAAG GATTTCGATG AAGAGCGCAT CGTGCCGCAA
151 TACGGCATA GCTTGGAAAC GCTGGCGATT AAAGGAATAC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TTCCGTTTAC TCTGTACAAA ACCGTCCGCG
251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCGT CATCGGCTTC
301 GCGGTTTTG TTACCTTTCC CGGCGTCTG GCGGCGAAAC TCTTGGGCGT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGCTTG TCCAACCGCC
401 AccTGTCGCG ctGGGCGAAA CGGGTGTGT ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGTTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGCGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCAGT TTGGGTGCGG ACGTTTTGAA CAAAACCGTA
601 CCGCAGGCGT TGGCACTGCT GCCTGAAGAG GTGCGCCGCG AGATGTACCA
651 CCAGTCGGGG CGTAACAAGC TGGGCAATCT TCAGGCGGAT TATGACGCGT
701 TGGGCGTGAA AGCGGAATGC GTGGAATTTA TTACCGACAT GGTGTCCGCC
751 TACCGTGATG CCGATTGGT GATTTGCCGT GCCGGCGCGC TGACGATTGC
801 CGAGTTGACG GCGGCGGGGC TGGGCGCGTT GTTAGTGCCG TATCCTCAGC
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTCATGGT GCAGGCAGAA
901 GCGGGCTGCG TGTTGCCGCA AACCAGTTG ACGGCGGAAA AACTCGCCGA
951 AATCCTCGGC AGCCTCAACC GCGAAAATG CCTCAAATGG GCGGAAAACG
1001 CCCGTACGTT GGCATTGCCG CACAGCGCGG ATGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

g087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRVR GHVVIWLGSK DSMEERIVPQ
51  YGIRLET Lai KGIRNGIKR KLMLPFTLYK TVREAQRIIR KHRVECVIGF
101 GGFVTFPGGL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTV

```

201 PQALALLPEE VRPQMYHQSG RNKLGNLQAD YDALGVKAEC VEFITDMVSA
 251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAUDDHQT ANARFMVQAE
 301 AGLLLPQTQL TAEKLAEILG SLNREKCLKW AENARTLALP HSADDVAEAA
 351 IACAA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

m087.seq
 1 ATGGGCGGTA AAACCTTTAT GCTGAwkkCG GCGGGAACGG GCGGACATAT
 51 TTTCCCCGCG CTGGCGGTGG CCGATTCAAT GCGCGCGCGC GGCCATCATG
 101 TGATTGGCT GGGCAGCAAG GATTGATGG AAGAGCGTAT CGTGCCGCAA
 151 TACGGCATAC GCTTGGAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
 201 CATCAAACGC AAATGATGC TGCCGTTTAC TTTGTATCAA ACCGTCCGCG
 251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCGT CATCGGCTTC
 301 GCGGCTTCG TTACCTTCCC CCGCGGTTTG GCGGCGAAGC TATTArGCGT
 351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC
 401 ACCTGTCGCG CTGGGCGAAG CCGGTGTTGT ACGCTTTTCC GAAAGCGTTC
 451 AGCCACGAAG GCGGCTTGGT CCGCAACCCC GTCCGCGCGC ATATTAGCAA
 501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
 551 TTTTGGTGGT CCGCGGCAGT TTGGGCGCGG ACGTTTGA CAAAACCGTA
 601 CCGCATGCAT TGGCTTTGCT GCCCGACAAT GCGCGTCCGC ATATGTACCA
 651 CCAATCGGGA CCGGCAAGC TGGGCATCTT GCAGGCGnnn nnnnnnnnnn
 701 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
 751 nnnGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG CGGTTGACGA
 801 TCACCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG GCGGGATTGC
 851 TGTGCGCGCA AACCAGTTG ACGGCGGAAA AACTCGCCGA GATTCTCGGC
 901 GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG CCCGTACGTT
 951 GGCACTGCCG CACAGTGCGG ACGACGTGGC GGAAGCCGCG ATTGCGTGTG
 1001 CGGCGTAA

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

m087.pep
 1 MGGKTFMLXX GGTGGHIFPA LAVADSLRAR GHVHVLGSK DSMEERIVPQ
 51 YGIRLETIAI KGVRGNGIKR KLMLPVTLYQ TVREAQRIIR KHRVECVIGF
 101 GGFVTFPGGL AAKLLXVPIV IHEQNAVAGL SNRHLRWAK RVLVAFPKAF
 151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVNLKTV
 201 PHALALLPDN ARPHMYHQSG RGKLGILQAX XXXXXXXXXX XXXXXXXXXX
 251 XAGLGALLVP YPHAUDDHQT ANARFMVQAE AGLLLPQTQL TAEKLAEILG
 301 GLNREKCLKW AENARTLALP HSADDVAEAA IACAA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/g087

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVHVLGSKDSMEERIVPQY	GIRLETIAI				
g087	MGGKTFMLMAGGTGGHIFPALAVADSLRVRGHHVHVLGSKDSMEERIVPQY	GIRLETIAI				
	10	20	30	40	50	60
	70	80	90	100	110	120
m087.pep	KGVRGNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
g087	KGIRGNGIKRKLMLPFTLYKTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
g087	IHEQNAVAGLSNRHLRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130	140	150	160	170	180

279

	190	200	210	220	229
m087.pep	RLKILVVGSSLGADVLNKTVP	PHALALLPDNARPHMYHQSGR	GKLGILQA-----		
g087	RLKILVVGSSLGADVLNKTVP	QALALLPEEVRPQMYHQSGR	NKLGNLQADYDALGVKAEC		
	190	200	210	220	230 240
m087.pep	-----			AGLGALLVPYPH	AVDDHQTANARFMVQAE
g087	VEFITDMVSAYRDADLVICR	AGALTIAELTAAGLGALLVP	YPH	AVDDHQTANARFMVQAE	
	250	260	270	280	290 300
m087.pep	AGLLLPQTQLTAEKLAEL	GLNREKCLKWAENARTLAL	PHSADDVAEAAIACAAX		
g087	AGLLLPQTQLTAEKLAEL	GLNREKCLKWAENARTLAL	PHSADDVAEAAIACAAX		
	310	320	330	340	350

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGGAACGG GCGGACATAT
51  TTTCCCGCG CTGGCGGTGG CGGATTCATT GCGCGCGCGC GGCCATCATG
101 TAATTTGGCT GGGCAGCAAG GATTCGATGG AAGAGCGCAT CGTGCCGCAA
151 TACGACATCC TGCTCGAAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TGCCGTTTAC TTTGTATCAA ACTGTCCGCG
251 AAGCGCAGCA GATTATCCGC AAACACCGTG TCGAGTGCGT CATCGGCTTC
301 GCGGCGTTCG TTACCTTTCC CGGCGGTTTG GCGGCGAAGT TATTAGGCGT
351 GCGGATTGTG ATTCACGAGC AAAACGCCGT GCGAGGTTTG TCCAACCGCC
401 ACCTGTCGCG CTGGGCGAAG CGGGTGTTGT ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCGC ATATTAGCAA
501 CCTGCCCGTG CTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCAGT TTGGGCGCGG ACGTTTTGAA CAAACCGTA
601 CCGCAGGCAT TGCTTTGCT GCCCGACAAT GCGCGTCCGC AGATGTACCA
651 CCAATCGGGA CGGGCAAGC TGGGCAGCTT GCAGGCGGAT TACGACGCGC
701 TGGGCGTGCA AGCGGAATGC GTGGAATTTA TTACCGATAT GGTGTCGCGC
751 TACCGCGATG CCGATTTGGT GATTTGCCGT GCCGCGCGCG TGACGATTGC
801 CGAGTTGACG GCGGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG
901 GCGGGATTGC TGTGCGCGCA AACCCAGTTG ACGGCGGAAA AACTCGCCGA
951 GATTCTCGGC GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG
1001 CCGTACGTT GGCAGTCCG CACAGTGCGG ACGACGTTGC CGAAGCCGCG
1051 ATGCGTGTG CCGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRAR GHVHVLGSK DSMEERIVPQ
51  YDILLETLAI KVRGNGIKR KLMLPFTLYQ TVREAQIIIR KHRVECVIGF
101 GGFVTFPGGL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTVP
201 PQALALLPDN ARPQMYHQSG RGKLGSLQAD YDALGVQAE VEFITDMVSA
251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE
301 AGLLLPQTQL TAEKLAELG GLNREKCLKW AENARTLALP HSADDVAEAA
351 IACAA*

```

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVHVLGSKDSMEERIVPQY	GIRLETLAI				
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVHVLGSKDSMEERIVPQY	DILLETLAI				
	10	20	30	40	50	60

280

	70	80	90	100	110	120
m087.pep	KGVRGNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVP					
a087	KGVRGNGIKRKLMLPFTLYQTVREAQQIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQ					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m087.pep	RLKILVVGGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQAXXXXXXXXXXX					
a087	RLKILVVGGSLGADVLNKTVPQALALLPDNARPMYHQSGRGKLGSLQADYDALGVQAE					
	190	200	210	220	230	240
			250	260	270	280
m087.pep	XX-----XXXXXXXXXAGLGALLVPYPHAVDDHQTANARFMVQAE					
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
	290	300	310	320	330	
m087.pep	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
a087	AGLLLPQTQLTAEKLAELGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

g088.seq

```

1  ATGTTTTTAT GGCTCGCACA TTTCAGCAAC TGGTAAACCG GTCTGAATAT
51  TTTTCAATAC ACCACATTCC GCGCCGTTAT GCGGCGTTG ACCGCCTTGG
101 CGTTTTCCCT GATGTTCCGC CCGTGGACGA TACGCAGGCT GACCGCGCTC
151 AAATGCGGGC AGGCAGTGCG TACCGACGGC CCGCAAACCC ACCTCGTCAA
201 AAACGGCAGC CCGACGATGG GCGGTTGCTG GATTCTGACC GCCATTACCG
251 TGTCCACCCCT GTTGTGGGGC AACTGGGCGA ACCCGTATAT CTGGATTCTC
301 TTGGGCGTAC TGCTTGCCAC CGGTGCGCTC GGTTTTTACG ACGACTGGCG
351 CAAAGTCGTT TATAAGACC CCAACGGCGT GTCCGCCAAA TTCAAATGG
401 TGTGGCAGTC AAGCGTTGCC GTTatcgcCG GTttggcaTT GTTTTACctt
451 gCcgcaAATT CCGCCAACAA TATTTTGATT GTCCCGtttT TCAAACAAAT
501 CGCCCTGCCG CTGGGCGTGG TCGGCTTttt gGtgttgTCT TACCTGACCA
551 TCGTCGGCAC ATCCAACGCC GTCAACCTCA CcgaCGGCTT GGACGGCCTT
601 GCCGCcttcc cgttcgtcct cgttgccgcC GGGCTCGCCA ttttcgccTA
651 CGTCAGCGGA CACTACCAAT TTCCCAATA CCTCCAGCTT CCCTATGTCG
701 CCGGCGCGAA CGAAGTCGCT ATATTCTGCA CCGCCATGTG CCGGCGGTGC
751 CTCGGATTTT TGTGGTTCAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA
801 TGTCCGCGCG CTGGCATTGG GTGCCGCGCT CGGTaccGtt gCCGTcaTcg
851 tCCGCCAAGA ATTTGTcttc gtcattaTGG GCGGTCTGTT cgtcgtagaa
901 gccgtgTCCG TTATGCTTCa tgtcggCTGG TACAAGAAAA Ccaaaaaacg
951 CATCTTcCTg acgGcaccga ttcacacca ttaCCaactt cgatgCTGga
1001 aagaaacgca agtcgctcgt CGTTtCTGGA TTAtTAccat cgtcggtgtt
1101 tTgataggtt tGagtacctT caAAattcgc ggaactatg ccgTCCGAAC
1101 ACCTTTTCTAGA CGGCATTGA ACGCGCAATA A

```

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

g088.pep

```

1  MFLWLAHFSN WLTGLNIFQY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSILIT AITVSTLLWG NWANPYIWIL
101 LGVLLATGAL GFYDDWRKV YKDPNGVSAK FKMVWQSSVA VIAGLALFYL
151 AANSANNILI VPFFKQIALP LGUVGFLVLS YLTIVGTSNA VNLTGDLGDL

```

201 AAFPEVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
301 AVSVMLHVGW YKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV
351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 285>:

```
m088.seq
1  ATGTTTTTAT  GGCTCGCACA  TTTCAGCAnC  TGGTTAACCG  GTCTGAATnn
51  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
101 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
151 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
201 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
251 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
301 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
351 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
401 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
451 nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn  nnnnnnnnnnn
501 nnnnnnnnnnn  nnnGGCGTGG  TCGGCTTTTT  GGTGTTGTCT  TACCTGACCA
551 TCGTCGGCAC  ATCAATGCG  GTCAACCTCA  CCGACGGCTT  GGACGGCCTT
601 GCGACCTTCC  CCGTCGTCT  CGTGCGCCG  GGCCTCGCCA  CTCTCGCTTA
651 TGCCAGCGGC  CACTCACAA  TTGCCAATA  CCTGCAATTA  CCTTACGTTG
701 CCGGCGCAAA  CGAAGTGGT  ATTTTCTGTA  CCGCATATGT  CGGCGCGTGC
751 CTCGGTTTCT  TGTGGTTAA  CGCCTATCCC  GCGCAAGTCT  TTATTGGGCA
801 TGTCCGTGCA  GTTGCAATT  GTGCCGCGCT  CGGTACCCTC  GCGGTTATCG
851 TCCGCCAAGA  GTTGTCTCT  GTCATTATG  GCGGATTATT  GTGCTGTAAG
901 GCCGTATCCG  TTATGCTTCA  GGTGGCTGG  TATAAGAAAA  CCAAAAAACG
951 CATCTTCCGT  ATGGCGCCCA  TCCATACCA  CTAGCAACAA  AAAGGCTGGA
1001 AAGAAACCCA  AGTCGTCGTC  CGCTTTTGTA  TTATTACCAT  CGTCTTGGTG
1051 TTGATCGGTT  TGAGTACCCT  CAAAAATCCG  TGAACCTATG  CCGTCTGAAC
1101 ATCTTTTCTC  GCGATTTTGA  CGGCAATA  A
```

1 MFLWLAHFSN WLTGLNIFOY TTFRAVMAAL TALAFSLMEG PWTIRRLTAL
51 KCGQAVRTDG PQTHLVKNGT PTMGSSLILT AITVSTLLWG NWANPYIWIL
101 LGVLLATGAL GFYDDWRKVY YKDPNGVSAK FKMVQSSVA VIAGLALFYL
151 AANSANNILI VPFFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTDGLDGL
201 AAFPFLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
301 AVSVMHLHWG YKTKKRIFL TAPIHHYQL RCWKETQVVV RFWIITIVVV
351 LIGLSTLKIR GNYAVRTPFR RHLNAQ*

This corresponds to the amino acid sequence <SEQ ID 286; ORF 088>:

```
m088.pep
  1  MFLWLAHFSX WLTGLNXXXX XXXXXXXXXXXX XXXXXXXXXXXX XXXXXXXXXXXX
51  XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
101 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX
151 XXXXXXXXXXX XXXXXXXXXXX XGVVGFVLVS YLTIVGTSNA VNLTDGLDGL
201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEV IFCTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGLFVVE
301 AVSVMLOVGW YKTKKRIFL MAPIHHHYEQ KGWKETOQVV RFWIITIVLV
351 LIGLSTLKIR XTYAVXTSFR RHLNAQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 088 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 088.ng) from *N. gonorrhoeae*:

m088/q088

m088.pep
 GVVGFVLVSYLTIVGTSNAVNLTGDLGDLA
 |||||
 g088
 IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFVLVSYLTIVGTSNAVNLTGDLGDLA
 150 160 170 180 190 200

```

                                40      50      60      70      80      90
m088.pep  TFPVVLVAAGLAI FAYASGHSQFAQYLQLPYVAGANEVVI FCTAMCGACLGFLWFNAYPA
           :|| ||||| ||||| :|| ||| :||| ||||| :||| ||||| ||||| |||||
g088      AFFPVLVAAGLAI FAYVSGHYQFSQYLQLPYVAGANEVAI FCTAMCGACLGFLWFNAYPA
           210      220      230      240      250      260

                                100     110     120     130     140     150
m088.pep  QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGLFVVVEAVSVMLQVGWYKTKKRIFLM
           ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g088      QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGLFVVVEAVSVMLHVGWYKTKKRIFLT
           270     280     290     300     310     320

                                160     170     180     190     200
m088.pep  APIHHHYEQKGWKETQVVVRFWIIITIVLVLIGLSTLKIRXTYAVXTSFRRHNAQX
           ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
g088      APIHHHYQLRCWKETQVVVRFWIIITIVVVLIGLSTLKIRGNYAVRTPFRRHNAQX
           330     340     350     360     370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 287>:

```

a088.seq
1  ATGTTTATAT  GGCTCGCACA  TTTTCAGCAAC  TGGTTAACCG  GTCTGAATAT
51  TTTTCAATAC  ACCACATTCC  GCGCCGCTCAT  GGCGCCGTGT  ACCCGCTTGG
101 CGTTTTCCTT  GATGTTTCGG  CCGTGGACGA  TACGCAAGGT  GACCGCGCTG
151 AAATGCGGGC  AGGCAGTGCG  TACCGACGGT  CCGCAAACCC  ACCTCGTCAA
201 AAACGCGACG  CCGACGATGG  GCGGTTTCGT  GATTCTGACC  GCCATTACCG
251 TGTCCACCCT  GTTGTGGGGC  AACTGGGGCA  ACCCGTATAT  CTGGATTCTC
301 TTGGGCGTAT  TGCTCGCCAC  GGGGCGCACT  GGTTTTACG  AGCACTGGCG
351 CAAAGTCGTC  TATAAAGACC  CCAACGGCGT  GTCCGCCAAA  TTCAAATGG
401 TGTGGCAGTC  AAGCGTTGCC  ATTATCGCCG  GTTTGGCATT  GTTTTACCTT
451 GCGGCCAATT  CCGCCAACAA  TATTTTGATT  GTCCCGTTCT  TCAAAACAA
501 CGCCCTGCGC  CTGGGCGTGG  TCGCGTTTTT  GGTGTGTGCT  TACCTGACCA
551 TCGTCGGCAC  ATCCAATGCC  GTCAACCTCA  CCGACGGCTT  GGACGGCCTT
601 GCGACCTTCC  CCGTCGTCTT  CGTTGCCGCC  GGCTTCGCGA  TCTTCGCCTA
651 TGCCAGCGGC  CACTACAATT  TTGCCCAATA  CCTGCAATTA  CCTTACGTTG
701 CGGGCGCAAA  CGAAGTGGTG  ATTTTCTGTA  CGCCCATGTG  CGCGCGGTGC
751 CTCGGTTTCT  TGTGGTTTAA  CGCCTATCCC  GCGCAAGTCT  TTATGGGCGA
801 TGTGCGTGCA  TTGGCATTGG  GTGCGCGCTT  CGGTACCGTC  GCGCTCATCG
851 TCCGCCAAGA  GTTTGTCTTC  GTCAATTATG  GCGGATTATT  TGTCGTAGAA
901 GCGGTATCCG  TTATGCTTCA  GGTGCGGTGG  TATAAGAAAA  CAAAAAAGC
951 CATCTTCTGT  ATGGCGCCCA  TCCATCACCA  CTACGAACAA  AAAGGCTGGA
1001 AAGAAACCCA  AGTCGTGCTC  CGCTTTTGGA  TTATTACCAT  CGTCTTGGTG
1051 TTGATCGGTT  TGAGTACCCT  CAAAATCCGC  TGAACCTATG  CCGTCTGAAC
1101 ACCTTTTCAG  CGGCATTTGA  ACGGCAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 288; ORF 088.a>:

```

a088.pep
1  MFLWLAHFSN WLTGLNIFQY TTFRAVMAAL TALAFSLMEG PWTIRRLTAL
51  KCGQAVRTDG PQTHLVKNGT PTMGGSLILT AITVSTLLWG NWANPYIWL
101 LGVLLLATGK GFYDDWRKVV YKDPNGVSAK FKVMWQSSVA I1AGLALFYL
151 AANSANNILI VPFFKQIALP LGDVGFLVLS YLTIVGTSNA VNLTGDLGDL
201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEVV IFTAMCGAC
251 LGFLWFNAYP AQVFMGDVGA LALGAALGYE AVIVRQEFVL VMGGGLFVVE
301 AVSVMLQVGR YKTKKKRIFL MAPIHHHHYQ KGWKETQVVV RFWIITIVLV
351 LIGLSTLKIR *TYAV*TPFR RHLNAO*

```

m088/a088 99.5% identity over a 205 aa overlap

```

                150      160      170      180      190      200
m088.pep XXXXXXXXXXXXXXXXXXXXXXXXXXXXGVVGFVLVSYLTIIVGTSNAVNLT DGLDGLA
                                     |||||
a088     IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFVLVSYLTIIVGTSNAVNLT DGLDGLA

```

283

	150	160	170	180	190	200
m088.pep	210	220	230	240	250	260
	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGFLWFNAYPA					
a088	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
m088.pep	270	280	290	300	310	320
	QVFMGDIVGALALGAALGTVAIVIRQEFVLVIMGGFLVVEAVSVMLQVGWYKTKKRIFLM					
a088	QVFMGDIVGALALGAALGTVAIVIRQEFVLVIMGGFLVVEAVSVMLQVGWYKTKKRIFLM					
	270	280	290	300	310	320
m088.pep	330	340	350	360	370	
	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

```

g089.seq
1  ATGCCGCCCA  AAATCACGAA  GAGCGGGTTT  TGCAAACCGG  CAATCGCGGC
51  GGCAGTCGCG  CCGACATTCG  TGCCTTTGCT  GTCGTCGATG  AATACCACGC
101 CGTTTTTCTC  GCCGATTTT  TCCACACGGT  GCGGCAAGCC  TTGGAAGGTT
151 TTGACGTGTT  CCAGCAATGC  TTCGCGCGGC  AAACCGACGG  CCTCGCACAA
201 AGCCACGGCA  GCCATAACGT  TGGCGGCGTT  GTGCAAACCT  TGCAGCGGGA
251 TGTCTTGCGT  AGAAATCAAA  TCTTCATTGC  CTTGTTTTAA  ACAGCCCGTC
301 CCGCGTTCCA  ACCAAAAATC  GGCTTCGTGT  TCCAAGGAAA  ACCGTTTCAC
351 TTCACGCCCT  GCCCGTTTCA  TGGCGCGGCA  GAACACGTCG  TCCGCATTCA
401 AAACCTGCAC  TCCATCGCCA  CGGAAAATCT  CGGCTTTGGT  ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

```

g089.pep
1  MPPKITKSGF  CKPAIAAAVA  PTFVPLLSSM  NTPFFSPIF  STRCGKPWKV
51  LTCSSNASRG  KPTASHKATA  AITLAALCKP  CSGMSCVEIK  SSLPCFKQPV
101 PRSNQKSASC  SKENRFTSRP  ARFMARQNTS  SAFKTCTPSP  RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

```

m089.seq
1  ATGCCGCCCA  AAATCACKAw  GAGCGGATTT  TGCAAACCGG  CAATCGCGGC
51  GGCAGTCGCG  CCGACATTCG  TGCCTTTGCT  GTCGTCGATA  AACACCACGC
101 CGTTTTTCTC  GCCGATTTT  TCCACGCGGT  GCGGCAGGCC  TTGGAAGGTT
151 TTGACGTGTT  CGAGCAATGC  TTCGCGCGAC  AAACCGATGG  CCTCACACAA
201 AGCCACkGCA  GCCATGACGT  TAGCGGCGTT  GTGCAKACCT  TGCAACGGwA
251 TGTCTTGCGT  GACAATCAAA  TCTTCATTGC  CTTGTTTCAG  GCGGCCTGTC
301 TCGCGTTCCA  ACCAGAAATC  AGCTTCGTGT  TCCAACGAAA  ACCATTTTAC
351 CTCGCGCCCC  GCACGCTTCA  TCGCGCGGCA  GAACGCATCG  TCCGCATTCA
401 AAACCTGCAC  GCCGTCGCCA  CGGAAAATCT  TGGCTTTGGT  ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

```

m089.pep
1  MPPKITXSGF  CKPAIAAAVA  PTFVPLLSSI  NTPFFSPIF  STRCGRPWKV
51  LTCSSNASRD  KPMASHKATA  AMTLAALCXP  CNMGSCVTIK  SSLPCFRPV
101 PRSNQKSASC  SNENHFTSRP  ARFIARQNAS  SAFKTCTPSP  RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng) from *N. gonorrhoeae*:

m089/g089

284

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPTFVPLLSSINTTFFFSPIFSTRCGRPWKVLTCSSNASRD					
	: : : : :					
g089	MPPKITKSGFCKPAIAAAVAPTFVPLLSSMNTTFFFSPIFSTRCGKPKWVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	: : : : : :					
g089	KPTASHKATAAITLAALCKPCSGMSCVBIKSSLPCFKQPVPRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : :					
g089	ARFMARQNTSSAFKTCTPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

a089.seq

1	ATGCCGCTTA	AAATCACGAA	GAGCGGATTT	TGCAAACCGG	CAATCGCGGC
51	GGCGGTCGCA	CCGACGTTCT	TGCCTTTGCT	GTCGTCGATG	AACACCACGC
101	CATTTTCTC	GCCGATTTT	TCCACGCGGT	GCGGCAGGCC	TTGAAAGGTT
151	TTGACGTGTT	CGAGCAATGC	TTGCGCGGGC	AAACCGACGG	CTTCGCACAA
201	GGCAACGGCA	GCCATCACGT	TAGTGCGGTT	GTGCAAGCCT	TGCAGCGGAA
251	TATCTTGCGT	GGCAATCAAA	TCTTCATTGC	CTTGTTTCAG	GCGACCTGTC
301	TCACGTTCCA	ACCAAAAATC	GGCTTCGTAT	TCCAACGAAA	ACCATTTCAC
351	CTCGCGCCCG	GCGCGCTTCA	TCGCACGACA	GAACGCATCG	TCCGCATTCA
401	AAACCTGCAC	ACCGTCGCCA	CGGAAAATCT	TGGCTTTGGT	ATGCGCGTAG

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

a089.pep

1	MPPKITKSGF	CKPAIAAAVA	PTFVPLLSSM	NTTFFFSPIF	STRCGRP*KV
51	LTCSSNASRG	KPTASHKATA	AITLVALCKP	CSGISCVAIK	SSLPCFRRPV
101	SRSNQKSASY	SNENHFTSRP	ARFIARQNAS	SAFKTCTPSP	RKILALVCA*

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPTFVPLLSSINTTFFFSPIFSTRCGRPWKVLTCSSNASRD					
	: : : : :					
a089	MPPKITKSGFCKPAIAAAVAPTFVPLLSSMNTTFFFSPIFSTRCGRPKWVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	: : : : : :					
a089	KPTASHKATAAITLVALCKPCSGISCVAIKSSLPCFRRPVSRSNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	: : : :					
a089	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

g090.seq

1	ATGCGCGTAG	TCGAGCAAAT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGAAA
---	------------	------------	------------	------------	------------



51	TGTTTCATCAC	CGTCGCCGCA	GTCGGGCGCA	GGCTTTCGGT	GTTTTCCAGT
101	TGGAAGCTGG	AAAGCTCcca	CACCCACACG	TCCGCCTTTT	TGCCTTCgcg
151	ctgCAATtct	gcctccaaga	cggcggtacc	gatATTGCCC	GCAATGAcgg
201	tatccagccc	gcacttgatg	CAGAGatagc	ggaccagggt	ggttaccgTG
251	GTTttgccgt	tgctgCcggt	aategCaatc	accttgctgc	CGCGGCGGtt
301	CAcaatGTCC	gccagCAATt	ggATGTCGCC	TAgCACGCGC	.ccgccgTTT
351	TGctttga				

This corresponds to the amino acid sequence <SEQ ID 296; ORF 090.ng>:

g090.pep
1 MRVVEQIVVA VEMVFGNVHH RRRSRAQAFG VFQLEAGKLP HPHVRLFAFA
51 LQFCLQDGRT DIARNNGIQP ALDAEIADQA GYRGFAVAAG NRNHLVAAAV
101 HNVROOLDVA XHAXERRFA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 297>:

```
m090.seq
1  ATGCGCATAG  TCGAGCAAGT  CGTCGTAGCG  GTCGAGATGG  TCTTCGAAAA
51  TGTTTCAGCA  CTGCGCCGCT  GTCGGGACGCA  GGCCTTCGGT  GTTTTCCAGT
101  TGGAAGACTG  AAAGCTCCAA  CACCCACACG  TCCGCTTTTG  TGCCTTCGCG
151  CTGCCATTCC  GCCTCCAAAA  CCGGCGTGCC  GATATTGCC  GCGATAACGG
201  TATCCAGCCC  GCACTTGATA  CAGAGATAGC  CGACCAGGCT  CGTTACCGTG
251  GTTTTGCCGT  TGCTGCCCGT  AATCGCAATT  ACCTTGTCGT  CCCGGCGGTT
301  CACAATGTCC  GCCAGCAATT  CGATGTCGCC  CAACACGCGT  .CCGCCGTTT
351  TGCTTGTG
```

This corresponds to the amino acid sequence <SEQ ID 298; ORF 090>:

m090.pep
1 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
51 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNYLVPVAV
101 HNVROOFDVA OHAXRREA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 090 shows 83.9% identity over a 118 aa overlap with a predicted ORF (ORF 090.ng) from *N. gonorrhoeae*:

m090/q090

	10	20	30	40	50	60
m090.pep	MRIVEQVVAVEMVFGNVQHRRRSRTQAFGVFQLEAGKLQHPHVRLFALPFLRLQNRR					
	: : : : : : : : : : :					
g090	MRVVEQIVVAVEMVFGNVHRRRSRAQAFGVFQLEAGKLPHPHVRLFALQFCLQDGR					
	10	20	30	40	50	60
	70	80	90	100	110	119
m090.pep	DIARDNGIQPALDTEIADQARYRGFAVAAGNRNYLVVPVHNVRQQFDVAQHAXRRFAX					
	: : : : : : : : : : : : : : : : : : : : : : :					
g090	DIARNNGIQPALDAEIAQAGYRGFAVAAGNRNHLVAAVHNVRQLDVAXHAXRRFAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 299>:

```

a090.seq
1  ATGCGCGTAG  TCGAGCAAGT  CGTCGTAGCG  GTCGAGATGG  TCTTCGAAAA
51  TGTTACAGCA  TGTCGCCGCA  GTCGGGCGCA  GGCTTTCGGT  GTTTTCCAGT
101 TGGAACACTG  AAAGCTCCAA  CACCCACACG  TCCGCCTTTT  TGCCTTCGCG
151 CTGCAATTCC  GCCTCCAAAA  CCGCGCGGCC  GATATTGCCC  CGGATAACGG
201 TATCCAGCCC  ACACTTGATG  CAGAGATAGC  CGACCAGGCT  CGTTACCGTG
251 GTTTTGCCGT  TGCTCCGGT  AATCGCAATC  ACCTTGTGCG  CGCGCGGGTT
301 CACAATTGTC  GCCAGCAATT  CGATGTCGCC  CAACACGCGT  C.CGCCGTTT
351 CGTTATTA

```

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

a090.pep

```

1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA
51 LQFRLQNRRA DIARDNGIQP TLDAEIADQA RYRGFAVAAG NRNHLVAAAV
101 HNVRRQQFDVA QHAXRRFA*

```

m09/a090 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAF	GVFQLEAGKLQ	HPHVRLFAF	ALPFRLQNRRA
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAF	GVFQLETGKLQ	HPHVRLFAF	ALQFRLQNRRA
	10	20	30	40	50	60

	70	80	90	100	110	119
m090.pep	DIARDNGIQP	ALDTEIADQA	RYRGFAVAAG	NRNHLVVP	PAVHNVRRQ	QFDVAQHAXRRFAX
a090	DIARDNGIQP	TLDAEIADQA	RYRGFAVAAG	NRNHLVAAV	HNVRRQQFDVA	QHAXRRFAX
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence < ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:

m090-1.seq

```

1 ATGACGGCGT TTGCATTCA GACGGCATCA CAAAGCCTTA AACGCTTCGA
51 TAAACACTTC CGAACGGTGC GCGTAGCCTT TGAACATATC AAAGCTCGCG
101 CAGGCGGGGC TGAGCAACAC AATATCGCCT GCTTCGGCTT GGGCATATGC
151 CGTCTGAACG GCTTCTCCCA AAGTGGCGCA GTCGGTCATA TTCAAGCCGC
201 AGCCGTCCAA ATCGCGGCGG ATTTGCGGCG CATCGACACC AATCAAGAAC
251 ACGCCTTTTG CCTTGCCTAC CAGTGCATCG CGCAGGGGCG TGAAGTCCTG
301 CCCTTTACCC ATGCCGCCCA AAATCACGAA GAGCGGATTT TGCAAACCGG
351 CAATCGCGGC GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA
401 AACACCACGC CGTTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC
451 TTGGAAGGTT TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG
501 CCTCACACAA AGCCACGGCA GCCATGACGT TAGCGCGGTT GTGCAGACCT
551 TGCAACGGAA TGTCTTGGCT GACAATCAA TCTTCATTGC CTTGTTTCAG
601 GCGGCCCTGC TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA
651 ACCATTTTAC CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG
701 TCCGCATTCA AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTTGGT
751 ATGCGCATAG TCGAGCAAAGT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA
801 TGTTACGACG CGTCGCCGCA GTCGGACGCA GGCTTTCGGT GTTTTCCAGT
851 TTGGAAGCTG AAAGCTCCAA CACCCACACG TCCGCTTTT TGCCTTCGCG
901 CTGCCATTTC GCCTCCAAAA CCGGCGTGCC GATATTGCCG GCGATAACGG
951 TATCCAGCCC GCACTTGATA CAGAGATAGC CGACCAGGCT CGTTACCGTG
1001 GTTTTGCCGT TGCTGCCGGT AATCGCAATT ACCTTGTCGT CCCGGCGGTT
1051 CACAATGTCC GCCAGCAATT CGATGTCGCC CAACACGCGT CCGCCGTTTT
1101 GCTTGAACGC CTCAATATCC GGCTGCCGCT CGCTGATGCC GGGACTGAGA
1151 GCCAGAATAT CGAAACCGTT GTCCAGCGCA TCTTTCAGAC GGCCCGTGTA
1201 AAACACCAAC CCGTCAAACA TCTTACCGAT TTGCGACACG CGTTCCGGCT
1251 TCAGTCCGCG ATCATACGCA GCAACCTCCG CGCCGTTTTT GCGCAGGTAG
1301 GCAATCATGG AAATACCGT ACCGCCGAGT CCGGCGACGA GGATTTTTTT
1351 GTTTTGAAAA GTCATTTTGG TTTGTCCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

m090-1.pep

```

1 MTAFAFQTAS QSLKRFDKHF RTVRVAFEH I KARAGGAEQH NIACFGLGIC
51 RLNGFSQSGA VGHQAQAAVQ IAADLRRI DT NOEHAFCLAY QCIAQGREVL
101 PFTHAAQNHE ERIQTGNRG GSRADIRAF VVDKHHAVFL ADFFHAVRQA
151 LEGFDVFEQC FARQTDGLTQ SHGSHDVSGV VQTLQRNVLR DNQIFIALEQ
201 AACLAFQPEI SFVFORKPFY LAPGTLHRAA ERIVRIQNLH AVATENLGFG
251 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
301 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NRNHLVVPVAV
351 HNVRRQQFDVA QHASAVLLER LNIRLPLADA GTESQNIETV VQRIQFQARV
401 KHQPVKHLTD LRHAFRLQLR IIRSNLRAVF AQVGNHGNTR TAESGDEDDF
451 VLKSHFGLS*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 303>:

```
g091.seq
1  ATGGAAATAC  CCGTGCCGCC  AAGTCCGGCG  ACGAGGATTT  TTTTGTTTGA
51  AAGTCATTTT  GGTTTTGTCT  TAAACAAAT  CATATTGGGC  AGGAGACGTC
101 CGCCTTGCC  CAAGCCGCTT  TCAGACGGCA  TCGCGAGCCG  ATTAATAACC
151 CGCCTTCAGG  CGTTGGTCAT  TGTCGCAGCT  GTTTTGGTCT  CCGTTTTGAC
201 AAGCCTTCGT  AAGCCATTGT  TGAGCGAGCG  CAAGGTCTTG  GCGCAGCCCG
251 CGTCCATCGT  AATACATCAA  GCCCAAATTG  TATTGGGCTT  GGGCATCCCC
301 TTTTCTGTA
```

This corresponds to the amino acid sequence <SEQ ID 304; ORF 091.ng>:

g091.pep
1 MEIPVPPSPA TRIFLFESHF GFVLKQIILG RRRPPLPKPL SDGIASRLIT
51 RLQALVIVAA VLVSVLTSLA KPLLSERKVL AHAASIVIHQ AQIVLGLGIP
101 LF*

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 305>:

```
m091.seq
  1  ATGGAAATAC  CCGTACCGCC  GAGTCCGGCG  ACGAGGATTT  TTTTGTTTGA
 51  AAAGTCATTT  TGGTTTGTC  TAAACAAAT  CATATTGAGC  AGGAGATGTC
101  CGCCCTGCC  CAAGCCGCTT  TCAGACGGCA  TCGCAGCTG  TTCAATAACC
151  CGCCTTCAGG  CGTTGGTCAT  TGTGCGAGCC  GTCTTGGTCT  CCGTTTTGAC
201  AAGCCTTGCC  AAACCATTCT  TGTGCAAGGG  CGCGGTCTTG  GCGCACGCCG
251  GCTCTTTCGG  CATACATCAC  GCCCAAATTG  TTTTGGGCTT  GGGCTACCCC
301  CTGCGC...
```

This corresponds to the amino acid sequence <SEQ ID 306; ORF 091>:

```
m091.pep
  1  MEIPVPPSPA TRIFLEKSF WFLVKQIILS RRCPLPKPL SDGIASCSIT
 51  RLQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLGLGYP
101  LR.
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 091 shows 84.2% identity over a 101 aa overlap with a predicted ORF (ORF 091.ng) from *N. gonorrhoeae*:

m091/g091

```

      10      20      30      40      50      60
m091.pep MEIPVPPSPATRIFLFEKSFVFLKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA
|||||:|||||:|||||
g091      MEIPVPPSPATRIFLFESHFGFVLKQIILGRRRPPLPKPLSDGIASRLITRLQALVIVAA
      10      20      30      40      50      60

      70      80      90     100
m091.pep VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLGLGYPLR
|||||:|:|||||:|:|||||
g091      VLVSVLTSLAKPLLSEKVLHAASIVIHQAQIVLGLGIPFLX
      70      80      90     100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 307>:

```

a091.seq
1  ATGGAAATAC  CCGTGCCGCC  AAGTCCGGCG  ACGAGGATT  TTTTGGTTTG
51  GAATCATTT  TGGTTTGTC  TAAACAAAT  CATATTGAG  AGGGGATGTC
101 TGATCTGCT  CAAGCCGCT  TCAGACGGCA  TCGCAGCTG  TTCAATAAACC
151 CGCTTTCAG  CGTTGGTCAT  TGTCGCAGCT  GTCTTGGTAT  CCGTTTTGAC
201 AAGCCTTGCC  AAGCCATTCT  TGTCGAAGG  CGCGGCTTGT  GCGCACGCCG
251 CGTCTTTCG  CATACTATC  GCCCAAAAT  TTTTGGGC

```

This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

a091.pep

```

1  MEIPVPPSPA TRIFLFWKSF WFLVKQIILS RGCLILLKPL SDGIASCSIT
51 RFQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLG

```

m091/a091 93.8% identity over a 96 aa overlap

```

              10      20      30      40      50      60
m091.pep      MEIPVPPSPATRIFLFEKSFWFLVKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA
               |||||
a091           MEIPVPPSPATRIFLFEKSFWFLVKQIILSRGCLILLKPLSDGIASCSITRFQALVIVAA
              10      20      30      40      50      60

              70      80      90      100
m091.pep      VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLGLGYPLR
               |||||
a091           VLVSVLTSLAKPFLCKGAVLAHAASFGIHHAQIVLG
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

g092.seq

```

1  ATGTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTGC GC
51  AACCGGTCAG ACCTTTAAAA TAACGCCTTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTTGTCCGT
151 ATCGGCGGCG TCGGCATGAG CCGTATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGGCATTCAA GTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTCGT TGCCTCTACC GCCGTCAAGA AAGAAaatcc
351 CGAAGTtgtc gcTGC GTTGG AGCGGCAAAT TCCGTTATT CCGCGCGCCT
401 TGATGCTGGC AGAGCTGATG CGCTTCCGTG ACGgcatcgc cattgccggT
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAACTC AACGCCGCGC
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTTCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTGTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GGC GCGCAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGc gtggcgCTg
1001 aagtcGgCGC ATcggttgAA GCGAtcCAA AaggCTTGCT CGGCTTTGAA
1051 GCGGTCGGCC GCCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgctGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgcTGCA CGCGGCGCGT ATCCGAAAAA acgtTTGGTG
1201 CtcgCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTACTCAATA CCGTTGatgC GCTGGTACTG ACCGAAGTTT
1301 AtgccgcccG CGAAGAGCCG GTTGCCGCCG CCGactcCCG CGCCTTGGCG
1351 CGTGCTATCC GCGTATTGGG CAAACTTGAG CCGATTACT GCGAAAatgt
1401 cgccgACCTG CCGCAAATGC TGATGAATGT TTTACAGGAT Ggcgatgttg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgttccttc cgcgctgttg
1501 gaattgtcga AACAGatttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

g092.pep

```

1  MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHFGV
51  IGGVGMGSGIA EVLHNLGFKV SGSDQARNAA TEHLSSLGIQ VYPGHTAEHV
101 NGADV VVAST AVKKNPEVV AALERQIPVI PRALMLAELM RFRDGI AIAAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```

```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

```

m092.seq
1 ATGTTT TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGGTCAG CCCTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTTGTCCGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTGGG
201 CTTTAAAGTT TCCGGTTCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACCT AACGCCGACG
551 GCACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GCGGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCGACCCT TGCCGCCGCA CGCGGCGCGT ATCTGAAAAA ACGTTTGGTA
1201 CTCGCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAAGTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCCGC CCGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTTGCAGGAC GCGGACATCG
1451 TGTTGAATAT GGGCGCGGGA AGCATCAACC GCGTCCCCGC CGCGCTGCTG
1501 GCATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

```

m092.pep
1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFVG
51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKNPEVV AALEQQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMGAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng) from *N. gonorrhoeae*:

m092/g092

```

10      20      30      40      50      60
m092.pep  MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVMSGIA

```

g092	MFFISIRYIFVRKLWCANGQTFKITPLRTKNQPERNINMMKNRVSNIHFTVGI	10	20	30	40	50	60
m092.pep	EVLHNLGFKVSGSDQARNAATEHLGSLGIQVYPGHTAEHVNAGADVVTSTAVKKENPEVV	70	80	90	100	110	120
g092	EVLHNLGFKVSGSDQARNAATEHLSSLGIQVYPGHTAEHVNAGADVVA	70	80	90	100	110	120
m092.pep	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL	130	140	150	160	170	180
g092	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL	130	140	150	160	170	180
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID	190	200	210	220	230	240
g092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID	190	200	210	220	230	240
m092.pep	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV	250	260	270	280	290	300
g092	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV	250	260	270	280	290	300
m092.pep	QMKGHEQGSFEVVLNMPGRHNVLNALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG	310	320	330	340	350	360
g092	QMKGHEQGSFEVVLNMPGRHNVLNALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG	310	320	330	340	350	360
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLAFQPHRYTRTRDLFEDFTK	370	380	390	400	410	420
g092	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYPEKRLVLAFQPHRYTRTRDLFEDFTK	370	380	390	400	410	420
m092.pep	VLNTVDALVLTEVYAAGEEPIAAADSRLARAIRVLGKLEPIYCENVADLPEMLLNVLQD	430	440	450	460	470	480
g092	VLNTVDALVLTEVYAAGEEPIAAADSRLARAIRVLGKLEPIYCENVADLPQMLMNVLQD	430	440	450	460	470	480
m092.pep	GDIVLNMGAGSINRVPAALLALSQIX	490	500				
g092	GDIVLNMGAGSINRVPSALLELSQIX	490	500				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 313>:

a092.seq

```
1 ATGTTTAAAAA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGGTCAG CCTTTAAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTGA CCAACATCCA TTTTGTCCGT
151 ATCCGCGGCG TCGGCATGAG CGGTATCGCC GAAGTCTTGC ACAATTTGGG
201 TTTTAAAGTT TCCGTTTCGG ATCAGGCGCG AAATGCCCTG ACCGAGCAT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCCG AGAACACGTT
```

```

301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACTC AACGCGCGAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCGCAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGGAACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGCGCACCTT TTCCGCCGCA CGCGCGCGCT ATCCGGAATA ACGTTTGGTA
1201 CTCGCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CTGATTCGCC CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTTGCAGGAC GCGGACATCG
1451 TGTGAATAT GGGTGCGGGA AGCATCAACC GCGTCCCCGC CGCGCTGCTG
1501 GAATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

a092.pep

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVGMGSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKNPEVV AALEQQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMGHEQGSF EVVLNMPGRH NVLNALAAIG VALEV GASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNLVD GDIVLNMAG SINRVPAALL
501 ELSKQI*

```

m092/a092 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092.pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMGSGIA					
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFVGIGGVGMGSGIA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m092.pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKNPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKNPEVV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m092.pep	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
a092	AALEQQIPVIPRALMLAELMRFRDGIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					

292

	190	200	210	220	230	240
	250	260	270	280	290	300
m092.pep	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
a092	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKFTVHV					
	310	320	330	340	350	360
m092.pep	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEVGASVEAIQKGLLGFEVGRRFQKYG					
a092	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEVGASVEAIQKGLLGFEVGRRFQKYG					
	370	380	390	400	410	420
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLAFQPHRYTRTRDLFEDFTK					
a092	DIKLPNGGTALLVDDYGHHPVEMAATLSAARGAYPEKRLVLAFQPHRYTRTRDLFEDFTK					
	430	440	450	460	470	480
m092.pep	VLNTVDALVLETVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
a092	VLNTVDALVLETVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
	490	500				
m092.pep	GDIVLNMGAGSINRVPAALLLSKQIX					
a092	GDIVLNMGAGSINRVPAALLELSKQIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

g093.seq

```

1  aTGCAGAAAtt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgcTGGACA GCgGTACCGC CATTTTGAAC GCCTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTTATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAAC TGGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCCTCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTACCCGTTC CCGAGTTCGC
351 CGTACTGTAC GATGATACCG ATTTCGATGC CGTCGAAGAA AAATTGGGTC
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggta
451 aaAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAAaCA
501 CCTTcagggg cgaAAtcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATAC ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaacCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTCCGGG CGCACAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

g093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLY DDTDFDAVEE KLGLPMFVKP AEGSSVGVV
151 KVKEKGRLKS VYEELKHLQG RNHCRTFYRR RRIFLPRPER QRAARHTHP
201 RNRVLRRLRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGSR RTGNRCGRLR
251 ARRFPPQRYRR QTLVSGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

m093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCfAA GACGGGGCGG TTCAGGGTGC ATTGGAAGTGTG TGGGGCATTTC
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTTCGATGC CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CCTTCAGGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATAAC ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACCGC GACGACACCA
651 TTTATCAATG TCCTTCGGAA GATTTCGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTCGCGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACGAGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

m093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGX DGA VQGALEL LGIPYTGSGV AASAI GMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAGSSVGVV
151 KVKGKGR LKS VYEELKHLQX RNHCRTFYRR RRIFLPRPER QRAARHTHVS
201 RNRVLR LRSQ VQPRRHLSM SFGFRD SRRR KPDARTGGS RAGNRCGR LR
251 ARRFQRYRR QTLVGNQHP ARYDEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

m093/g093

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKAQGFQTA					
g093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKERGFQTA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m093.pep	FNILHGTYGX DGA VQGALELL LGIPYTGSGV AASAI GMDKY RCKLIWQAL GLPVPEFAVLH					
g093	FNILHGTYGED GAVQGALELL LGIPYTGSGV AASAI GMDKY RCKLIWQAL GLPVPEFAVLV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m093.pep	DDTDFDAVEE KLGLPMFVKP AAGSSVGVV KVKGKGR LKS VYEELKHLQX RNHCRTFYRR					
g093	DDTDFDAVEE KLGLPMFVKP AAGSSVGVV KVKGKGR LKS VYEELKHLQX RNHCRTFYRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m093.pep	RRIFLPRPER QRAARHTH SRNRVLR LRSQVQPRRHLSM SFGFRD SRRR KPDARTGGS R					
g093	RRIFLPRPER QRAARHTH PRNRVLR LRSQVQPRRHLSM SFGFRD SRRR KPDARTGGS R					
	190	200	210	220	230	240
	250	260	270			
m093.pep	RAGNRCGR LRARRFPQRYRR QTLVGNQHP ARYDEPX					
g093	RTGNRCGR LRARRFPQRYRR QTLVGNQHP ARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

a093.seq

```

1  ATGCAGAAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAACCTG TTGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTTCGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTTCGATG CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTACGAAG AATTGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCTG TGTGAAACCG CAAAGGCCTG CCCGGCATA ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGAAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

a093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGSSVGVV
151 KVKGKGR LKS VYEELKHFQX RNHCRTVYRR RRIFLPCVER QRPARTHHP
201 RDRV L* LRSQ VQQRHLSM SFGSRDSRRR KPDARTGGSR RAGNRCGR LR
251 ARRF PQRYRR QTL SVGNQHP ARYDRP*

```

m093/a093 95.7% identity over a 276 aa overlap

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKAQGFQTA					
a093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKAQGFQTA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m093.pep	FNILHGTYGDGAVQGALELLGIPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLH					
a093	FNILHGTYGEDGAVQGALELLGIPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m093.pep	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVVVKVGKGR LKSVYEELKHLQXRNHCRTFYRR					
a093	DDTDFDAVEEKLGLPMFVKPAAEGSSVGVVVKVGKGR LKSVYEELKHFQXRNHCRTVYRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m093.pep	RRIFLPRPERQRAARHTHHSRNRVLRSLRSQVQPRRHLSMSFGRFDRSRRKPDARTGGSR					
a093	RRIFLPCVERQRPARTHHP RDRV LXLRSQVQQRHLSMSFGRSDRSRRKPDARTGGSR					
	190	200	210	220	230	240
	250	260	270			
m093.pep	RAGNRCGR LRARRFPQRYRRQTLSVGNQHPARYDEPX					
a093	RAGNRCGR LRARRFPQRYRRQTLSVGNQHPARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 321>:

```
g094.seq
1  ATGTATTGCG CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTGG GTTCGAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT AGTGGTCTGT GTTTTGCCGT GCGTAccggc aatggcgatg
151 cCGTCACGGA AGCGCATCAG CTCTGCCAGC ATCAAGGCGC GCGGAATAAC
201 GGGAAATTGC GCTCCAACG CAgcgacaAC TTCGgattT TCTTTCTTGA
251 CGCGGGTAGA GGCAACGACG ACATccgcAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

g094.pep
1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPVCPAMAM
51 PSRKRISSAS IKARGITGIC RSNAATTSGF SFLTAVEATT TSAPLTCSAV
101 WPG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 323>:

```
m094.seq
1  ATGTATTTCG CTTTGCCCAA GCGGGCGTTA GTGCTGCGG CGTTGAGTTT
51  GCCGCCGATA ACGAAAGTCG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CGGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTGCCGGC AATGGCGATG
151 CCGTCACGGA AGCGCATCAA CTCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATTT TCTTTTTTGA
251 CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCGGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

m094.pep

1	MYSPLPKRAL	VPAALSLPPI	TKVGSSPAAP	RMEAVRLVVV	VLPCVPAMAM
51	PSRKRINSAN	IRARGITGIC	CSNAATTSGF	SFLTAVEVTT	TSAPLTCSAV
101	WPG*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 094 shows 95.1% identity over a 103 aa overlap with a predicted ORF (ORF 094.ng) from *N. gonorrhoeae*:

m094/q094

```

              10      20      30      40      50      60
m094.pep    MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLP CVPAMAMPSRKRINSAN
              |||||
g094         MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLP CVPAMAMPSRKRISAS
              10      20      30      40      50      60

              70      80      90      100
m094.pep    IRARGITGICCSNAATTSGFSFLTAVEVTTTTSAPLTCSAVWPGX
              :|||
g094         IKARGITGICRSNAATTSGFSFLTAVEATTTTSAPLTCSAVWPGX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 325>:

```
a094.seq
1  ATGTATTTCG  CTTTGCCCAA  GCGGGCGCTG  GTGCTGCGG  CGTTGAGTTT
51  GCCGCCGATA  ACGAAAGTCG  GGTCAAGTCC  TGCCGCGCCG  AGGATGAGAG
101 CGGTCAGGCT  GGTGTCGTG  GTTTGCCGT  CGGTGCCCGT  AATGGCCGATG
151 CCGTCACGGA  AGCGCATCAA  CTCGCCAAC  ATCAGGGCGC  GCGGAATAAC
201 GGGAAATTGC  TGCTCCAACG  CAGCGACAA  TTCGGGATT  TCTTTTTTGA
251 CGGCGGTAGA  GGTAACGACG  ACATCCGCAC  CGTTAACGTG  TTCTGCGGTA
301 TGGCCGGGAT  AA
```

This corresponds to the amino acid sequence <SEO ID 326: ORF 094.a>:

a094.pep

```

1  MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
51  PSRKRINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*

```

m094/a094 100.0% identity over a 103 aa overlap

```

              10      20      30      40      50      60
m094.pep      MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRINSAN
               |||||
a094           MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRINSAN
               |||||
              10      20      30      40      50      60

              70      80      90     100
m094.pep      IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
               |||||
a094           IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
               |||||
              70      80      90     100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 327>:

```

g095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
51  TTTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
151 AACACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGGGTCA GTGTAGGAAA
301 GAGGCATCGG ATCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 328; ORF 095.ng>:

```

g095.pep
1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCCKR
101 EASDRRLRQR CIRLCPGRW CLRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 329>:

```

m095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT
51  TTTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG
351 CGGGCGTTAG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 330; ORF 095>:

```

m095.pep
1  MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCCKR
101 DASDRRLRQR CIRLCPGRX CLRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 095 shows 97.6% identity over a 124 aa overlap with a predicted ORF (ORF 095.ng) from *N. gonorrhoeae*:

m095/g095

```

              10      20      30      40      50      60
m095.pep      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
               |||||

```

297

```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
g095      HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKEASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
1   ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTGTC GCGCCGACGT
51  TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTCG CGTAGAAGGG CACACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGCTTC TCAAACTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCACGA TGTATTCGCC TTGCCCCAAG
351 CGGGCGTTGG TGCCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
1   MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQLLNTVPVG IHMFVDIGN DGHNRCQCRK
101 DASDRRLRQR CIRLCPSGRW CLRR*

```

m095/a095 96.0% identity in 124 aa overlap

```

           10      20      30      40      50      60
m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           |||||
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

           70      80      90      100     110     120
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           |||||
a095      HTVDEIDKRLMQLLNTVPVGIIHMFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRW
           70      80      90      100     110     120

m095.pep  CLRRX
           ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
1   ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGTGCGC CGCGAACGCG CAGTTCGCGC ATCAGGCTTT CTTGCGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGAtaat ggtgTCGTCT CGGttgtact

```

298

```

201  tggcttcgta gTCGTAAAC TCGGTGCGG GGATGATGTG TATGCCGGGC
251  AGCCCTTTGC CGTTCAGGAC GGGGCAGGAA TATTCGCCGC CGCCGATAAA
301  AcgtTcggca atgaTTtcgc ccctgAAGGT GttTCAattc ttcgtaAACG
351  CTTTTCAGAc ggccttTTTC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 334; ORF 096.ng>:

g096.pep

```

1  MAGHTGQGVDFQQIEFAVGI FEEIDAHA AFRTDCLCAANR QFAHQAFFGF
51  GQIFRRTLIN GVVSVVLGFV VVKLGCGDDV YAGQPFQAVQD GAGIFAAADK
101 TFGNDFAXEG VSILKRKFS DGLFL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 335>:

m096.seq

```

1  ATGGCTCGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTCG CGGTTGTACT
201 TGGCTTCGTA GTCGTAAAC TCGGTGCGG GAATGATGTG TATGCCGGGC
251 AGCCCTTTGC CGTTCAGGAC GGGGCAGGAA TATTCGCCGC CGCCGATAAA
301 ACGTTCGGCA ATGATTTCGC CC.TGAAGGT GTTCAATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 336; ORF 096>:

m096.pep

```

1  MARHTGQGVDFQQIEFAVGI FEEIDAHA AFRTDCLRAANR QFAHQAFFGF
51  GQIFRRTLIN GVVAVVLGFV VVKLGCGNDV YAGQPFQAVQD GAGIFAAADK
101 TFGNDFAXEG VSILKRKFS DGLFL*

```

m096/g096 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGI	FEEIDAHA AFRTDCLRAANR	QFAHQAFFGF	GQIFRRTLIN		
g096	MAGHTGQGVDFQQIEFAVGI	FEEIDAHA AFRTDCLCAANR	QFAHQAFFGF	GQIFRRTLIN		
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDV	YAGQPFQAVQD	GAGIFAAADK	TFGNDFAXEG	VSILKRKFS	DGLFLX
g096	GVVSVVLGFVVVKLGCGDDV	YAGQPFQAVQD	GAGIFAAADK	TFGNDFAXEG	VSILKRKFS	DGLFLX
	70	80	90	100	110	120
m096.pep	GLFLX					
g096	GLFLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 337>:

a096.seq

```

1  ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACC GCAGTTCGCGC ATCAGGCTTT CTTCGGCTTC
151 GGTCAATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTTG CGGTTGTACT
201 TGGCTTCGTA GTCATAAAC TCGGTGCGG GGATGATGTG TATGCCGGGC
251 AGGCCTTTGC CGTTCAACAC AGGCAGGAA TATTCGCCGC CGCCGATAAA
301 CCGTTCGGCA ATGATTTCGC CCT.GAAAGT GTTCAATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 338; ORF 096.ng>:

a096.pep

```

1  MAGHTGQGVDFQQIEFAVGI FEEIDAHA AFRTDCLRAANR QFAHQAFFGF

```

51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK
 101 PFGNDFAXES VSILRKRFSD GLFL*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHAAFR	TDC	LRAANRQFAHQAFFGFGQIFRRTLIN			
a096	MAGHTGQGVDFQQIEFAVGIFEEIDAHAAFR	TDC	LRAANRQFAHQAFFGFGQIFRRTLIN			
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDVYAGQPF	FAVDGAGIFAAADKTFGND	FAXEGVSILRKRFSD			
a096	GVVAVVLGFVVVKLGCGNDVYAGQAF	VQHRAGIFAAADKPF	GNDFAXESVSILRKRFSD			
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

1	ATGGATATTT	CAAAACAAAC	ATTGCTGGAT	AGGGTTTTTA	ACCTGAAGGC
51	AAACGGTACG	ACGGTACGTA	CCGAGTTGAT	GGCGGGTTTG	ACGACCTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAATC	CCCTGATTTT	GGGCGAGACC
151	GGAATGGATA	TGGGGGCGGT	ATTCGTCGCT	ACCTGTATCG	CATCCGCCAT
201	CGGCTGTTTT	GTCATGGGTT	TTATCGGCAA	CTATCCGATT	GCGCTTGCCC
251	CGGGGATGGG	GCTGAATGCC	TATTTACCT	TTGCCGTCGT	TAAGGGTATG
301	GGCGTGCCTT	GGCAGGTGGC	GTTGGGTGCG	GTGTTCAATT	CCGCTCTGAT
351	TTTCATCCTG	TTTCACTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCCTATGGG	TTTGAAATG	TCGATTGCCG	CCGGTATCGG	TTTGTTTTTG
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTGTCCA	ATCCGGCAAC
501	CTTGCTCGGC	TTGGGCGATA	TTTCATCAGC	CAGCGCACTG	TTGGCATTGT
551	TCGGTTTTGT	CATGGTGGTC	GTATTGGGGT	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATTCTGAC	GATTACCGTC	ATTGCCAGCC	TGATGGGTTT
651	GAACGAGTTT	CACGGCGTGG	TCGGCGAAGT	ACCGGGCATT	GCGCCGACCT
701	TTATGCAGAT	GGATTTTAAA	GGTCTGTTTA	CCGTCAGCAT	GGTCAGCGTG
751	ATTTTCGTCT	TCTTCTTGGT	CGATTGTTC	GACAGTACCG	GAACGCTGGT
801	CGGCGTATCC	CACCGTGCCG	GACTGCTGGT	GGACGGTAAG	CTGCCCGGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CCATTGTGGC	AGGTGCGGCT
901	TTGGGTACTT	CTTCAACCAC	GCCTTATGTG	GAAAGCGCGG	CGGGCGTATC
951	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC
1001	TGGCGTGTCT	GATGTCTCTC	CCATTGGCGA	AAAGTGTTCC	GGTATTTGCC
1051	ACCGCGCCCC	CACTGCTTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCGAG
1101	GGACATTGAT	TGGGACGATA	TGACTGAAGC	CGCGCCCGCG	TTCTTGACCA
1151	TTGTCTTCAT	GCCGTTTACC	TATTCGATTG	CAGACGGCAT	CGCCTTCGGC
1201	TTTCATCAGCT	ATGCCGTGGT	CAAACCTTTG	TGTCGCCGGA	CTGGGGACGT
1251	GCCGCCTATG	GTATGGGTTG	TTGCCGTATT	GTGGGCATTG	AAATTCTGGT
1301	ATTTGGGCTG	A			

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

1	MDISKQTLLED	RVFNLKANGT	TVRTELMAGL	TTFLTMCYIV	IVNPLILGET
51	GMDMGAVFVA	TCIASAIGCF	VMGFIGNYPI	ALAPGMGLNA	YFTFAVVKGM
101	GVPWQVALGA	VFISGLIFIL	FSFFKVREML	VNALPMGLKM	SIAAGIGLFL
151	ALISLKGAGI	IVANPATLVG	LGDIHQPSAL	LALFGFVMV	VLGYFRVQGA
201	IIITILTITV	IASLMGLNEF	HGVVGEVPGI	APTFMQMDFK	GLFTVSMVSV
251	IFVFFLVDLF	DSTGTLVGVS	HRAGLLVDGK	LPRLKRALLA	DSTAIVAGAA
301	LGTSSSTPYV	ESAAGVSAGG	RTGLTAVTVG	VMLACL MFS	PLAKSVPVFA
351	TAPALLYVGT	QMLRSARDID	WDDMTEAAPA	FLTIVFMPFT	YSIADGIAFG

401 FISYAVVKLL CRRTGDVPPM VWVAVLWAL KFWYLG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 341>:

m097.seq

```

1 ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51 AAACGGTACK ACGGTGCGTA CCGAGTTGAT GGCGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCyGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCTGCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TTGCCGTCGT TAAGGGTATG
301 GGCCTGCCTT GGCAGGTTGC GTTGGGTGCG GTGTTTCATCT CCGGTCTGAT
351 TTTTATCCTG TTCAGCTTTT TTAAAGTCAG GAAATGCTG GTCAAACGCAC
401 TGCCTATGGG TTTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTCGGT TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCATTGT
551 TCGGTTTTGC TATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATCTTGAC CATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAATGAATTT CACGCGATCA TCGGCGAAGT ACCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTGAA GGCCTGTTTA CCGTCAGCAT GGTCAGTGTG
751 ATTTTCGTCT TCTTCTTGGT CGATCTATTT GACAGTACCG GAACGCTGGT
801 CGGCATATCC CACCGTGCCG GGCTGCTGGT GGACGGTAAG CTGCCCGGCC
851 TGAACGCGC ACTGCTTGCA GACTCTACCG CCATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTTCCACCAC GCCTTATGTG GAAAGCGCGG CGGGCGTATC
951 GGCAGGCGGA CGGACCGGCC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TCGCCTGCCT GATGTTTTCA CCTTTGGCGA AAAGTGTTCC CGCTTTTGCC
1051 ACCGCGCCCG CCCTGCTTTA TGTCGGCACG CAGATGCTCC GCAGTGCAG
1101 GGATATTGAT TGGGACGATA TGACGGAAGC CGCACCTGCG TTCCTGACCA
1151 TTGTTTTTCAT GCCGTTTACT TATTCGATTG CAGACGGCAT CGCTTTTCGGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCGCGCA CCAAAGACGT
1251 TCCGCCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT
1301 ATTTGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 342; ORF 097>:

m097.pep

```

1 MDTSKQTLDD GIFKLKANGT TVRTELMAGL TTFLTCYIV IVNPXILGET
51 GMDMGAVFVA TCIASAIGCF VMGFVGNYP IALAPGMGLNA YFTFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFE GLFTVSMVSV
251 IFVFLVDLF DSTGTLVGIS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVP PM VWIIVAVLWAL KFWYLG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 097 shows 96.3% identity over a 436 aa overlap with a predicted ORF (ORF 097.ng) from *N. gonorrhoeae*:

m097/g097

```

          10      20      30      40      50      60
m097.pep MDTSKQTLDDGIFKLKANGTTVRTELMAGLTTFLTCYIVIVNPXILGETGMDMGAVFVA
          || ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g097      MDISKQTLDDRNFNLKANGTTVRTELMAGLTTFLTCYIVIVNPLILGETGMDMGAVFVA
          10      20      30      40      50      60

          70      80      90      100     110     120
m097.pep TCIASAIGCFVMGFVGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL
          ||||| ||||| :||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g097      TCIASAIGCFVIGNYP IALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL
          70      80      90      100     110     120

          130     140     150     160     170     180

```

m097.pep	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
g097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL
	130 140 150 160 170 180
m097.pep	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGIIGEVPSIAPTTFMQMDFE
g097	LALFGFAMVVVLGHFRVQGAIITILTITVIASLMGLNEFHGVVGEVPGIAPTTFMQMDFK
	190 200 210 220 230 240
m097.pep	GLFTVSMVSVIFVFFLVDFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA
g097	GLFTVSMVSVIFVFFLVDFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA
	250 260 270 280 290 300
m097.pep	LGTSTTPYVESAAAGVSAGGRGLTAVTVGVMLACLMPSPAKSVPAFATAPALLYVGT
g097	LGTSTTPYVESAAAGVSAGGRGLTAVTVGVMLACLMPSPAKSVPAFATAPALLYVGT
	310 320 330 340 350 360
m097.pep	QMLRSARDIDWDDMTEAAPFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM
g097	QMLRSARDIDWDDMTEAAPFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTGDVPPM
	370 380 390 400 410 420
m097.pep	VWIVAVLWALKFWYLGX
g097	VWVAVLWALKFWYLGX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097.seq

```

1  ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51  AACGGTACG ACGGTGCGTA CCGAGTTGAT GCGGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCTGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGATGGG GCTGAATGCC TATTCACCT TTGCCGTCGT TAAGGGTATG
301 GCGGTGCCTT GGCAGGTTGC GTTGGGTGCG GTGTTTCATCT CCGGTCTGAT
351 TTTCATCCTG TTCAGCTTTT TTAAAGTCAG GGAAATGCTG GTCAACGCAC
401 TGCCTATGGG TTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTTCGGC TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCACTGT
551 TCGGTTTTGC CATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTTTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAATTT CACGGCATCA TCGGCGAAGT GCCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTAAA GGGTTGTTTA CCGTCAGCAT GGTGAGCTGT
751 ATTTTCGTCT TTTTCCTAGT CGATCTGTTC GACAGTACCG GAACACTGGT
801 CGGTGTATCG CATCGTGCCG GACTGCTGGT GGACGGTAAG CTGCCCGGCC
851 TGAACGCGC ACTGCTTGCA GACTCTACCG CTATTGTGGC AGGTGCGGCT
901 TTGGTACTT CTTCAACCAC GCCTTATGTG GAAAGTGCGG CGGCGGTATC
951 GGCAGGCGGG CCGACAGGTC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TCGCCTGCCT GATGTTTTCA CCTTTGGCGA AAAGTGTTCC CGCTTTTGCC
1051 ACCGCGCCCG CCCTGCTTTA TGTGGGCACG CAGATGCTCC GCAGTGCGAG
1101 GGACATCGAT TGGGACGATA TGACGGAAGC CGCACCAGCA TTCCTGACCA
1151 TTGTCTTCAT CCGGTTTACC TATTCGATTG CAGACGGCAT CGCTTTCGGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCGCGGCA CCAAAGACGT
1251 TCCGCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT

```

1301 ATTTGGGCTG A

This corresponds to the amino acid sequence <SEQ ID 344; ORF 097.a>:

a097.pep

```
1  MDTSKQTLLD GIFKLGKANGT TVRTELMAGL TTFLTMCYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YTFFAVVKGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIGLFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IITILTITV IASLMGLNEF HGIIGEVPSI APTFMQMDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPM VWIVAVLWAL KFWYLG*
```

m097/a097 99.3% identity in 436 aa overlap

m097.pep	10	20	30	40	50	60
	MDTSKQTLLDGIFKLGKANGTTVRTELMAGLTTFLTMCYIVIVNXPILGETGMDMGAVFVA					
a097	MDTSKQTLLDGIFKLGKANGTTVRTELMAGLTTFLTMCYIVIVNPLILGETGMDMGAVFVA					
	10	20	30	40	50	60
m097.pep	70	80	90	100	110	120
	TCIASAIGCFVMGFVGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
a097	TCIASAIGCFVMGFVGNYPIALAPGMGLNAYFTFAVVKGMGVPWQVALGAVFISGLIFIL					
	70	80	90	100	110	120
m097.pep	130	140	150	160	170	180
	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
a097	FSFFKVREMLVNALPMGLKMSIAAGIGLFLALISLKGAGIIVANPATLVGLGDIHQPSAL					
	130	140	150	160	170	180
m097.pep	190	200	210	220	230	240
	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFE					
a097	LALFGFAMVVVLGHFRVQGAIIITILTITVIASLMGLNEFHGIIGEVPSIAPTFMQMDFK					
	190	200	210	220	230	240
m097.pep	250	260	270	280	290	300
	GLFTVSMVSVIFVFFLVDLFDSTGTLVGISHRAGLLVDGKLPRLKRALLADSTAIVAGAA					
a097	GLFTVSMVSVIFVFFLVDLFDSTGTLVGVS HRAGLLVDGKLPRLKRALLADSTAIVAGAA					
	250	260	270	280	290	300
m097.pep	310	320	330	340	350	360
	LGTSSTTPYVESAAGVSAGGRTGLTAVTVGVLMACLMFSPLAKSVPAFATAPALLYVGT					
a097	LGTSSTTPYVESAAGVSAGGRTGLTAVTVGVLMACLMFSPLAKSVPAFATAPALLYVGT					
	310	320	330	340	350	360
m097.pep	370	380	390	400	410	420
	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
a097	QMLRSARDIDWDDMTEAAPAFLTIVFMPFTYSIADGIAFGFISYAVVKLLCRRTKDVPPM					
	370	380	390	400	410	420
m097.pep	430					
	VWIVAVLWALKFWYLGX					
a097	VWIVAVLWALKFWYLGX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 345>:

```
g098.seq
  1  ATGACCGCCG  ACGGTCTCTT  CGTCGCTTTC  AACTTCAATA  CGTTTGCCGT
 51  TGTGCGAATA  TTGATACCAG  TACAGCAGGA  TGCTGCCAG  GCTGGCGATC
101  AGTTTGTCCG  CGATGTCGCG  CGCTTCGCTG  TCGGGATGGC  TTTCCGCTTC
151  GGGATGAACG  CAGCCGAGCA  TGGACACGCC  GGTACGCATC  ACGTCCATCG
201  GATGGGTATG  TGCAGGCAGG  CTTTCCAAAA  CTTTAATCAC  ACGGATAGGC
251  AGGCCGCGCA  TGGATTGAG  CTTGGTTTTA  TAAGCGGCCA  GCTCGAATTT
301  GTTGGGCAGA  TGGCCGTGAA  TCAGCAAGTG  TCGACTTCT  TCAAACTCGC
351  ATTTTGTGTC  CAAATTAGAA  TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

```
g098.pep
  1  MTADGLFVAF  NFNTFAVVRI  LIPVQQDAAQ  AGDQFVGDDVA  RFAVGMAFAF
 51  GMNAAEHGHA  GTHVHRMGM  CRQAFQNFNH  TDRQAAHGFE  LGFISGQLEF
101  VGQMAVNQQV  CDFFKLAFLC  QIRMS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

```
m098.seq
  1  ATGACCGCCG  ATGGTCTCTT  CGTCGCTTTC  AACCTCAATG  CGTTTGCCGT
 51  TGTGCGAATA  TTGATACCAG  TACAAGAGGA  TGCTGCCAG  GCTGGCGATC
101  AGTTTGTCCG  CGATGTCGCG  CGCTTCACTT  TCCGGATGGC  TTTCACGTTT
151  AGGATGAACG  CAGCCCAGCA  TGGATACGCC  GGTACGCATT  ACGTCCATCG
201  GATGGGTATG  TGCAGGCAGG  CTTTCCAAAA  CTTTAATCAC  ACGGATAGGC
251  AGGCCGCGCA  TGGATTGAG  CTTGGTTTTA  TAAGCGGCCA  GCTCGAATTT
301  GTTGGGCAGA  TGGCCGTGAA  TCAGCAGGTG  GCGACTTCT  TCAAACTCGC
351  ATTTTGTGTC  CAAATCAGAA  TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

```
m098.pep
  1  MTADGLFVAF  NLNAFAVVRI  LIPVQEDAAE  AGDQFVGDDVA  RFTFRMAFTF
 51  RMNAAQHGYA  GTHVHRMGM  CRQAFQNFNH  TDRQAAHGFE  LGFISGQLEF
101  VGQMAVNQQV  GDFFKLAFLC  QIRMS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng) from *N. gonorrhoeae*:

```
m098/g098

      10      20      30      40      50      60
m098.pep  MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g098       MTADGLFVAFNFNTFAVVRI LIPVQQDAAQAGDQFVGDDVARFAVGMAFAFGMNAAEHGHA
          10      20      30      40      50      60

      70      80      90     100     110     120
m098.pep  GTHVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQVGDFFKLAFLC
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g098       GTHHVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQVCDFFKLAFLC
          70      80      90     100     110     120

m098.pep  QIRMSX
          |||||
g098       QIRMSX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

```
a098.seq
  1  ATGACCGCCG  ATGGTCTCTT  CGTCGCTTTC  AACCTCAATG  CGTTTGCCGT
 51  TGTGCGAATA  TTGATACCAG  TACAAGAGGA  TGCTGCCAG  GCTGGCGATC
```

304

```

101 AGTTTGTCGG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTGAG CTTGGTTT TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GCGACTTCT TCAAACGCG
351 ATTTTGTGC CAAATCAGAA TGTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

```

1 MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
51 RMNAAQHGYA GTHYVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*

```

m098/a098 100.0% identity in 125 aa overlap

	10	20	30	40	50	60
m098.pep	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARETFRMAFTFRMNAQHGYA					
a098	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARETFRMAFTFRMNAQHGYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m098.pep	GTHYVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV GDFFKLAFLC					
a098	GTHYVHRMGMC RQAFQNFNHTDRQAAHGFE LGFISGQLEFVGQMAVNQQV GDFFKLAFLC					
	70	80	90	100	110	120
m098.pep	QIRMSX					
a098	QIRMSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTGGA
51 GCTGACGGGC AAACGCGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGG
101 CACTGACCGA ATTCTTGCGT AAAGAGCGCG TGGTCGGGGC GTTTGTGCAA
151 TTTTTCGGCG AGGCGCGGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGAGT TCGGCGCGAC TGCCGCCATG TTCGCCATCG
251 ACGCGCAAAC TATTGATTAT TTGAACTGA CCGGACGTGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTAT GGGCAGGTGG
351 CTTGAAAACC GCCGTTTATC CGCGCGTTTT GAAATTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
451 GCCGATTGG CCGCGAAAGG GCTGGCGAAG CTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCGTGTA
551 CCAATACTTC CAACCCGCGC AACGTTGTCG CCGCCGCACT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GAAACGCAA CTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGGAATCTA TTTGAAAGAA GCAGGCTTGT
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAgcgG CGCGCTCgaC CCGAAAATCC AACAAGAAAT
801 CATCGACCGC GAttgtacg cCACC GCCGT ATTGT CAGGC AACCGCAACT
851 TCGACGCGCC TATCCATCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCCT
901 CCTTTGGTCG TTGCCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCCG CGAAATCCGC CTGAAAGATA
1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAACAAT TCCGCGACAT TTATATCCCG ATGTCGACAC CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGACCGATG TCCACCTACA
1151 TCCGCGGTCC GCCCTATTGG GAAGGCGCAC TGGCAGGGGA ACGTACATTA
1201 AGAGGTATGC GTCCGCGGCG GATTTTGCCC GACAACATCA CCACCGACCA
1251 CATCTCgcca tCCAATGCGA TTTTGGCCGG cagTGCcgca ggtgaATATT

```

```

1301 TGGCGAAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451 tggcacgcgT tgaacCAGAA GGCCAAACCA TGGCGATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC GCGGAAGGGC GTGCGGCTGG
1601 CGGGTGTGGA AGCCATCGCC GCCGAAGGTT TCGAGCGCAT CCACCGCACC
1651 AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGGC CTGACCCTCG TGATTCACCG TAAAAACGGA
1801 GAAACCGTCG AAGTTCGGGT TACCTGCCGC CCCGATACCG CAGAAGAAGC
1851 ATTGGTATAT GAAGCCGGCG GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901 TGAAGGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1 MLGRASMMRL PDIVGVELTG KRQAGITATD IVLALTEFLR KERVVGAFVE
51 FFEGEGARSLS IGDRAATISM TPEFGATAAM FAIDAQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNP HARFAT
151 ADLAAKGLAK PYEPPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRR PWVKSSFAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQEIIDR DLYATAVLGS NRNFDGRIHP YAKQAF LASF
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDIYIP MSDTGTAQKA PSPLYDWRPM STYIRPPYVW EGALAGERTL
401 RGMRRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMRKQPL I IAGADYQG GSSRDWAAGK VRLAGVEAIA AEGFERIHRF
551 NLIGMGVLP L QFKPGTNRHT LQLDGTETYD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAEEALVY EAGGVLRQFA QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51 GCTGAACGGC AAACGGCAGG CCGGCATTAC GGCGACGGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACCGG TGGTCGGGGC GTTTGTGCGA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAACC GCAGGCTTGT GGGCAGATGC
351 CTGAAACC GCCGTTTATC CTCGCGTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCAGCC
451 GCCGATTGG CGGCGAAAGG GCTGGCGAAG CTTACGAAG AGCCTTCGGA
501 CGCCAAATG CCCGACGGCT CGGTCATCAT CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCACGC
601 AATGCCAACC GTCTCGGCTT GAAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCGGGCCTGT
701 TGCCCGAAAT GGAAGAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CCGCTGGAT CCGAAATCC AGAAAGAAAT
801 CATCGACCGC GATTGTACG CCACCGCCGT ATTATCAGGC AACCGCAACT
851 TCGACGGCCG TATCCACCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCCT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTGACA CCGGACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCCGTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCGA TTTTGGCCGT CAGTGCCGCA GCGGAGTATT
1301 TGGCGAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTGC GC CAAGGCTCGT
1451 TCGCCCGCGT CGAACCCGAA GCGGAAACCA TCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

```

```

1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTCACCG TAAAAACGGC
1801 GAAACCGTTG AAGTTCCCGT TACCTGCTGC CTCGATACTG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGCGC GCGTGTGCA ACGGTTTGA CAGGATTTT
1901 TGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
  1  MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
 51  FFGEGARSLs IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101  VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNP HARFAT
151  ADLAAKGLAK PYEEPSDQOM PDGSVIAAI TSCTNTSNPR NVVAAALLAR
201  NANRLGLKRK PWVKSSFAPG SKVAEIYLKE AGLLPEMEKL GFGIVAFAC
251  TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAF LASP
301  PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
351  PQQFRDVYVP MFDTGTAQKA PSPLYDWRPM STYIRPPYEW EGALAGERTL
401  RGMRLAILLP DNITTDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
451  RGDHLTAQRA TFANPKLFNE MVKNEDGSVR QGSFARVEPE GETMRMWEAI
501  ETYMNRRKQPL I IAGADYQG GSSRDWAAKG VRLAGVEAIV AEGFERIHRT
551  NLIGMGVLP L QFKPDNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601  ETVEVPVTCC LDTAEVLVY EAGGVLRFA QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng) from *N. gonorrhoeae*:

m099/g099

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFEGEGARSLs					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFEGEGARSLs					
	10	20	30	40	50	60
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDY LKLTGRDDAQVKLVETYAKTAGLWADALKT					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDY LKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNP HARFATADLAAKGLAKPYEEPSDQOMPDGSVIAAI					
g099	AVYPRVLKFDLSSVTRNMAGPSNP HARFATADLAAKGLAKPYEEPSDQOMPDGAVIAAI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m099.pep	GFGIVAFAC TT CNMGSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF LASP					
g099	GFGIVAFAC TT CNMGSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAF LASP					
	250	260	270	280	290	300
	310	320	330	340	350	360

m099 . pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIIWPADEEIDAVVAEYVKPQQFRDVIYP						
g099	PLVVAYALAGSIRFDIENDVLGVADGREIRLKDIIWPTDEEIDAIVA EYVKPQQFRDIYIP	310	320	330	340	350	360
m099 . pep	MFDTGTAQKAPSPLYDWRPMSTYIRRPYPYEWEGALAGERTLRGMRPLAILPDNITTDHLS	370	380	390	400	410	420
g099	MSDTGTAQKAPSPLYDWRPMSTYIRRPYPYEWEGALAGERTLRGMRPPAILPDNITTDHISP	370	380	390	400	410	420
m099 . pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR	430	440	450	460	470	480
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR	430	440	450	460	470	480
m099 . pep	QGSFARVEPEGETMRMWEAIIETYMNRKQPLIIAGADYQGSSRDWAAKGVRLAGVEAIV	490	500	510	520	530	540
g099	QGSLARVEPEGQTMRMWEAIIETYMNRKQPLIIAGADYQGSSRDWAAKGVRLAGVEAIA	490	500	510	520	530	540
m099 . pep	AEGFERIHRTNLIGMGVLPLOQFKPDNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG	550	560	570	580	590	600
g099	AEGFERIHRTNLIGMGVLPLOQFKPGTNRHTLQLDGTETYDVVGERTPRCGLTLVIHRKNG	550	560	570	580	590	600
m099 . pep	ETVEVPVTCCLDTAE EVLVYEAGGV LQRFAQDFLEGNAAX	610	620	630	640		
g099	ETVEVPVTCRPDTAE EALVYEAGGV LQRFAQDFLEGNAAX	610	620	630	640		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099.seq

1	ATGCTGGGAC	GCGCGTCCAT	GATGCGCCTG	CCCGATATTG	TCGGCGTTGA
51	GCTGAACGGC	AAACGGGAAG	CGGGCATTAC	GGCGACGGAT	ATTGTGTTGG
101	CAC TGACCGA	GTTTCTGCGC	AAAGAACGCG	TGGTCTGGGGC	GTTTGTGCGAA
151	TTCTTCCGGC	AGGGCGCGAG	AGGCCTGTCT	ATCGGCGACC	GGCGCACCAT
201	TTCCAACATG	ACGCCGGAGT	TCGGCGCGAC	TGCCGCGATG	TTCGCTATTG
251	ATGAGCAAAAC	CATTGATTAT	TTGAAACTGA	CCGGACGCGA	CGACGCGCAG
301	GTGAAATTGG	TGGA AACCTA	CGCCAAAACC	GCAGGCTTGT	GGGCAGATGC
351	CTTGAAAAACC	GCGCTTTATC	CGCGCGTTTT	GAAATTGTAT	TTGAGCAGCG
401	TAAACGCGCAA	TATGGCAGGC	CCGAGCAACC	GCACGCGCG	TTTTGCGACC
451	GCCGATTTGG	CCGGCAAAGG	CTTGGCTAAA	CCTTACGAAG	AGCCTTCAGA
501	CGCGCAAATG	CCTGACGGTG	CAGTGATTAT	TGCCGCGGAT	ACTTCTCTGA
551	CCAATACTTC	CAATCCGCGC	AACGTTGTGC	CGCCGCGCCT	GTTGGCAGCG
601	AATGCCAACCC	GCCTCGGCTT	GCAACGCAPA	CCTTGGGTGA	AATCTTCGTT
651	TGCCCCGGGT	TCAAAAGTAG	CCGAAATCTA	TTTGAAGAGAA	GCAGATCTGC
701	TGCCCCGAAAT	GGAAAAAATC	GGCTTCGGTA	TCGTTGCGCT	CGCATGTACC
751	ACCTGTAAACG	GCATGACGCG	CGCGCTGGAT	CCGAAAATCC	AGAAAGAAAT
801	CATCGAACCGC	GATTTGTACG	CCACCGCGCT	ATTGTGAGCG	AACCGCAACT
851	TTGACGGCCG	TATCCATCCG	TATGCGAAAC	AGGCTTTCCT	CGCTTCGCCT
901	CCGTTTGGTGC	TTGCCTACGC	GCTGGCAGCG	AGCATCCGTT	TCGATATTGA
951	AAACGACGTA	CTCGGCCGTTG	CAGACGGCAA	AGAAATCCCG	CTGAAAGACA
1001	TTTGGCCTAC	CGATGAAGAA	ATCGATGCCA	TCGTTGCCGA	ATATGTGAAA
1051	CCGCAGCAAT	TTCGCGACGT	TTATATCCCG	ATGTTTCGACA	CCGGCACAGC
1101	GCAAAAAGCA	CCAAGCCCCG	TGTACGACTG	GCGTCCAATG	TCTACCTATA
1151	TCCGCGCCGC	ACCTTACTGG	GAAAGCGCAC	TGGCAGGGGA	ACGCACATTA
1201	AGCGGTATGCG	TTCCGCTGGC	GATTTTGGCC	GACAACCATC	CCACCGACCC

```
1251 TCTCTCGCCA TCCAATGCGA TTTTGGCAAG CAGTGCCGCA GGCGAATATT
1301 TGGCAAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTCCG
1451 TGGCACGCGT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTTG TGATTCACCG TAAAAACGGC
1801 GAGACCGTCG AAGTCCCAT TACCTGCCGC CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTTT
1901 TGAAGGGAA CCGCGCTTAG
```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```
1 MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRTISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAGKGLAK PYEPPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK PWKSSFAPG SKVAEIYLKE ADLLPEMEKL GFGIVAFACF
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFILASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDVYIP MFDTGTAQKA PSPLYDWRPM STYIRPPYW EGALAGERLT
401 SGMRLPLAILP DNITDHLSP SNAILASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMNKQPL IIIAGADYGQ GSSRDWAAKG VRLAGVEAIV AEGFERIHRF
551 NLIGMGVPL QFKPGTNRHT LQLDGTETD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEVLVY EAGGVLRFA QDFLEGNA*
```

m099/a099 97.5% identity in 639 aa overlap

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
a099	MLGRASMMRLPDIVGVELNGKRKAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDYLKLTGRDDAQVKLVETYAKTAGLWADALKT					
a099	IGDRATISNMTPEFGATAAMFAIDEQTIDYLKLTGRDDAQVKLVETYAKTAGLWADALKT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEPPSDGQMPDGSVIAAI					
a099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAGKGLAKPYEPPSDGQMPDGAIVIAAI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
a099	TSCTNTSNPRNVVAAALLARNANRLGLQRPWKSSFAPGSKVAEIYLKEADLLPEMEKL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m099.pep	GFGIVAFACFCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFILASP					
a099	GFGIVAFACFCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFILASP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m099.pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVYVP					

a099	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIIWPTDEEIDAIVA EYVKPQQFRDVYIP	310	320	330	340	350	360
m099.pep	MFDTGTAQKAPSPLYDWRPMSITYIRRPYPYEGALAGERTLRGMRPLAILPDNITTDHLS	370	380	390	400	410	420
a099	MFDTGTAQKAPSPLYDWRPMSITYIRRPYPYEGALAGERTLSGMRPLAILPDNITTDHLS	370	380	390	400	410	420
m099.pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR	430	440	450	460	470	480
a099	SNAILASSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR	430	440	450	460	470	480
m099.pep	QGSFARVEPEGETMRMWEAIETYMNKRQPLIIAGADYQGSSRDWAAGVRLAGVEAIV	490	500	510	520	530	540
a099	QGSLARVEPEGQTRMWEAIETYMNKRQPLIIAGADYQGSSRDWAAGVRLAGVEAIV	490	500	510	520	530	540
m099.pep	AEGFERIHRTNLIGMGVLPLOQFKPDTNRHTLQLDGTETDVGERTPRCDLTLVIHRKNG	550	560	570	580	590	600
a099	AEGFERIHRTNLIGMGVLPLOQFKPGTNRHTLQLDGTETDVGERTPRCDLTLVIHRKNG	550	560	570	580	590	600
m099.pep	ETVEVPVTCCLDTAEVVLVEAGGVLQRFAQDFLEGNAAX	610	620	630	640		
a099	ETVEVPITCRLDTAEVVLVEAGGVLQRFAQDFLEGNAAX	610	620	630	640		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 357>:

```

g102.seq
1      AtgtCCGCCA  AAactccgtc  gctcttcggc  ggcgcgatga  Ttatcgccgg
51     gaaggttatc  ggcgcAGgta  tgttcccaa  cccacacgcc  aacttggggg
101    acgggttaat  aggcctcgct  attgtgtgc  tgtacacgtg  gtttccattc
151    tcctccggcg  cctctcatgat  tttggaagtc  aacaccata  acCCcggagg
201    ggcaAGtttt  gacaccATTg  tCAaagacct  gctcgGACgc  ggctggaaca
251    tcatcaacgy  catccgcgtc  gctttggTc  taccggctc  gacctacggc
301    tacattttag  tcggcggtga  cctGACGCC  AAAGGCATg  GCAGCGCAGT
351    AGGCGGCCAA  ATTTCgctca  CCGTCGGACA  actcgtcttc  tTCGGCATCC
401    TCGCCTTTTG  CGTATGGGCA  TCCGCACGCT  TGGTFCAGCG  CTTTACCGCG
451    GTCTCATCG  GCGGCATGGT  ATTAACCTTT  ATTTGGGCAA  CCGCGGCCT
501    GGTTCGCCAT  GCCAAACCGT  CCGTCTCTTT  CGACACCCAA  GCCCCCGCTG
551    GCACCCGGTA  CTGGATTATC  GCGCGCACCG  CCCTGCCCGT  CTGCTTCGCT
601    TCCTTCGGCT  TCCACGGCAA  CGTTCCAGC  CTGCTCAAAT  ACTTTAAAGG
651    GCACGcgCc  aaagtGgCA  aATCcatctg  gGcaggtaca  ttgtTTGCCT
701    tggtaattta  cgtctCTGg  caaacgcgca  TCaaagcaca  ctTGCcgcaa
751    aacgagttcg  cCCcCgtgat  tgcgcgcgag  aggcaactCT  CCGTCTGgac
801    tgaaacccTG  tccaaattcg  cccaaacccg  cgatatggt  aAaatattgt
851    cctatttcc  ctcataggca  atcgccacct  cctttttagg  cgTAAcctta
901    ggctgtttg  acaaacatcg  cgacatcttc  aaatggaagc  acagtatgtc
951    cggcgggggc  accaaaaccg  tcgcgctgaa  cttctcggc  CCCCTgattt
1001   cctggtgtct  cctccccacc  gccctttcta  ccgccattgg  tgcgtctcga
1051   ctggcgggcaa  cgtcttggga  ggaatGcatc  atccccgcca  tgcgtcgcta
1101   cgtttccccc  caaaaaattG  gcGaggcgaa  gacttataAa  gtttaCGCG
1151   gcttgtggct  gatgttagtc  ttcttttcg  gcatcgccaa  catcgcgcga
1201   CAGGTATTGA  GccaAatGgA  ACTcgtCccc  GTATTAAAG  GATAA

```

This corresponds to the amino acid sequence <SEQ ID 358; ORF 102.ng>:

g102.pep

```

1  MSAKTPSLFG GAMIAGKVI GAGMFPNPTA NLGDGLIGSL IVLLYTWFPF
51  SSGALMILEV NTHNPRGASF DTMVKDLLGR GWNIINGIAV ALVLYGSTYA
101 YILVGGDLTA KGIGSAVGGK ISLTVGQLVF FGILAFVCWA SARLVDRFTG
151 VLIGGMVLTF IWATGGLVAD AKPSVLFDQ APVGTGYWIY AATALPVCLA
201 SFGFHGNVSS LLKYFKGDAP KVAKSIWAGT LVALVIYVLW QTAIQSNLPR
251 NEFAPVIAAE RQLSVLNETL SKFAQTGDM D KILSLFPYMA IATSEFLGVTL
301 GLFDNIADIF KWNDSMSGRG TKTVALNFLP PLISWLLLP GFFTAIGASG
351 LAATVWDQGI IPAMLLYVSP QKIGAGKTYK VYGGWLMLV FLFGIANIAA
401 QVLSQMEVLP VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA AAACCCCTTC ACTGTTCCGC GCGCGCATGA TTATCGCCGG
51  CACGGTCATC GCGCGAGGCA TGCTCGCCAA CCCGACCGCC ACATCCGGCG
101 TATGGTTTAC CGCTCGCTG GCGGTGTTC TGTACACCTG GTTTCTATG
151 CTTCCACGCG GCCTGATGAT TTTGGAAGTC AACACCCATT ATCCGCACGG
201 CGCAAGTTTC GACACGATGG TCAAAGACCT GCTCGGACGC GGCTGGAACA
251 TCATCAACGG CATCGCCGTC GCCTTCGTTT TATACCTGCT TACTTAGCCT
301 TATATCTTCG TCGGCGGCGA CCTGACCGCC AAAGGCTTAG GCAGCGCGGC
351 AGCGCGCGAC GTTCACTCA CCGTCGGACA ACTCGTCTTC TTCGGCATCC
401 TCGCCTTTTG CGTATGGGCA TCCGACGCT TGGTCGACCG CTTACCCGGC
451 GTCCTTATCG GCGGCATGGT ATTGACCTTT ATTTGGCGG CCGCGCGGCT
501 GATTGCCGAT GCCAAGCCGT CCGTCTCTT CGATACCCAA GCGCCGCGC
551 GCACAAACTA CTGGATTAC GCGGCCACCG CCCTGCCCGT CTGCCTCGCT
601 TCCTTCGGCT TCCACGGCAA CGTCTCCAGC CTGCTCAAA ACTTTAAAGG
651 CGACGCGCCC AAAGTGGCTA AATCCATCTG GACGGGCACA CTGATTGCGC
701 TGGTAATTTA CGTCTCTGG CAAACCGCCA TCCAAGGCAA CCTGCGCGC
751 AACGAGTTCG CCCCCGTCAT CGCGCCGAA GGGCAAGTCT CCGTCTCAT
801 CGAAACCCCTG TCCAAATTCG CCCAAACCGG CAATATGGAC AAAATATTGT
851 CCCTGTTTTT CTATATGGCG ATCGCCACCT CGTTTTTAGG CGTAACGCTC
901 GGACTCTTCG ACTACATCGC CGACATCTT AAATGGAACG ACAGCATCTC
951 CGGCGCGACC AAAACCGCGC CGCTGACCTT CTGCGCGCCC CTGATTTCCT
1001 GCGTGTCTTT CCCCACGGC TTCGTTACCG CCATCGGCTA CGTCGGCTG
1051 GCGGCAACCG TCTGGACAGG CATCATCCCC GCCATGCTGC TCTACCGTTC
1101 GCGCAAAAAA TTCGCGCGAG GCAAAACCTA TAAAGTTTAC GCGCGCTTGT
1151 GGCTGATGGT TTGGGTCTTC CTTTCGGCA TCGTCAACAT CGCCGCACAG
1201 GTATTGAGCC AAATGGAAC CTGCCCGTA TTAAAGGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep.
1  MPNKTPSLFG GAMIAGTVI GAGMLANPTA TSGVWFTGSL AVLLYTWFSM
51  LSSGLMILEV NTHYPHGASF DTMVKDLLGR GWNIINGIAV AFVLYLLTYA
101 YIFVGGDLTA KGLGSAAGGD VSLTVGQLVF FGILAFVCWA SARLVDRFTG
151 VLIGGMVLTF IWAAGGLIAD AKPSVLFDQ APAGTNYWIY AATALPVCLA
201 SFGFHGNVSS LLKYFKGDAP KVAKSIWGT LIALVIYVLW QTAIQGNLPR
251 NEFAPVIAAE GQVSVLIETL SKFAQTGNMD KILSLFSYMA IATSEFLGVTL
301 GLFDYIADIF KWNDSISGRT KTAALTFLEP LISCLLEPTG FVTAIGYVGL
351 AATVWTGIIP AMLLYRSRKK FGAGKTYKVY GGLWLMVWVF LFGIVNIAAQ
401 VLSQMEVLPV FKG*

```

m102/g102 86.0% identity in 415 aa overlap

	10	20	30	40	50	60
m102.pep	MPNKTPSLFGGAMIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
g102	MSAKTPSLFGGAMIAGKVIAGMFPNPTANLGDGLIGSLIVLLYTWFPFSSGALMILEV					
	10	20	30	40	50	60
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIINGIAVAFVLYLLTYAIFVGGDLTAKGLGSAAGGD					
g102	NTHNPRGASFDTMVKDLLGRGWNIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK					
	70	80	90	100	110	120
m102.pep	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDQ					
g102	ISLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIATGGLVADAKPSVLFDQ					
	130	140	150	160	170	180
m102.pep	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTIALLVIYVLW					
g102	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTIALLVIYVLW					

g102	APVGTGXYWIIYAATALPVC	190	200	210	220	230	240
	250	260	270	280	290	300	
m102.pep	QTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL						
g102	QTAIQSNLPRNEFAPVIAAERQLSVLNETLSKFAQTGDMDKILSLFPYMAIATSFLGVTL						
	250	260	270	280	290	300	
	310	320	330	340	350		
m102.pep	GLFDYIADIFKWNDSISGR-TKTAALTFLPPLISCLFPPTGFVTAIGYVGLAATVWVT-GI						
g102	GLFDNIADIFKWNDSMSGRGRTKTVALNFLPPLISWLLPTGFETAIGASGLAATVWDQGI						
	310	320	330	340	350	360	
	360	370	380	390	400	410	
m102.pep	IPAMLLYRSRKKFGAGKTKYKVYGGWLWMVWVFLFGIVNIAAQVLSQMELVPVFKGX						
g102	IPAMLLYVSPQKIGAGKTKYKVYGGWLML-VLFGIANIAAQVLSQMELVPVFKGX						
	370	380	390	400	410		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 361>:

a102.seq

1	ATGCCACCA	AAACCCCTTC	ACTGTTTCGGC	GGCGCGATGA	TTATCGCCGG
51	CACGNTCATC	GGCGCAGGTA	TGCTCGCCAA	CCCGACCGCC	ACATCCGGCG
101	TATGTTTAC	CGGCTCGCTG	GCCGCTGTTG	TGTACACCTG	GTTTTCATGAT
151	CTCTCCACGG	GCGTGATGAT	TTTGGAAATC	AACACCCACT	ATCCCCACGG
201	CGCGANCTTC	GACACCATGG	TTAAAGACCT	GCTCGGACGG	AGCTGGAACA
251	TCATCAACGG	CATCGCCGTC	GCCTTCGTTT	TATACCTGCT	TACTTAGCGT
301	TATATCTTCG	TCGGCGGCGA	CCTGACCGCC	AAAGGCTTAG	CGACGCGCGC
351	AGGCGGCAAT	GTTTCACTCA	CCGTCCGACA	ACTCGTCTTC	TTCCGGCATTC
401	TCGCTTTTGG	CGTATGGGCA	TCCGCACGCT	TGGTCGACCG	ATTACACGAG
451	GTCTCATCG	GCGGCATGGT	ATTAACCTTT	ATTTGGGCAA	CCGGCGGCCT
501	GATTGCGCAT	GCCAACTGTC	CCGTCTCTTT	CGACACCCAA	GCCCCTACCG
551	GCACCAACTA	CTGGATTTAT	GTCGCCACCG	CCCTGCCCGT	CTCGCTTGGC
601	TCATTGCGGT	TCCACGGCAA	CTGCTCCAGC	CTGCTCAAAAT	ACTTTTAAAG
651	CGACGCGCCC	AAAGTGGCTA	AATCCATCTG	GACGGGCACA	CTGATTGCGC
701	TGGTAATTTA	CGTCTCTGG	CAAAACCGCA	TCCAANGCAA	CCTGCCGGCG
751	AACGAGTTTC	CCCCCGTGAT	TGCCGCGGAA	GGGCAAGTCT	CCGCTNTGAT
801	TGAAACCTCG	TCCAAATTCG	CCCAAACCGG	CAATATGGAC	AAAATTAATGT
851	CCCTGTTTTC	CTATATGGCG	ATCGCCACCT	CGTTTTTAGG	CGTAACGCTC
901	GGACTCTTCG	ACTACATCGC	CGACATCTTC	AAATGGAACG	ACAGCGTGTC
951	CGGCCGCACC	AAAACCGCGC	CGCTGACCTT	CCTGCCGCCT	NTAATTTCTT
1001	GCTGTCTT	CCCCACGGC	TTTGTTACCG	CCATCGGNTA	CGTCGGCTGC
1051	GCGGCACAACG	TCTGGACAGG	CATCATCCCC	GGCATGCTG	TNTACGGTTC
1101	GCGCAAAAAA	TTGGGCGCAG	GCAAAACCTA	TAAAGTTTAC	GGCGGCTTGT
1151	GGCTGATGGT	TTGGGTCTTC	CTTTTCGGCA	TCNTCAACAT	CGCCGCGACAN
1201	GTATTGAGCC	AAATGGAAC	CGTCCCCGTA	TTTAAAGGAT	AA
1202					

This corresponds to the amino acid sequence <SEQ ID 362; ORF 102.a>:

a102.pcp

1	MPTKTPSLFG	GAMIIAGTXI	GAGMLANPTA	TSGVWFTGSL	AVLLYTWFMS
51	LSSGLMILEV	NTHYPHGAXF	DTMVKDLLGR	SWNIINGIAV	AFVLYLLTYA
101	YIFVGGDLTA	KGLGSAAGGN	VSLTVGQLVF	FGILAFVCWA	SARLVDRFST
151	VLIGMGVLTG	IWATGGLIAD	AKLPVLFDTG	APTGTNIWYI	VATALPVCLA
201	SFGFHGNVSS	LLKYFKGDAP	KVAKSIWTFG	LIALVIYVLW	QTAIQXNLPR
251	NEFAPVIAAE	GOVSXKIETL	SKFAQTGNMD	KILSLFSYMA	IATSFLGVTL
301	GLFDYIADIF	KWNSDVSGR	KTAALTFLPP	XISCLLFTFG	FVTAIGYVGL
351	ALVTWETGI	P	AMLLYRSRKL	FGAGKTYKVY	GGLWLMVWVF
401	VLSSOMELPV	FKG*			LFGIXNIAAX

m102 / a102 95.9% identity in 413 aa overlap

m102.pep	10	20	30	40	50	60
	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
a102	MPTKTPSLFGGAMIIAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
	10	20	30	40	50	60
m102.pep	70	80	90	100	110	120
	NTHYPHGASEFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXFDTMVKDLLGRSWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGN					
	70	80	90	100	110	120
m102.pep	130	140	150	160	170	180
	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFVCWASARLVDRFTSVLIGGMVLTFFIWAAGGLIADAKLPVLFDTQ					
	130	140	150	160	170	180
m102.pep	190	200	210	220	230	240
	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
a102	APTGTNYWIYVATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
	190	200	210	220	230	240
m102.pep	250	260	270	280	290	300
	QTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
a102	QTAIQXNLPRNEFAPVIAAEGQVSVXIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
	250	260	270	280	290	300
m102.pep	310	320	330	340	350	360
	GLFDYIADIFKWNDSISGRTKTAALTFPLPPLISCLLFPTGFVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDSVSGRTKTAALTFLPPIXISCLLFPTGFVTAIGYVGLAATVWTGIIP					
	310	320	330	340	350	360
m102.pep	370	380	390	400	410	
	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIVNIAAQVLSQMELVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIXNIAAXVLSQMELVPVFKGX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

g105.seq

```

1   Atgtccgcag aaaCATACac acAAAatcggc tGGgtaggct taggGcaaat
51  gGgtctgcct atgGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCgcg CAAAGGAGCA
151 AAAGTTTACG GCagcACCGC CGAACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAACAAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAACA CGCTTCCAAA GacctTAACC TCGcggtcAA AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 364; ORF 105.ng>:

g105.pcp

1	MSAETTYQIG	VWGLGQMGLP	MVTRLDDGGI	EVGVYNRSPD	KTAPISAKGA
51	KVYGSTAEIV	<u>RACPVIFLMV</u>	<u>SDYAAVCDIL</u>	NGVRDGLAGK	IVNMSTISP
101	TENLAVKALV	EAAAGQFAEA	PVSGSVGPAT	NGTLILIFGG	SEAVLNPLQK
151	IFSLVGKKT	HFPGDVGKSG	AKLVNLSLGL	IFGEAYSEAM	LMARQFGIDT
201	DTIVEATGGS	AMDSMPFQTK	KLWANREFP	PAFALKHASK	DLNLAVKELE
251	QAGNTLPAVE	TVAASYRKAV	EAGYGEQDVS	GVYLKLAEH	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 365>:

m105.seq

1	ATGTCGCGCAA	ACGAATACGC	ACAAATCGGC	TGgaTAGGCT	TAGGGCAAAT
51	GGGTCTGCCT	ATGGTAACGC	GGCTCTTGGA	CGGCGGCATC	GAAGTCGCGC
101	TATACAACCG	CTCGCCCGAC	AAAAC TGCCC	CCATCTCCGC	CAAAGGCGCA
151	AAAGTTTACG	GCAACACCGC	CGAACTCGTC	CGCGACTATC	CCGTCAATTT
201	CTGATGGTT	TCCGACTATG	CCGCGCTGTG	CGACATCTCG	AACCGAGTCC
251	GCGACGGATT	GGCCGGCAAm	ATCATCGTCA	ACATGAGCAC	CATCTCCCCG
301	ACCGAAAGC	TCGCCGTCAA	AGCACTTGTC	GAAGCGCAGm	GaCAGTTTGC
351	CGAAGCACCC	GTTTCGCGAT	CGGTCTGGGC	CGCACCAAC	GGCACGCTGC
401	TGATTCTGTT	CGGCGGCAGC	GAACCGtTTT	AAACCCGCTG	CAAAAAATAT
451	TTTCCCTCTG	CGGCAAAAAA	ACCTTCCATT	TCGGCGATGT	CGGCAAAAGT
501	TCGGGCGCGA	AACTCGTCTT	GAACCTCGCT	TTGGGCAATT	TCGGCGAaCG
551	TAcAGCGAAs	GmTgCTGATG	GCGCGGCAGT	TCGGCATCGA	TACCGACACC
601	ATCGTCGAAG	CCATCGGGA	CTCGGCAATG	GACTCGCCCA	TGTTCCAAAC
651	CAAAAAATCC	CTGTGGGCAA	ACCGGAATT	CCCGmCCGmC	TTGCGCCTCA
701	AACACGCCTC	CAAAGACCTC	AACCTCGCCG	TCAAAGAGCT	TGAACAGGCA
751	GGCAACACCC	TGCCCGCCGT	CGAAACCGTT	GCTGCCAGCT	ACCGCAAAAGC
801	AGTCGAAGCC	GGTACGGGA	CACAGGACGT	TTCCGGCGTT	TACCTGAAAC
851	TGGCAGAACA	CTGA			

This corresponds to the amino acid sequence <SEQ ID 366; ORF 105>:

m105.pep

1	MSANEYAQIG	WIGLGQMGLP	MVTRLDDGGI	EVGVYNRSPD	KTAPISAKGA
51	KVYGNTAELV	RDYPVIFLMV	<u>SDYAAVCDIL</u>	NGVRDGLAGX	IIVNMSTISP
101	TEKLAVKALV	EAQRQFAEP	VSSGVGPATN	GTLLILFGGG	EPFXTRCKKY
151	FPSSAKKPSI	SAMSQKVRAR	NSXSTRSPAF	SANVRQXXLM	ARQFGIDTDT
201	IVEAIGDSAM	DSPMFGTKKS	LWANREFPPX	FALKHASKDL	NLAVKELEQA
251	GNTLPAVETV	AASYRKAVEA	GYGTQDVSGV	YLKLAEH	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 105 shows 79.9% identity over a 289 aa overlap with a predicted ORF (ORF 105.ng) from *N. gonorrhoeae*:

m105/g105

		10	20	30	40	50	60
g105.pep		MSAETYTQIGWVGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGSTAE					L
		: : :					:
m105		MSANEYAQIGWIGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAE					L
		10	20	30	40	50	60
		70	80	90	100	110	120
g105.pep		RACPVIIFLMVSDYAAVCDILNGVRDGLAGKIIVN					MS
							:
m105		RDYPVFIIFLMVSDYAAVCDILNGVRDGLAGXIIVN					MS
		70	80	90	100	110	
		130	140	150	160	170	180
g105.pep		PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLV					GK
							:
m105		PVSGSVGPATNGTLLILFGGSEPFTRCKKYFPSSAKKP-					SISAMSAKVRARNSSXTRSW
		120	130	140	150	160	170

314

	190	200	210	220	230	240
g105.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK					
m105	AFSANVQRXXLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPXXFALKHASK					
	180	190	200	210	220	230
	250	260	270	280	289	
g105.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEH					
m105	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGTQDVSGVYLKLAEH					
	240	250	260	270	280	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 367>:

a105.seq

```

1  ATGTCCGCAA  ACGAATACAC  ACAAATCGGC  TGGATAGGCT  TAGGGCAAAT
51  GGGTCTGCCT  ATGGTAACGC  GGCTCTGGA  CGGCGGCATC  GAAGTCGGCG
101 TATACAACCG  CTCGCCCGAC  AAAACTGCCC  CCATCTCCGC  CAAAGGCGCA
151 AAAGTTTACG  GCAACACCGC  CGAACTCGTC  CGCGACTATC  CCGTCATTTT
201 CCTGATGGTT  TCCGACTATG  CCGCCGTGTG  CGACATCCTG  AACGGAGTCC
251 GCGACGGATT  GGCCGGCAAA  ATCATCGTCA  ACATGAGCAC  CATCTCCCGG
301 ACCGAAAACC  TCGCCGTCAA  AGCACTTGTC  GAAGCCGCAG  GCGGACAGTT
351 TGCCGAAGCA  CCCGTTTCCG  GATCGGTCGG  GCCCGCCACC  AACGGCACGC
401 TGCTGATTCT  GTTCGGCGGC  AGCGAAGCCG  TTTTAAACCC  GCTGCAAAAA
451 ATATTTTCCC  TCGTCGGCAA  AAAAACCTTC  CATTTCGGCG  ATGTCGGCAA
501 AGGTTGGGGC  GCGAACTCG  TCTTGAATC  GCTCTGGGC  ATTTTCGGCG
551 AAGCGTACAG  CGAAGCGATG  CTGATGGCG  GGCAGTTCGG  CATCGATACC
601 GACACCATCG  TCGAAGCCAT  CGGCGGCTCG  GCAATGGACT  CGCCCATGTT
651 CCAAACCAA  AAATCCCTGT  GGGCAAACCG  CGAATCCCA  CCCGCCTTCG
701 CCCTCAAACA  CGCCTCCAAA  GACCTCAACC  TCGCCGTCAA  AGAGCTTGAA
751 CAGGCAGGCA  ACACCTGCC  CGCCGTCGAA  ACCGTTGCTG  CCAGCTACCG
801 CAAAGCAGTC  GAAGCCGGCT  ACGGCGAACA  GGACGTTTCC  GGCCTTACC
851 TGAAATTGGC  AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 368; ORF 105.a>:

a105.pep

```

1  MSANEYTQIG  WIGLGQMGLP  MVTRLLDGGI  EVGVYNRSPD  KTAPISAKGA
51  KVGNTAELV  RDYPVIFLMV  SDYAAVCDIL  NGVRDGLAGK  IIVNMSTISP
101 TENLAVKALV  EAAGGQFAEA  PVSGSVGPAT  NGTLLILFGG  SEAVLNPLQK
151 IFSLVGKKT  FFGDVKGKSG  AKLVLNSLLG  IFGEAYSEAM  LMARQFGIDT
201 DTIVEAIGGS  AMDSPMFQTK  KSLWANREFP  PAFALKHASK  DLNLAVKELE
251 QAGNTLPAVE  TVAASYRKAV  EAGYGEQDVS  GVYLKLAEH*

```

m105/a105 96.5% identity in 289 aa overlap

	10	20	30	40	50	60
m105.pep	MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
a105	MSANEYTQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m105.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISP TENLAVKALVEAAG-QFAEA					
a105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISP TENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
	120	130	140	150	160	170
m105.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLVLNSLLG					
a105	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVKGSGAKLVLNSLLG					
	130	140	150	160	170	180
	180	190	200	210	220	230

```

m105.pep    IFGDV-QRXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPXAFALKHASK
             |||:: :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
             190      200      210      220      230      240

m105.pep    240      250      260      270      280
             DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
             250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 369>:

```

g105-1.seq
1  ATGTCCGCAG AAACATACAC ACAAATCGGC TGGGTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGAGCA
151 AAAGTTTACG GCAGACCCGC CGAACTCGTC CGCGCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCGGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAACAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCCTTG
701 CACTCAAAAC CGCTTCCAAA GACCTTAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GGCCTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 370; ORF 105-1.ng>:

```

g105-1.pep
1  MSAETYTIQIG WVGLGQMGLP MVTRLDDGGI EVGVYNRSPD KTAPISARGA
51  KVYGSTAEVLV RACPVIIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGQGFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
151 IFSLVGKKTFF HFGDVGKGS GAKLVNLSLG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 371>:

```

m105-1.seq
1  ATGTCCGCAA ACGAATACGC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACCCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCGGCG ATGTCGGCAA
501 AGGTTCGGGC GCGAAACTCG TCTTGAATC GCTCTGGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGAGACTCG GCAATGGACT CGCCCATGTT
651 CCAAACAAA AAATCCCTGT GGGCAAACCG CGAATTCCTG CCCGCCCTTG
701 CCCTCAAAAC CGCTTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GGCCTTACC
851 TGAAACTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 372; ORF 105-1>:

```

m105-1.pep
1  MSANEYAQIG WIGLGQMGLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51  KVYGNTAEVLV RDPVIFILMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP

```

316

```

101  TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
151  IFSLVGKKTFF HFGDVGRGSG AKLVNLSLLG IFGEAYSEXLMARQFGIDT
201  DTIVEAIGDS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251  QAGNTLPVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

m105-1/g105-1 96.9% identity in 289 aa overlap

```

              10      20      30      40      50      60
m105-1.pep  MSANEYAQIGWIGLGQMG LPMVTRLLDGGIEVG VYNRSPDKTAPISAKGAKVYGN TAEVLV
              |||: ||:||||:|||||
g105-1      MSAETYTQIGWVGLGQMG LPMVTRLLDGGIEVG VYNRSPDKTAPISAKGAKVYGS TAEVLV
              10      20      30      40      50      60

              70      80      90     100     110     120
m105-1.pep  RDYPVIFILMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
              | |||||
g105-1      RACPVIIFILMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
              70      80      90     100     110     120

              130     140     150     160     170     180
m105-1.pep  PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS GAKLVNLSLLG
              |||||
g105-1      PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKGS GAKLVNLSLLG
              130     140     150     160     170     180

              190     200     210     220     230     240
m105-1.pep  IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK
              |||||
g105-1      IFGEAYSEAMLARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190     200     210     220     230     240

              250     260     270     280     290
m105-1.pep  DLNLAVKELEQAGNTLPVETVAASYRKAVEAGYGEQDVS GVYLKLAEHX
              |||||
g105-1      DLNLAVKELEQAGNTLPVETVAASYRKAVEAGYGEQDVS GVYLKLAEHX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 373>:

```

a105-1.seq
1  ATGTCCGCCAA ACGAATACAC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101  TATACAACCG CTCGCCCGAC AAAACTCGCC CCATCTCCGC CAAAGCGCA
151  AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201  CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCTCG AACGGAGTCC
251  GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCGG
301  ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351  TGCCGAAGCA CCCGTTTCCG GATCGGTCGG GCCCGCCACC AACGGCACGC
401  TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451  ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGCG ATGTCGGCAA
501  AGGTTCCGGC GCGAACTCG TCTTGAATC GCTCTTGGG ATTTCGGCG
551  AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601  GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCCATGTT
651  CCAAACCAAA AAATCCCTGT GGGCAAACCG CGAATTCCCA CCCGCTTCG
701  CCCTCAACAA CGCCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751  CAGGCAGGCA ACACCTGCC CGCCGTGCAA ACCGTTGCTG CCAGCTACCG
801  CAAAGCAGTC GAAGCCGCTC ACGGCGAACA GGACGTTTCC GCGCTTACC
851  TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 374; ORF 105-1.a>:

```

a105-1.pep
1  MSANEYTQIG WIGLGQMG LPMVTRLLDGGI EVGVYNRSPD KTAPISAKGA
51  KVVYGN TAEVL RDYPVIFILMV SDYAAVCDIL NGVRDGLAGK IIIVNMSTISP
101  TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
151  IFSLVGKKTFF HFGDVGRGSG AKLVNLSLLG IFGEAYSEAM LMARQFGIDT
201  DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251  QAGNTLPVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

a105-1/m105-1 99.0% identity in 289 aa overlap

```

              10      20      30      40      50      60
a105-1.pep  MSANEYTQIGWIGLGQMG LPMVTRLLDGGIEVG VYNRSPDKTAPISAKGAKVYGN TAEVLV
              |||||

```

```

m105-1      MSANEYAQIGWIGLGQMG LPMVTRL LDGGIEVGVNRS PDKTAPISAKGAKVYGNTAELV
              10      20      30      40      50      60

              70      80      90      100     110     120
a105-1.pep  RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
              |||||
m105-1      RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA
              70      80      90      100     110     120

              130     140     150     160     170     180
a105-1.pep  PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVNLSLLG
              |||||
m105-1      PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVNLSLLG
              130     140     150     160     170     180

              190     200     210     220     230     240
a105-1.pep  IFGEAYSEAMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
              |||||
m105-1      IFGEAYSEAMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190     200     210     220     230     240

              250     260     270     280     290
a105-1.pep  DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
              |||||
m105-1      DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

```

g107.seq
1   ATGGTATTAA CCTTTATTG GGC AACCGC GGCCTGGT G CCGATGCCAA
51  ACCGTCCGTC CTCTTCGACA CCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCCttggta atttacgtcc
251 TCTggcaaac cgccatCcaa agcaaccTGC cgcgcaacga gttcgcCCCC
301 gtgattgccg ccgagaggca actCTCCGTC CTgaatgaaa cccTGtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc cacctccttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cggcaccaaa
501 accgtcgcgc tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

```

g107.pep
1   MVLTFIWATG GLVADAKPSV LFDTQAPVGT GYWIYAATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAAERQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSF LGVTGLGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

```

m107.seq
1   ATGGTATTGA CCTTTATTG GCGGCCGCGC GGGCTGATTG CCGATGCCAA
51  GCCGTCCGTC CTCTTCGATA CCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGc CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTCT CCAGCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCGCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCTGTCCAA
351 ATTGCCCCAA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

```

m107.pep..
1   MVLTFIWAAG GLIADAKPSV LFDTQAPAGT NYWIYAXTAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP

```

101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IAHLOMERQH LRAAPKPPR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng) from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
g107	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWGTGLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	: : : : :					
g107	KGDAPKVAKSIWGTGLIALVIYVLWQTAIQGNLPRNEFAPVIAAERQSLVNETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSFGLVTLGLFDYIA-HLOMERQHLRAAPKPPR					
	: : : : :					
g107	TGDMDKILSLFPYMAIATSFGLVTLGLFDNIAGHLQMERQYVRAAPKPSR					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTATTG GGCACCGGC GGCCTGATTG CCGATGCCAA
51  ACTGCCCCGC CTCTCGACA CCCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTCGC CACCGCCCTG CCCGTCTGCC TTGCGTCATT CGGTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGGGCA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTCGCCCCA ACCGGCAATA TGGACAAAAT ATTGTCCTTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCCGCGCTG ACCTTCCTGC CGCCTCTAAT TTCCTGCCTG CTCTTCCCCA
551 CCGGCTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCGTCTGG
601 ACAGGCATCA TCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTCGG
651 CGCAGGCAAA ACCTATAAAG TTTACGGCGG CTTGTGGCTG ATGTTTGGG
701 TCTTCCTTTT CGGCATCGTC AACATCGCCG CACAGGTATT GAGCCAAATG
751 GAACTCGTCC CCGTATTTAA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWAAGGLIADAKLPV LFDQAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTLGLFDY
151 IADIFKWNDS VSGRTKTAAL TFLPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKFGAGK TYKVYGLLWL MVVFLFGIV NIAAQVLSQM
251 ELVPVFKG*

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	: : : : :					
a107	MVLTFIWAAGGLIADAKLPVLFDTQAPTGTNYWIYVATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60

```

              70      80      90      100      110      120
m107.pep      KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ
              |||||
a107           KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ
              70      80      90      100      110      120

              130      140      150      160      170
m107.pep      TGNMDKILSLFSYMAIATSFLGVTLGLFDYIAHLQMERQHLRAAPKPPRX
              |||||
a107           TGNMDKILSLFSYMAIATSFLGVTLGLFDYIADIFKWNDSVSGRTKTAALTFLPPLISCL
              130      140      150      160      170      180

a107           LFPTGFVTAIGYVGLAATVWTGIIPAMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIV
              190      200      210      220      230      240

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

```

g108.seq
1   ATGttgcccgg gCTTCAACCG GATATTCAaa cggTTTGCTC CAACACTCGG
51  AAcggCGCAT AAAACGCCGc ccTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATCCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTGCGCGCG GCAATCTTAC TCGGCGGGTG
201 CGCCGCCGCG GCACAACAT TCGGCAGCTT AGACGGCGGC ACGGGTATGG
251 GTGGCAGCAT CGTCAAAATG ACGGTAGAAA gccAATGCCG TCGGGAATTG
301 GACAGGCGCA GCGAATGGCG TTGACCGCG CTGGCGATGA GTCCGAAAAA
351 ACAGGCGGAA TGGGAAAACA AGATTTCGGG CTGCGCTACC GAAGAAGCAC
401 CTAACCAAGT GACCGGCAAC GATGTGATGC AGATGCTGaa ccagtccacG
451 CGCaatcagg cacTtgccgc CCTgaccgTC AAAacgggTT CgcgctgcTT
501 CAAacgcctg tACCGCTAa

```

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

```

g108.pep
1   MLPGFNRIFK RFAPTLGTAH KTPPFALSRT GRLIRSYRHK RRGFNRKGIE
51  MNKTLSILPA AILLGGCAAG GNTFGSLDGG TGMGGSIVKM TVESQCRAEL
101 DRRSEWRLTA LAMSAEKQAE WENKICGCAT EBAPNQLTGN DVMQMLNQST
151 RNQALAAALTV KTVSACFKRL YR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

```

m108.seq
1   ATGTTGCCGG GCTTCAACCG GATATTCAAA CGGTTTGTTT CAACACTCGG
51  AACGGCGCAT AAAACGCCGC CCTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATTCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTGCGCGTG GCAATCTTAC TCGGCGGGTG
201 CGCCGCCGGA GGCGGTAAAC CATTCGGCAG CTTAGACGGT GGCACAGGCA
251 TGGCGGCAG CATCGTCAA ATGGCGGTTG GGAGCCAATG CCGTGCGGAA
301 TTGGACAAAC GCAGCGAATG GCGTTTGACC GCGCTGGCGA TGAGTGCCGA
351 AAAACAGGCG GAGTGGGAAA ACAAGATTG CGCTTGCGTC GCCCAAGAAG
401 CACCGAACG GATGACCGGC AACGATGTA TGCAGATGCT GGCTCCGTCC
451 ACGCGCAATC AGGCATTGC CGCCTGACC GCCAAACGG TTTCCGCCTG
501 CTTCAAACAC CTGTACCGCT AA

```

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

```

m108.pep
1   MLPGFNRIFK RFVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNRKGIE
51  MNKTLSILPV AILLGGCAAG GGNTFGSLDG GTMGGSIVK MAVGSQCRAE
101 LDKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPERMTG NDVMQMLAPS
151 TRNQALAAALT AKTVSACFKH LYR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng) from *N. gonorrhoeae*:

m108/g108

a108.seq

This corresponds to the amino acid sequence <SEQ ID 386; ORF 108.a>:

1 MLPGFNRIKF RFVPTLGTAH KTPPFALSRT GLRIRFYRHK RRGFNKRKIE
51 MNKTLTSLPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE
101 LNKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS
151 TRNOALAALT AKTVSACFKH LYS*

	10	20	30	40	50	60
m108.pep	MLPGFNRI	FKRFVPTL	GTAHKTPP	FALSRTGR	LIRFYRHK	RGRGFENR
a108	MLPGFNRI	FKRFVPTL	GTAHKTPP	FALSRTGR	LIRFYRHK	RGRGFENR
	10	20	30	40	50	60
	70	80	90	100	110	120
m108.pep	AILLGGCA	AAGGGNTF	GSLDGGT	GMGGSIVK	MAVGSQCR	AELDKRSE
a108	AILLGGCA	AAGGGNTF	GSLDGGT	GMGGSIVK	MAVESQCR	AELNKRSE
	70	80	90	100	110	120
	130	140	150	160	170	
m108.pep	EWENKICAC	VAEAPERMT	GNQNDVMQ	MLAPSTRN	QALAAALT	AKTVSACF
a108	EWENKICAC	VAEAPNQLT	GNQNDVMQ	MLDPSTRN	QALAAALT	AKTVSACF
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:



This corresponds to the amino acid sequence <SEQ ID 388; ORF 109.ng>:

1 MYRRVVGLS DGLGDLAAGI DRRRLTAFG SGHGNDARQ RQ NHPIRRHRGV
51 LFRLLNPNVFG WALTMLLDNL GLIGCKERSA QLGFVGRVLI PAVGFLILCV
101 AMGAVGMLPG IPPFLEOFKS LG

m109.seq

```

1   ATGTATTATC GCCGGGTTAT GGGGCTATCC GATGGACTTG GCGATTTTGGC
51  AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CATCGTGGTG TTCTCTCCG CCTTGTC AAT CCGGTTTTCG GCTGGGCGTT
201 GACGATGCTG TTGGATAATT TGGGCTTAAT CGGCTGCAAA GAGCGCAGTG
251 CGCAATTAGG TTTCGCCGGA CGCGTGTTGA TACCCGCAGT AGGTTTCTTG
301 ATCTTTGTGT TGCGCATGGG TGCGTGCGG ATGCTGCCCG GTATCCCGCC
351 GTTTTTGGAA CAGTCAAAT CTTTGGGCTA G

```

m109.pep

1 MYRRVMGLS DGLGDLAAGI ERLGRRRII TAFSGHGND AQRQNHPIRR
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFAG RVLIPAVGFL
101 ILCVAMGAVG MLPGIPPFLE HFKSLG*

Homology with a predicted ORF from *N. gonorrhoeae*

m109/q109

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 391>:

a109.seq

1 ATGTATTATC GCCGGGTGT GGGGCTATCC GATGGACTTG GCGATTTGGC
51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCACCC AATCCGCCGC
151 CACCGTGGTG TTCTCTCCG CTTGGTCAAT CCGGTTTTCG GCTGGGCGTT

a109.pep

q111.seq

corresponds to the amino acid sequence <SEQ ID 304: ORE 111 aa>:

g111.pap

following partial DNA sequence was:

m111.seq

323

```

601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCGATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTTCTCTG ATTGTCAGGG
1001 ATAAAGGCGG cTACCGCACC GCCATGTCTT CCGAATTGTA AAAAGTGCtTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 396; ORF 111>:

```

m111.pep
1  MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLQGET MGTITYXVKYL
51  SNNRDKLPSP AEIXKRIDDA LKEXNRXMST YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTGVL VNLWGFDPK SVTREPSP EQ
151 IKQAASYTGI DKIIILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHKG GKNARGEPWR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVDASAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

ORF 111 shows 88.7% identity over a 97 aa overlap with a predicted ORF (ORF 111.ng) from *N. gonorrhoeae*:

m111.pep/g111.pep

	10	20	30	40	50	60
m111.pep	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTITYXVKYLSNNRDKLPSP					
	: : : : : : : : : : :					
g111	MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLQGETMGTITYXVKYLSNNRDKLPSP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m111.pep	AEIXKRIDDALKEXNRXMSTYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	: : :					
g111	AKIQKRIDDALKEVNRQMSTYQTDSEISRFIQTXAGELFAXHAXSITDSAEDCLPNTPI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m111.pep	GALDVTGVLVNLWGFDPKSVTREPSPQIKQAASYTGIDKIIILKQKDYASLSKTHPK					
g111	SALX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 397>:

a111.seq

```

1  ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTGC
51  CCTGAGTTTT ATCTTCTCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAAATATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG
351 CCTGACACAC GGCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAA TCCGTACCC GTGAACCGTC GCCGGAACAA
451 ATCAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAACA
501 AGGCAAAGAT TACGTTCTCT TGAGCAAAAC CCACCCAAG GCCTATTGCG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TGCGGGCGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA

```

324

```

801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTG ATTGTAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAAGTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

```

1 MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLQGET MGTTYTVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFDPK SVTREPSPEQ
151 IKQAASYTGI DKIIKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLAS SISVVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSP					
a111	MPSETRLPNFIRTLIFALSFIPLNACSEQTAQTVTLQGETMGTTYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISDFAHVTA EAVHLNRLTH					
a111	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISDFAHVTA EAVHLNRLTH					
	70	80	90	100	110	120
m111.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
a111	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIKQKGDYASLSKTHPK					
	130	140	150	160	170	180
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRWIGIEQPNIVQ					
a111	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRWIGIEQPNIVQ					
	190	200	210	220	230	240
m111.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVADSAM					
a111	GGNTQIIVPLNNRSLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVADSAM					
	250	260	270	280	290	300
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

```

1 ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTGTC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTT GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCCCCT GCCAAAATAC AAAAGCGCAT
201 TGATGATGCG CTTAAGAAG TCAACCGCA GATGTCCACC TACCAGACCG

```

325

```

251 ATTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ATTTGCGACA CGTTACCGCC GAAGCCGTCC GCCTGAACCG
351 CCGTACTCAC GCGCCTGGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGGTTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAACAA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAA GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCggcGAGTT
651 GCACGGCAAA GGCAAAAATG CGCAGCGCGA ACCGTGGCGC ATCGGTATAG
701 AGCAACCCAA TATcatccaa ggcggcaata cgcAGattat cgtcccgctg
751 aaCaaccgtt cgcttgccac ttccggcgAT taccgtaTTT tccacgtcgA
801 TAAAAACGGC Aaacgccttt cccacATCAT CAATCCCAAC AACAAACGAC
851 CCATCAGcCA CAacctcgcc tcCATCagCg TGGTCTCAGA CAGTGCATG
901 ACGGCGGACG GTTTATCCAC AGGATTATTT GTTTTAGCGC AAACCGAAGC
951 CTTAAGGCTG GCAGAACAAG AAAAACTCGC TGTTCCTTA ATTGTCCGGG
1001 ATAAGGACGG CTACCGCACC GCCATGTCTT CCGAATTGTC CAAGCTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 400; ORF 111-1.ng>:

g111-1.pep

```

1 MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLQGET MGTITYVKYL
51 SNNRDKLPSP AKIQKRIDDA LKEVNRQMSY YQTDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGPK SVTREPSPEQ
151 IKQAASYTGI DKIIILQOGKD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNHGEFWR IGIEQPNIIQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVSADSAM
301 TADGLSTGLF VLGETEALRL AEQEKLAFL IVRDKDGYRT AMSSEFAKLL
351 R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 401>:

m111-1.seq

```

1 ATGCCGTCTG AAACACGCCT GCCGAACCTT ATCCGCGTCT TGATATTGTC
51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAACCG
101 TTACCCTGCA AGGCGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAAATAAT GGGACAAACT CCCCTCACTT GCCGAAATAC AAAAAACGAT
201 CGATGACGGG CTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC GCCTGAACCG
351 CCTGACACAC GCGCGCTGGG ACGTAACCGT CGGCCCTTTG GTCAACCTTT
401 GGGGATTTCG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAAACAGG CGGCATCTTA TACGGGCATA GACAAAATCA TTTTGAACAA
501 AGGCAAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAA GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGGCGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GCGGGAATA CGCAGATTAT CGTCCCCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGCGC AAACCGAAGC
951 CTTAAGCTG GCAGAGCGCG AAAAACTCGC TGTTCCTTA ATTGTAGGG
1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGTA AAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 402; ORF 111-1>:

m111-1.pep

```

1 MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLQGET MGTITYVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFPGPK SVTREPSPEQ
151 IKQAASYTGI DKIIILQOGKD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNHGEFWR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKNG KRLSHIINPN NKRPISHNLA SISVVSADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAFL IVRDKDGYRT AMSSEFEKLL
351 R*

```

m111-1/g111-1 96.6% identity in 351 aa overlap

	10	20	30	40	50	60
m111-1.pep	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTITYVKYLSNNRDKLPSP					
g111-1	MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLQGETMGTITYVKYLSNNRDKLPSP					

326

	10	20	30	40	50	60
m111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNROMSTYQPDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
g111-1	AKIQKRIDDALKEVNROMSTYQTDSEISRFNQHTAGKPLRISSDFAHVTAEAVRLNRLTH					
	70	80	90	100	110	120
m111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPKSVTREPSPQIKQAASYTGIDKIILKQKDYASLSKTHPK					
g111-1	GALDVTVGPLVNLWGFGPKSVTREPSPQIKQAASYTGIDKIILKQKDYASLSKTHPK					
	130	140	150	160	170	180
m111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKFGVDKVGAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQ					
g111-1	AYLDLSSIAKFGVDKVGAGELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIIQ					
	190	200	210	220	230	240
m111-1.pep	250	260	270	280	290	300
	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPISHNLASISVVADSAM					
g111-1	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPISHNLASISVVSDSAM					
	250	260	270	280	290	300
m111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
g111-1	TADGLSTGLFVLGETEALRLAEQEKLAFLIVRDKDGYRTAMSSEFAKLLRX					
	310	320	330	340	350	

g111-1/p44550

sp|P44550|YOJL_HAEIN HYPOTHETICAL LIPOPROTEIN HI0172 PRECURSOR >gi|1074292|pir||C64144
 hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)
 lipoprotein, putative [Haemophilus influenzae Rd] Length = 346
 Score = 349 bits (885), Expect = 2e-95
 Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSPAEIXKRIDDALKEVNRMSTYQ 82
 L AC + + T + + L G + TMGTTY VKYL + S + + I + LK + N MSTY +
 Sbjct: 17 LAACQKET -KVISLSGKTMGTTYHVKYLDGGSITATS - EKTHEEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRFNQHT - AGKPLRISSDFAHVTAEAVRLNRLTHGALDVTVGPLVNLWGFGPKS 141
 DSE + SRFNQ + T P + IS + DFA V AEA + RLN + + T GALDVTVG + VNLWGFGP + K
 Sbjct: 75 KDSELSRFNQNTQVNTPIEISADFAKVLAEAIRLNKVTGALDVTVGPPVNLWGFGPEKR 134

Query: 142 VTREPSPQIKQAASYTGIDKIILKQKDYASLSKTHPKAYLDLSSIAKFGVDKVGAGEL 201
 + + P + PEQ + + + + GIDKI L K + A + LSK P + Y + DLSSIAKFGVD + VA + L
 Sbjct: 135 PEKQPTPEQLAERQAWVGIDKITLDTNKEKATLSKALPQVYVDLSSIAKFGVDQVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQGGNTQIIIVPLNNRSLATSGDY 261
 E + QNY + VEIGGE + KGKN G + PW + I IE + P + + LNN + A + SGDY
 Sbjct: 195 EQLNAQNYMVEIGGEIRAKGNIEGKPPWQIAIEKPTTTGERAVEAVIGLNNMGMASSGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNKRPISHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321
 RI + + + NGKR + H I + P PI H + LASI + V + A + + MTADGLSTGLFVLGE + AL + + A
 Sbjct: 255 RIY - FEENGKRFAHEIDPKTYPIQHHLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLAVFLIVRDKGGYRTAMSSEFEKL 349
 E + LAV + LI + R G + T SS F + KL
 Sbjct: 314 EKNNLAVYLIIRTDNGFVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

a111-1.seq

```

1  ATGCCGCTCG AAACACGCCT GCCGAAC TTT ATCCGCACCT TGATATTTC
51  CCTGAGTTTT ATCTTCCTGA ACGCCTGTT C GGAACAAACC GCGCAAACCG
101 TTACCCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCCTCCGC
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG

```

327

```

351 CCTGACACAC GGGCGGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCGG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAATCA TTTTGAAACA
501 AGGCAAAAGT TACGCTTCTT TGAGCAAAAC CCACCCCAAG GCCTATTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGCGGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGC AAAACG CGCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GGGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATT TCCACGTCGA
801 TAAAAGCGCG AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAA ACTCG TGT TTTCTG ATTGTCAGGG
1001 ATAAAGCGCG CTACCGCACC GCCATGTCTT CCGAATTGA AAAACTGCTC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

a111-1.pep

```

1 MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLQGET MGTITYTVKYL
51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFPGDK SVTREPSPEQ
151 IKQAASYTGI DKILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPRW IGIEQPNIVQ GGNTQIIVPL
251 NNRLSLATSGD YRIFHVDKSG KRLSHIINPN NKRPISHNLA SISVVDASAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

a111-1.pep	10	20	30	40	50	60
	MPSETRLPNFIRTLIFALSFIFLNACSEQTAQTVTLQGETMGTITYTVKYLNNRDKLPSP					
m111-1	MPSETRLPNFIRVLFALGFIFLNACSEQTAQTVTLQGETMGTITYTVKYLNNRDKLPSP					
	10	20	30	40	50	60
a111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVHLNRLTH					
m111-1	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH					
	70	80	90	100	110	120
a111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKILKQKGDYASLSKTHPK					
m111-1	GALDVTVGPLVNLWGFPGDKSVTREPSPEQIKQAASYTGIDKILKQKGDYASLSKTHPK					
	130	140	150	160	170	180
a111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGNARGEPRWIGIEQPNIVQ					
m111-1	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGNARGEPRWIGIEQPNIVQ					
	190	200	210	220	230	240
a111-1.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRLSLATSGDYRIFHVDKSGKRLSHIINPNNKRPISHNLA SISVVDASAM					
m111-1	GGNTQIIVPLNNRLSLATSGDYRIFHVDKNGKRLSHIINPNNKRPISHNLA SISVVDASAM					
	250	260	270	280	290	300
a111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
m111-1	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

g114.seq

```

1 ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51 GACTTTTTTA TGTCCGCCG GCGGGACGAG TATGGGGCGG TCAATGTCGG

```

```

101 TAACGGTAGG TTTGTTTTGT GTTCCATTA ACTTAACAAT ATCTGTCGAA
151 TACGGTCAAA GCGGCTATTT TACCAGAGCC GCCGAATGTA AAACAGGGTG
201 TCAGGGCATC AGCCCAGAGCT GCCTGAACGA ACGGACGGTT TGCGAGGTAA
251 CGATAAAATG GTCGAGCAGC GAAACATCAA CCAGCGACAT GGCCTGTGCC
301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGGTCAG GCGAGCCGCC
351 CGGATGGTTG TGCGCGATAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 406; ORF 114.ng>:

```

g114.pep
  1 MASITSPLHG AQQECSTFL CPPGGTSMGR SMSVTVGLFC VSINLTISVE
  51 YGQSGYFTRA AECKTGCGI SPSCLNERTV CEVTIKWSSS ETSTSDMACA
 101 SRLVNMSSC EGSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 407>:

```

m114.seq
  1 ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCACAGAG AATGCAGCAA
  51 GACTTTTTTA TGTCCACCGG GCGGACGAG TATAGGCGG TCAATGTCGG
 101 TAACGGTAGG TTTGTTTTGT GTTCCATTA ACTTAACAAT ATCTGTTGAA
 151 TACGGTTGAA GCGGCTATTT TATCAGAGCC GCCGCATGTA AAACAGAGTG
 201 TCAGGGCATC AACCCGAGCT GTCTGAACGA ACAGACGCTT TGCGAKGTAA
 251 CGATAAAATG GTCGAGCAGC GACACATCGA CCAGCGACAT TGCCTGTGCC
 301 AGCCGCCTTG TGAACATGAT GTCTTCCTGC GAAGTTCsG GCGAGCCGCcC
 351 CGgATGGTTG TGCGCAATAA TCAGGCTGTC GGCATATTCG TCCAATGCCA
 401 GTTTGACGAT TTCGCGGATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 408; ORF 114>:

```

m114.pep
  1 MASITSPLHG AHRECSKFL CPPGGTSIGR SMSVTVGLFC VSINLTISVE
  51 YGXSGYFIRA AACKTECQGI NPSCLEQTL CXVTIKWSSS DTSTSDIACA
 101 SRLVNMSSC EXSGEPPGWL CAIIRLSAYS SNASLTISRM *

```

m114/g114 90.0% identity over a 140 aa overlap

	10	20	30	40	50	60
m114.pep	MASITSPLHGAHRECSKFLCPPGGTSIGRSMSTVGLFCVSINLTISVEYGXSGYFIRA					
g114	MASITSPLHGAQQECSKFLCPPGGTSMGRSMSTVGLFCVSINLTISVEYQSGYFTRA					
	10	20	30	40	50	60
m114.pep	AACKTECQGINPSCLEQTLCXVTIKWSSSDTSTSDIACASRLVNMSSCEXS					
g114	AECKTGCGGISPSCLNERTVCEVTIKWSSSETSTSDMACASRLVNMSSCEGS					
	70	80	90	100	110	120
m114.pep	GEPGWL					
g114	GEPGWL					
	70	80	90	100	110	120
m114.pep	CAIIRLSAYSSNASLTISRMX					
g114	CAIIRLSAYSSNASLTISRMX					
	130	140				
m114.pep	CAIIRLSAYSSNASLTISRMX					
g114	CAIIRLSAYSSNASLTISRMX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 409>:

```

a114.seq
  1 ATGCCGAGG CAAGCATCGC CTCCATCACT TCGCCGCTGC ACGGGGCGCA
  51 ACAGGAATGC AGCAAGACTT TTTTATGTCC GCCGGGCGGG ACGAGTATGG
 101 GGGCGTCAAT GTCGGTAACG GTAGGTTTGT TTTGTGTTTC CATTAACTTA
 151 ACGATATCTG TCGAATACGG TTGAAGCGGC TATTTTATCA GAGCCGCCGC
 201 ATGTAAAACA GGGTGTGAGG GCATCAGCCC GAGCTGCCTG AACGAACGGA
 251 CGGTTTGC GCATTACGATA AAATGGTCGA GCAGCGACAC ATCGACCAGC
 301 GACATTGCCT GTGCCAGCCG CCTTGTGAAC ATGATGTCTT CCTGCGAAGG
 351 TTCGGGCGAG CCGCCCGGAT GGTGTGCGC GATAATCAGG CTGTCGGCAT
 401 ATTCGTCAA TGCCAGTTTG ACAATTTCAC GGATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 410; ORF 114.a>:

a114.pep

```

1  MPEASIASIT SPLHGAQQEC SKTFLCPPGG TSMGRSMSVT VGLFCVSINL
51  TISVEYG*SG YFIRAAACKT GCQGISPSCL NERTVCAVTI KWSSSDTSTS
101 DIACASRLVN MMSSCEGSGE PPGWLCIIIR LSAYSSNASL TISM*
```

m114/a114 92.9% identity in 140 aa overlap

```

              10      20      30      40      50
m114.pep      MASITSPLHGAHRECSKTFLCPPGGTSIGRSM SVTVGLFCVSINLTISVEYGXSG
              :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a114           MPEASIASIT SPLHGAQQEC SKTFLCPPGGTSMGRSM SVTVGLFCVSINLTISVEYGXSG
              10      20      30      40      50      60

              60      70      80      90      100     110
m114.pep      YFIRAAACKTECQGINPSCLNEQTL CXVTIKWSSSDTSTSDIACASRLVNMMSSCEXS GE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a114           YFIRAAACKTGCQGISPSCLNERTVCAVTIKWSSSDTSTSDIACASRLVNMMSSCEGS GE
              70      80      90      100     110     120

              120     130     140
m114.pep      PPGWLCIIIRLSAYSSNASLTISM X
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a114           PPGWLCIIIRLSAYSSNASLTISM X
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 411>:

g117.seq

```

1  atggtcgacg aactcgacCT GCTGCCCCGAT GCCGTCGCCG CCACCCGTGCT
51  TGCCGACATC GGACGCTACG TCCCCGATTG GAACCTATTG GTTCCGAGC
101 GCTGCAACAG CACCGTCGCC GAGCTGGTCA AAGGTGtgga CGAAGTGCAG
151 AAACCTACCC ACTTCGCCCG GGTGGACAGC CTCGCCACGC CGGAAGAACG
201 CGCACAGCAA GCGGAAACCA TGCGGAAAT GCTGCTGGCg atggttaccg
251 Acatccgcgt cgtatTAATC AAACCTGGCGA TGCGTaccg caccCTGcta
301 ttTTtaaGCA ACGCCCCGA CAGCCCTGAA AAACgcgccc TCgccaaAga
351 aacccTCGAC ATCTTCGCCC CGCTCGCCAA CCGCTTGGGC GTGTGGCAGC
401 TCAAATGGCA GCTCGAAGAT TTGGGCTTCC GCCATCAAGA ACCCGAAAAA
451 TACCGCGAAA TCGCCCTGCT TTTGGACGAA AAACGCACCG AACGCCTCGA
501 ATACATCGAA AACTTCCTCG ATATCCTGCG TACGGAATC AAAAAATACA
551 ATATCCAATT TGAAGTCGCC GGCCGTCCGA AACACATCTA CTCCATTAC
601 AAAAAAATGG TGAAGAAAAA ACTCAGCTTC GACGgctTGT TCGACATCCG
651 CGCCGTGCGG ATTCTGGTCG ATACCGTCCC CGaGTGTAC ACCACGCTGG
701 gcaTCGTCCA CAGCCTCTGG CAGCCCATT CCGGCGagtt CGAcgactAC
751 ATCGCCAACC CCAAAGgcaA CGgttATAAA AGtTTGCACA CCGTCATCGT
801 cggcccGGAa gacaaaggtg tggaaGtgCA AATCCGCACC TTCGAtatGC
851 accAATTCAA CgaatTcggT gtcgcccGCC ACTGGCGtta caaagaaggc
901 ggcaaaaggcg attccGCCtA cgaacaaAAA ATcgccTggt TGCgccaACT
951 CTTGGACTGG CGCGAAAATA TGGCGGAAAG CGGCAAGGAA GACCTCGCCG
1001 CCGCCTTCAA AACCGAGCTT TTCAACGACA CGATTATGT TTTGACCCCG
1051 CACGCAAAAG TCCTCTCTCT GCCAACGGGC GCAACCCCA TCGACTTCGC
1101 CTACGCCCTG CACAGCAGCA TcggCGACCG CTGCCGGGGC GCGAAAGTCG
1151 AaggGCAGAT TGTGCGCTG TCCACCCGC TCGAAAACGG ACAGCGCGTC
1201 GAAATcatta cCGCcaaAGA AGGGCATCCT TCCGTCAACT GGCTTTACGA
1251 AGGctgGGtc aAATCCGCA AGGCCATCGG caaAATCCGC GCCTAcacCC
1301 GCCAGcaaAa cgCgaCACC GTGCGGAAG AAGGCCGTGT CCAACTCGAC
1351 AAGCAGCTTG CCAAACTCAC GCCCAAACCC AACCTGCAAG AGCTTgcccga
1401 aaATCTCGGC taaaaAAGC cagaagacct ctacacCGCc gtcggacaag
1451 gcgaatttc caaccgcgcc atCcaaaaag cctgcggcac GCTgaacgaa
1501 ccgccccCGG TGCCCGTCAG CGCAACCACC ATCGTCAAAC AGTCCAAAT
```

```

1551 CAAAAAAGGT GGCAAACCG GCGTGCTCAT CGACGGCGAA GACGGCTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAACCG CGCCGCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTC GTCCACCGCA AACCTGCCC
1701 CTCTTTCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAGGAA GGGCAAGTGT TCGCCGTCGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCGG GCTTTTGC GC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTTA CCGCCGTGCA AACCCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTTCACG CTCGAAGTCA AACAAGtCAA CGacCTCCCC
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAA GCGTATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

g117.pep

```

1 MVDEL DLLPD AVAATLLADI GRYPDWNLL VSERCNSTVA ELVKGVDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVLI KLAMRTRTLL
101 FLSNAPDSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHQEPEK
151 YREIALLLDE KRTERLEYIE NFDLILRTEL KKYNIHFVA GRPKHIYSIY
201 KKMVKKKLSF DGLFDIRAVR ILVDTVPECY TTLGIVHSLW QPIPGFDDY
251 IANPKNGYK SLHTVIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 KGKDSAYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLTLP
351 HGKVLSLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQRV
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIRQONADT VREEGRVQLD
451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLINE
501 PPPVPVSATT IVKQSKI KKG GKTGV LIDGE DGLMTTLAKC CKPAPPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GOVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTA VQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLG DVK GVL SVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

m117.seq (partial)

```

1 ..GTGAACTCA AGAAATACAA TGTCCATTTC GAAGTCGCCG GCCGCCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCTCTT TGACATCCGC GCCGTGCGAA TTCTGGTTGA TACCGTCCCC
151 GAGTGTACA CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCCATTC
201 CGGCGAGTTC GACGACTACA TCGCCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTGCACAC CGTCATCGTC GGCCCGGAAG ACAAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATTCAAC GAATTCGGTG TCGCCGCCCA
351 CTGgCGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAACTC TTGGACTGGC GCGAAAACAT GCGCGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAA ACCGAGCTTT TCAACGACAC
501 GATTATATGTT TTGACCCCGC ACGGCAAAGT CCTCTCCCTG CCCACGGGCG
551 CGACCCCAT CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCCGGGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCCGCT
651 CGAAACCGGA CAGCGCGTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CCTACATCCG CCAGCAAAAC GCCGACACCG TGCGCGAAGA
801 AGGCCGCGTC CAACTCGACA AACAGCTTGC CAAACTCACG CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGCT ACAAAAAGCC AGAAGACCTC
901 TACACCGCGG TCGGACAAGG CGAAATTTC AACCGCGCCA TCCAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCCGT ACCCGTCAGC GAAACCACCA
1001 TCGTCAAACA GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCACGCTT GCCAAATGCT GCAAACCCGC
1101 GCCGCCGAC GATATTATCG GCTTCGTTAC CCGCGAGCGC GgCATTTCAG
1151 TGCACCGCAA AwwwTkCyCG TCTTTCCAAC ACCTCGCCGA ACACGCGCCC
1201 GAwAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCCGTCGAT ATCGAAATCC GCGCCCAAGA CCGCTCCGGG CTTTGTGCGC
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAAC TCAACGTTAC CGCCGTGCAA
1351 ACCCAGTCCC GCGACTTGGa AGCCAGCATG AGGTTACAGC TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCGCG GCGTCCTCGC CAGCCTCGGC GACGTCAAAG
1451 GCGTATTGAG CGTTACCCG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

m117.pep (partial)

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 117 shows 97.6% identity over a 490 aa overlap with a predicted ORF (ORF 117.ng) from *N. gonorrhoeae*:

m117/q117

m117.pep
VKLKKYNVHFVEVAGRPKHIYSIYKKMVKKKL
:
g117
EKYREIALLLDEKRTERLEYIENFLDILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKKL

10 20 30
150 160 170 180 190 200

40 50 60 70 80 90
 m117.pep SFDGLFDIRAVRILVDTVPCEYTTGLGVHSLWQPIPGGEFDDYIANPKGNGYKSLHTVIVG
 |||||
 g117 SFDGLFDIRAVRILVDTVPCEYTTGLGVHSLWQPIPGGEFDDYIANPKGNGYKSLHTVIVG
 210 220 230 240 250 260

100 110 120 130 140 150
 m117.pep PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESG
 |||||
 g117 PEDKGVEVQIRTFDMHQFNEFGVAAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESG
 270 280 290 300 310 320

160 170 180 190 200 210
 m117.pep KEDLAAAFKTELFNDTIYVLTPHGKVLSPPTGATPIDFAYALHSSIGDRCRGAKVEGQIV
 |||||
 g117 KEDLAAAFKTELFNDTIYVLTPHGKVLSPPTGATPIDFAYALHSSIGDRCRGAKVEGQIV
 330 340 350 360 370 380

220 230 240 250 260 270
 m117.pep PLSTPLENGQRVEIIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQ
 |||||
 g117 PLSTPLENGQRVEIIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQ
 390 400 410 420 430 440

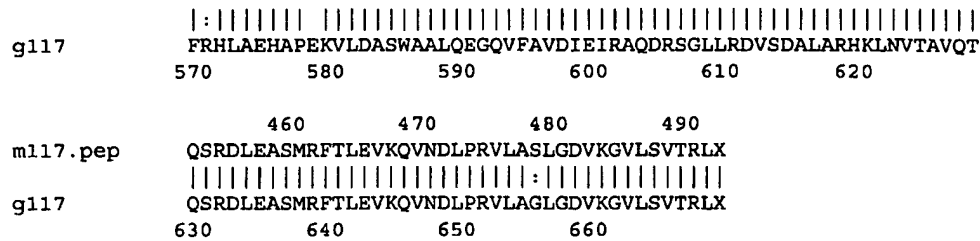
280 290 300 310 320 330
m117.pep LDKQLAKLTPKPNLQELAENLGYYKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPPVPVSE
g117 LDKQLAKLTPKPNLQELAENLGYYKKPEDLYTAVGQGEISNRAIQKACGTLNEPPPPVPVSA
450 460 470 480 490 500

```

          340      350      360      370      380      390
m117.pep  TTIVKQSKIKKGGKNGVLIDGEDGLMTTLAKCKKPAPDDIIGFVTRERGISVHRKXXXS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g117      TTIVKQSKIKKGGKTGVLIDGEDGLMTTLAKCKKPAPDDIAGFVTRERGISVHRKTCPS
          510      520      530      540      550      560

```

400 410 420 430 440 450
m117.pep FOHLAEHAPXKVLDSWAALQEGQVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAVOT



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 415>:

a117.seq

```

1  ATGGTTCATG  AACTCGACCT  GCTCCCGCAT  GCCGTCGCCG  CCACCCTGCT
51  TGCCGACATC  GGACGCTACG  TCCCGACTG  GAACCTATTG  GTTCCGAAC
101 GCTGCAACAG  TACCGTCGCC  GAGCTGGTCA  AAGGTGTGGA  CGAAGTGCAG
151 AAACCTACCC  ACTTCGCCCC  GGTGGACAGC  CTCGCCACGC  CGGAAGAACG
201 CGCCCAGCAG  GCAGAACTA  TCGGAAAT  GCTGCTGGCG  ATGGTTACCG
251 ACATCCGCGT  CGTGTTAATC  AAACCTGGCG  TCGGTACGCG  CACCCTGCAA
301 TTTTAAAGCA  ACGCCCCCGA  CAGCCCCGAA  AAACGCGCCG  TCGCCAAAGA
351 AACCCTCGAC  ATCTTCGCCC  CGCTCGCCAA  CCGTTTGGGC  GTGTGGCAGC
401 TCAAAATGGCA  GTCGAAGAT  TTGGGCTTCC  GCCATCAAGA  ACCCGAAAAA
451 TACCGCGAAA  TCGCCCTGCT  TTTGGACGAA  AAACGCACCG  AACGCCTCGA
501 ATACATCGAA  AACTTCCTTA  ATATCCTGCG  TACGGAATC  AAAAAATACA
551 ATATCCACTT  TGAAGTCGCG  GGCCGTCCGA  AACACATCTA  CTCCATTTAC
601 AAAAAAATGG  TGAAGAAAAA  ACTCAGCTTC  GACGGGTGT  TCGACATCCG
651 CGCCGTGCGG  ATTCTGGTTG  ATACCGTCCC  CGAGTGTAC  ACCACACTGG
701 GCATTGTCCA  CAGCCTCTGG  CAGCCCATTC  CCGGCGAGTT  CGACGACTAC
751 ATCGCCAACC  CGAAAGGCAA  CGGCTATAAA  AGTTTGACA  CCGTCATCGT
801 CGGCCCGGAA  GACAAAGGCG  TGGAAGTGCA  AATCCGCACC  TTCGATATGC
851 ACCAATTCAA  CGAATTCGGT  GTCGCCGCGC  ACTGGCGTTA  CAAAGAGGGC
901 GGCAAAGGCG  ATTCCGCCTA  CGAACAAAA  ATCGCCTGGT  TACGCCAACT
951 TTTGGACTGG  CGCGAAAACA  TGGCGGAAAG  CGGCAAGGAA  GACCTCGCCG
1001 CCGCCTTCAA  AACCGAGCTT  TTCAACGACA  CGATTTATGT  TTTGACCCCG
1051 CACGGCAAAG  TCCTCTCCT  GCCACAGGC  GCGACCCCA  TCGACTTCGC
1101 CTACGCCCTG  CACAGCAGCA  TCGGCGACCG  TTGCCGCGGT  GCGAAAGTCG
1151 AAGGGCAGAT  TGTGCCGCTG  TCCACCCCGC  TCGAAAACGG  ACAGCGTGTG
1201 GAAATCATT  CCGCCAAAGA  AGGGCATCCT  TCCGTCAACT  GGCTTTACGA
1251 AGGCTGGGTC  AAATCCAACA  AGGCAATCGG  CAAAATCCGC  GCCTACATCC
1301 GCCAGCAAAA  CGCCGACACC  GTGCGCGAAG  AAGGCCGCGT  CCAACTCGAC
1351 AAACAGCTTG  CCAAACCTAC  GCCCAACCC  AACCTGCAAG  AGCTTGCCGA
1401 AAATCTCGGC  TACAAAAGC  CAGAAGACCT  CTACACCGCC  GTCGGACAAG
1451 GCGAAATTC  CAACCGCGCC  ATCCAAAAG  CCTGCGGCAC  GCTGAACGAA
1501 CCGCCGCCCG  TACCGTCAG  CGAAACCACC  ATCGTCAAAC  AGTCCAAAT
1551 CAAAAAGGC  GGCAAAAACG  GCGTGCTCAT  CGACGGCGAA  GACGGTCTGA
1601 TGACCACGCT  TGCCAAATGC  TGCAAAACCG  CGCCGCCCGA  CGACATTGTC
1651 GGCTTCGTTA  CCCGCGATCG  CGGCATTCG  GTACACCGCA  AAACCTGCCC
1701 CTCTTTCCGA  CACCTCGCCG  AACACGCGCC  CGAAAAAGTA  CTGGACGCAA
1751 GTTGGGCGGC  GTTGCAAGAA  GGACAAGTGT  TCGCCGTCGA  TATCGAAATC
1801 CGCGCCCAAG  ACCGCTCCGG  GCTTTTGCGC  GACGTATCCG  ACGCGCTCGC
1851 CCGCCACAAA  CTCAACGTTA  CCGCCGTGCA  AACCAGTCC  CGCGACTTGG
1901 AAGCCAGCAT  GAGGTTCACG  CTCGAAGTCA  AACAAGTTAC  CGACCTCCCA
1951 CGCGTCCTCG  CCAGCCTCGG  CGACGTCAA  GCGTATTGA  GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 416; ORF 117.a>:

a117.pep

```

1  MVHELDLLPD  AVAATLLADI  GRYVPDWNLL  VSERCNSTVA  ELVKGVDEVQ
51  KLTHFARVDS  LATPEERAQQ  AETMRKMLLA  MVTDIRVLI  KLAMRTRTLQ
101 FLSNAPDSPE  KRAVAKETLD  IFAPLANRLG  VWQLKWQLED  LGFRHQPEPK
151 YREIALLLDE  KRTERLEYIE  NFLNILRTEL  KKYNIHFEVA  GRPKHIYSIY
201 KKMVKKKLSF  DGLFDIRAVR  ILVDTVPECY  TTLGIVHSLW  QPIPGFDDY
251 IANPKNGYK  SLHTVIVGPE  DKGVEVQIRT  FDMHQFNEFG  VAAHWRYKEG
301 GKGDSEYEQK  IAWLRQLLDW  RENMAESGKE  DLAAAFKTEL  FNDTIYVLTP
351 HGKVLSLPTG  ATPIDFAYAL  HSSIGDRCRG  AKVEGQIVPL  STPLENGQRV

```

					10		20		30
m117.pep					VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL				
					:	:	:	:	:
a117	EKYREIALLLDEKRT	ERLEYIENFLN	ILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKKL						
	150	160	170	180	190	200			
		40	50	60	70	80	90		
m117.pep	SFDGLFD	IRAVRILVDTV	PECYTTLGIVHSLWQPI	PGEFDDYIANPKGNGYKSLHTV	IVG				
	:	:	:	:	:	:	:	:	:
a117	SFDGLFD	IRAVRILVDTV	PECYTTLGIVHSLWQPI	PGEFDDYIANPKGNGYKSLHTV	IVG				
	210	220	230	240	250	260			
		100	110	120	130	140	150		
m117.pep	PEDKGVE	QIRTFDMHQF	NFEFGVAAHWRYKEGGK	GD	SAYEQKIAWLRQLLDWRENMAESG				
	:	:	:	:	:	:	:	:	:
a117	PEDKGVE	QIRTFDMHQF	NFEFGVAAHWRYKEGGK	GD	SAYEQKIAWLRQLLDWRENMAESG				
	270	280	290	300	310	320			
		160	170	180	190	200	210		
m117.pep	KEDLAAAFKTELF	NDTIYVLT	PHGKVL	SLPTGATPIDFAYALHSSIGDR	CRGAKVEG	QIV			
	:	:	:	:	:	:	:	:	:
a117	KEDLAAAFKTELF	NDTIYVLT	PHGKVL	SLPTGATPIDFAYALHSSIGDR	CRGAKVEG	QIV			
	330	340	350	360	370	380			
		220	230	240	250	260	270		
m117.pep	PLSTPLENGQ	RVEIITAKEGH	PSVNWLYEGWVKS	NAIGKIRAYIRQ	QNADTVREEG	RVQ			
	:	:	:	:	:	:	:	:	:
a117	PLSTPLENGQ	RVEIITAKEGH	PSVNWLYEGWVKS	NAIGKIRAYIRQ	QNADTVREEG	RVQ			
	390	400	410	420	430	440			
		280	290	300	310	320	330		
m117.pep	LDKQLAKLT	PKPNLQELAE	NLGykkPEDLYTAVGQGEIS	NR	AIQKACGTLNEPPVPVSE				
	:	:	:	:	:	:	:	:	:
a117	LDKQLAKLT	PKPNLQELAE	NLGykkPEDLYTAVGQGEIS	NR	AIQKACGTLNEPPVPVSE				
	450	460	470	480	490	500			
		340	350	360	370	380	390		
m117.pep	TTIVKQSKIKKGGK	NGVLIDGEDGLMTT	LAKCKPAPDDI	IGFVTRERGISVHRKXXS					
	:	:	:	:	:	:	:	:	:
a117	TTIVKQSKIKKGGK	NGVLIDGEDGLMTT	LAKCKPAPDDI	IGFVTRERGISVHRKXXS					
	510	520	530	540	550	560			
		400	410	420	430	440	450		
m117.pep	FQHLAEHAPXK	VLDASWAALQEGQVFAVDIEIRAQDRSGLLRD	VSDALARHKL	NVTAVQT					
	:	:	:	:	:	:	:	:	:
a117	FRHLAEHAPXK	VLDASWAALQEGQVFAVDIEIRAQDRSGLLRD	VSDALARHKL	NVTAVQT					
	570	580	590	600	610	620			
		460	470	480	490				
m117.pep	QSRDLEASMR	FTLEV	KQVNDLPRVLASLGDVKG	VLSVTRLX					
	:	:	:	:	:	:	:	:	:
a117	QSRDLEASMR	FTLEV	KQVNDLPRVLASLGDVKG	VLSVTRLX					
	630	640	650	660					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1   ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTCGTGG CGCAGGAACA TTATCCTGCC
151 GATGCCGCCA GCCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GCGCAAAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCCCGGCCA
251 CCCTGCTTGC CGACATCGGA CGTACGTCC CCGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACGCGC ACAGCAAGCG GAAACCATGC GAAAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT ATTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCTGAAAAA CGCGCCGTCG
551 CCAAGAGAAC CCTCGACATC TTCGCCCCGC TCGCCAACCG CTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAGAAC
651 CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAC TTCCTCGATA TCCTGCGTAC GGAACCAAAA
751 AAATACAATA TCCACTTGA AGTCGCCGGC CGTCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGCCTGTTTC
851 ACATCCGCGC CGTGGCGATT CTGGTCGATA CCGTCCCGCA GTGTTACACC
901 ACCTGCGGCA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGagttCGA
951 cgactACATC GCCAACCCCA AAGgcaACGg ttATAAAAGt TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtgg aagtgcAAAT CCGCACCTTC
1051 GATATGcacc AATTCAaCga ATTCGGTGTC GCCGCCCACT GCGTTACAA
1101 AGAAGCGCGC AAAGCGGATT CCGCCTACGA AAAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGACTGGCGC GAAATATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAGAAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCGGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGTGTCCA
1551 ACTCGACAAG CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAAGCG AATTTTCCAA CCGCGCCATC CAAAAAGCCT CGCGCACGCT
1701 GAACGAACCG CCGCCCGTGC CCGTCAGCGC AACCACCATC GTCAAAACAGT
1751 CCAAAATCAA AAAAGGTGGC AAAACCGGCG TGCTCATCGA CGGCGAAGAC
1801 GGCCTTGATG CCACGCTTGC CAAATGCTGC AAACCCGCGC GCCTCCGACG
1851 TATTGCCGGC TTCGTTACCC GCGAGCGCGG CATTTCCGTC CACCGCAAAA
1901 CCTGCCCTCT TTTCCGACAC CTTGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 KAGCGCAAGT GGGCGGCGTT GCAGGAAGGG CAAAGTGTTC CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAAC CCAGTCCCGC
2101 GACTTGGGAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCCGCGC GTCCTCGCGC GCCTCGGCGA TGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

```

1   MTAISPIQDT QSATLQELRE WFD SYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNHFEVAG RPKHIYSIYK KMKVKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKGNGYKS LHTVIVGPPE KGEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAFAFKTELF NDTIYVLTPL GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQORVE IITAKEGHPS VNWLYEGWVK SGKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSATTI VKQSKIKKGG KTGVLIDGED
601 GLMTTLAKCC KPAPPDIDAG FVTRERGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLAGLDGVKG VLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

m117-1.seq

```

1   ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

```

```

51  ATTGCGCGAA  TGGTTCGACA  GCTACTGCGC  CGCTCTGCCG  GACAACGATA
101 AAAACCTCAT  CGGTACCGCA  TGGTTGCTGG  CGCAGGAACA  TTACCCCGCC
151 GATGCCGCGA  CGCCGTATGG  CGAGCCGCTG  CCCGACCACT  TCCTCGGCGC
201 GGCAGCAATG  GTTCATGAAC  TCGACCTGCT  CCCCAGTGCC  GTCGCCGCCA
251 CCCTGCTTGC  CGACATCGGA  CGCTACGTCC  CCGACTGGAA  CCTATTGGTT
301 TCCGAACGCT  GCAACAGTAC  CGTCGCCGAG  CTGGTCAAAG  GTGTGGACGA
351 AGTGCAGAAA  CTCACCCACT  TCGCCCGGGT  GGACAGCCTC  GCCACGCCGG
401 AAGAACCGCG  CCAGCAGGCA  GAAACTATGC  GGAATAATGCT  GCTGGCGATG
451 GTTACCGACA  TCCGCGTCGT  GTTAATCAAA  CTGGCGATGC  GTACGCGCAC
501 CCTGCAATTT  TTAAGCAACG  CCCCAGACAG  CCCCAGAAAA  CGCGCCGTCG
551 CCAAGAAAC  CCTCGACATC  TTCGCCCGCG  TCGCCAACCG  TTTGGCGGTG
601 TGGCAGCTCA  AATGGCAGCT  CGAAGATTG  GGCTTCCGCC  ATCAAAAGCC
651 CGAAAAATAC  CGCGAAATCG  CGCTGCTTTT  GGACGAAAAA  CGCACCGAAC
701 GCCTCGAATA  CATCGAAAC  TTCCTCAACA  TCCTGCGCGG  TGAATCAAG
751 AAATACAATG  TCCATTTCGA  AGTCGCCGGC  CGCCGAAAC  ACATCTACTC
801 CATTACAAA  AAATGGTGA  AGAAAAACT  CAGCTTCGAC  GGCCTCTTTG
851 ACATCCGCGC  CGTGCGAATT  CTGGTTGATA  CCGTCCCCGA  GTGTTACACC
901 ACCTGGGTA  TCGTCCACAG  CCTCTGGCAG  CCCATTCCCG  GCGAGTTCGA
951 CGACTACATC  GCCAATCCCA  AAGGCAACGG  CTATAAAAGT  TTGCACACCG
1001 TCATCGTCGG  CCCGGAAGAC  AAAGGCGTGG  AAGTACAAAT  CCGCACCTTC
1051 GATATGCACC  AATTCAACGA  ATTCGGTGTC  GCCGCCCACT  GGCATTACAA
1101 AGAGGGCGCG  AAGGGCGATT  CCGCCTACGA  ACAGAAAAAT  GCCTGGTTGC
1151 GCCAACTCTT  GGACTGGCGC  GAAAACATGG  CGGAAAGCGG  CAAGGAAGAC
1201 CTGCGCCCGC  CCTTCAAAAC  CGAGCTTTTC  AACGACACGA  TTTATGTTTT
1251 GACCCCGCAC  GGCAAAGTCC  TCTCCCTGCC  CACGGGCGCG  ACCCCCATCG
1301 ACTTCGCCTA  CGCCCTGCAC  AGCAGCATCG  GCGACCGTTG  CCGCGGTGCG
1351 AAAGTCGAAG  GGCAGATTGT  GCCGCTGTCC  ACCCGCTCG  AAAACGGACA
1401 GCGCGTCGAA  ATCATTACCG  CCAAGAAGG  GCATCCTTCC  GTCAACTGGC
1451 TTTACGAAGG  CTGGGTCAA  TCCAACRAG  CAATCGGCAA  AATCCGCGCC
1501 TACATCCGCC  AGCAAAACGC  CGACACCGTG  CGCGAAGAAG  GCCGCGTCCA
1551 ACTCGACAAA  CAGCTTGCCA  AACTCACGCC  CAAACCCAAC  CTGCAAGAGC
1601 TTGCCGAAAA  TCTCGGCTAC  AAAAAGCCAG  AAGACCTCTA  CACCGCGCGT
1651 GGACAAGGCG  AAATTTCCAA  CCGCGCCATC  CAAAAAGCCT  GCGGCACGCT
1701 GAACGAACCG  CCGCCCGTAC  CCGTCAGCGA  AACCACCATC  GTCAAACAGT
1751 CCAAAATCAA  AAAAGGCGGC  AAAACCGCG  TGCTCATCGA  CGGCGAAGAC
1801 GGTCTGATGA  CCACGCTTGC  CAAATGCTGC  AAACCCGCGC  CGCCCGACGA
1851 TATTATCGGC  TTCGTTACCC  GCGAGCGCGG  CATTTCACTG  CACCGCAAAA
1901 CCTGCCCGTC  TTTCCAACAC  CTCGCCGAAC  ACGCGCCCGA  AAAAGTGCTG
1951 GACGCAAGCT  GGGCGGCATT  GCAGGAAGGA  CAAGTATTCG  CCGTCGATAT
2001 CGAAATCCGC  GCCCAAGACC  GCTCCGGGCT  TTTGCGCGAC  GTATCCGACG
2051 CGCTCGCCCG  CCACAAATC  AACGTTACCG  CCGTGCAAAC  CCAGTCCCGC
2101 GACTTGGAAG  CCAGCATGAG  GTTCACGCTC  GAAGTCAAAC  AAGTCAACGA
2151 CCTCCCGCGC  GTCCTCGCCA  GCCTCGGCGA  CGTCAAAGGC  GTATTGACCG
2201 TTACCCGGCT  TTAA

```

This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

m117-1.pep

```

1  MTAISPIQDT  QSATLQELRE  WFDSYCAALP  DNDKNLIGTA  WLLAQEHYPA
51  DAATPYGEPL  PDHFLGAAQM  VHELDLLPDA  VAATLLADIG  RYVPDWNLLV
101 SERCNSTVAE  LVKGVDEVQK  LTHFARVDSL  ATPEERAQQA  ETMRKMLLAM
151 VTDIRVVLIK  LAMRTRTLQF  LSNAPDSPEK  RAVAKETLDI  FAPLANRLGV
201 WQLKWQLEDL  GFRHQKPEKY  REIALLLDEK  RTERLEYIEN  FLNILRGELK
251 KYNVHFEVAG  RPKHIYSIYK  KMKKKLSFD  GLFDIRAVRI  LVDTVPECYT
301 TLGIVHSLWQ  PIPGEFDDYI  ANPKGNGYKS  LHTVIVGPED  KGVEVQIRTF
351 DMHQFNEFGV  AAHWRYKEGG  KGDSAYEQKI  AWLRQLLDWR  ENMAESGKED
401 LAAAFKTELF  NDTIYVLTPH  GKVLSLPTGA  TPIDFAYALH  SSIGDRCRGA
451 KVEGQIVPLS  TPLENGQRVE  IITAKEGHPS  VNWLYEGWVK  SNKAIGKIRA
501 YIRQONADTV  REEGRVQLDK  QLAKLTPKPN  LQELAENLGY  KKPEDLYTAV
551 GQGEISNRAI  QKACGTLNEP  PPVPVSETTI  VKQSKIKKGG  KNGVLIDGED
601 GLMTTTLAKCC  KPAPPDDIIG  FVTRERGISV  HRKTCPSFOH  LAEHAPEKVL
651 DASWAALQEG  QVFAVDIEIR  AQDRSGLLRD  VSDALARHKL  NVTAVQTQSR
701 DLEASMRFTL  EVKQVNDLPR  VLASLGDVKG  VLSVTRL*

```

m117-1/g117-1 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFDSDYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFDSDYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120

m117-1.pep	PDHFLGAAQMVHEDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
g117-1	PDHFLGAAQMVDELDPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK
	70 80 90 100 110 120
m117-1.pep	130 140 150 160 170 180
g117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK
	130 140 150 160 170 180
m117-1.pep	190 200 210 220 230 240
g117-1	RAVAKETLDIFAPLANRLGVWLKQWLEDLGFRHQKPEKYREIALLLDEKRTTERLEYIEN
	RAVAKETLDIFAPLANRLGVWLKQWLEDLGFRHQEPEKYREIALLLDEKRTTERLEYIEN
	190 200 210 220 230 240
m117-1.pep	250 260 270 280 290 300
g117-1	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
	FLDILRTELKKYNHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT
	250 260 270 280 290 300
m117-1.pep	310 320 330 340 350 360
g117-1	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV
	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEEKGVEVQIRTFDMHQFNEFGV
	310 320 330 340 350 360
m117-1.pep	370 380 390 400 410 420
g117-1	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH
	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPH
	370 380 390 400 410 420
m117-1.pep	430 440 450 460 470 480
g117-1	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS
	430 440 450 460 470 480
m117-1.pep	490 500 510 520 530 540
g117-1	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY
	490 500 510 520 530 540
m117-1.pep	550 560 570 580 590 600
g117-1	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED
	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSATTIVKQSKIKKGGKTGVLIDGED
	550 560 570 580 590 600
m117-1.pep	610 620 630 640 650 660
g117-1	GLMTTLAKCKKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAWALQEG
	GLMTTLAKCKKPAPPDDIAGFVTRERGISVHRKTCPSFRLAEHAPEKVLDAWALQEG
	610 620 630 640 650 660
m117-1.pep	670 680 690 700 710 720
g117-1	QVFAVDIEIRAQDRSGLLRDVSALARHKLNVAVQTQSRDLEASMRFTLEVQVNDLPR
	QVFAVDIEIRAQDRSGLLRDVSALARHKLNVAVQTQSRDLEASMRFTLEVQVNDLPR
	670 680 690 700 710 720
m117-1.pep	730
g117-1	VLASLGDKVKGVLVSVTRLX
	VLASLGDKVKGVLVSVTRLX
	730

m117-1/RelA

sp|P55133|RELA_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744
Score = 536 bits (1366), Expect = e-151
Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATLLADI---GRYVPDWNLLVSERCNSTVAELVKGVDEVQKLTHFARVDSL 130
L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S
Sbjct: 68 LSMADATLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQVEQMCAIS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEKRAVAKETLDI 190
A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I
Sbjct: 122 AEETAQAAQVDNIRMLLSMVDDFRVCVVIKLAERICNLREVKDQPDDEV-RRAAAQECANI 180

Query: 191 FAPLANRLGVWQLKWQLEDLGRHQKPEKYREIALLLDEKRTERLEYIENFLNIRGELK 250
+APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K
Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDQTYKQIAQLSERRIDREDYITHFVDDLSDAMK 240

Query: 251 KYNVHFVAGRPKHIYSIYKKMVKKLSFDGLDIRAVRILVDTVPECYTTLGIVHSLWQ 310
N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++
Sbjct: 241 ASNIRAEVQGRPKHIYSIWRKMQKKSLEFDELFDVRAVRIVAEELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTDFMHQFNEFGVAHWRKYKEG- 369
+P EDDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAHWR+YKEG
Sbjct: 301 HLPKEFDDYVANPKPNGYQSIHTVVLGPEGKTIEIQIRTKMHHESELGVAHWRKYKEGT 360

Query: 370 --GKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTPHGKVLSP 427
G SAY++KI WLR+LL W+E M++SG ++ +++++F+D +Y TP G V+ LP
Sbjct: 361 ASGGAQSAYDEKINWLRKLLAQEEMSDSG--EMLDELRSQVFDREVYAF+PKGVDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRRCRGAKVEGQIVPLSTPLENGQVEIITAKEGHPSVNWLYE- 486
+ ATP+DFAY +HS +G RC GAKVEG+IVP + L+ G +VEIIT KE +PS +WL
Sbjct: 419 SNATPLDFAYHIHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAIGKIRAYIRQONADTVREEGRVOLDKQLAKL--TPKPNLQELAENLGKYP 543
G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P
Sbjct: 479 LGFVTSSRAKAVHAWFRKQDRDNIIAGKEILEAELVKIHATLKDAQYAAKRFNVKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQKACGTLENEPPVPVSETTIVKQSKI-----KKGKNGV 594
E+LY +G G++ N+ I +N+P + + K S+ KK ++ V
Sbjct: 539 EELYAGIGSGDLRINQVINHINALVNKPTAEEDQQLLEKLSEASNKQATSHKKPQRDAV 598

Query: 595 LIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDSW 654
+++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W
Sbjct: 599 VVEGVNDLMTHLARCCQPIPGDDIQGFVTQGRGISVHRMDCEQLEELRHHAPERIIDTVW 658

Query: 655 AALQEGQVFVAVDIEIRAQDRSGLLRDVSALARHKLNVTAQTQ--SRDLEASMRFTLEV 712
G + + + + A +R+GLL++++ L K+ V +++++ + + M F LE+
Sbjct: 659 GGGFVGN-YTITVRVTASERNGLLKLNTLMNEKVKVAGMKSRVDYKQMSIMDFEEL 717

Query: 713 KQVNDLPRVLASLGDVKGVLSVTRL 737

+ L RVL + VK V RL
Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

a117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACACGATA
101  AAAAAGTTGT CTTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151  GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201  GGCACAAATG GTTCATGAAC TCGACCTGCT CCCGATGCC GTCGCGGCCA
251  CCCTGCTTGC CGACATCGGA CGTACGTCC CCGACTGGAA CCTATTGGTT
301  TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351  AGTGCAGAAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401  AAGAACGCGC CCAGCAGGCA GAAACTATGC GGAAATGCT GCTGGCGATG
451  GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501  CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCCAGAAAA CGCGCCGTCG
551  CCAAGAAAC CCTCGACATC TTCGCCCCGC TCGCAACCG TTTGGCGGTG
601  TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTCCGCC ATCAGAACCC
651  CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701  GCCTCGAATA CATCGAAAC TTCCTTAATA TCCTGCGTAC GGAACCAAA
751  AAATACAATA TCCACTTTGA AGTCGCCGCG CGTCCGAAAC ACATCTACTC
801  CATTACAAA AAAATGGTGA AGAAAAAAGT CAGCTTCGAC GGGTTGTTCG

```

```

851 ACATCCGCGC CGTGCGGATT CTGGTTGATA CCGTCCCCGA GTGTTACACC
901 ACACTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAACCCGA AAGGCAACGG CTATAAAGT TTGCACACCG
1001 TCATCGTCGG CCGGAAGAC AAAGGCGTGG AAGTGCAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTGCGGTGC GCCGCGCACT GCGGTTACAA
1101 AGAGGGCGGC AAAGGCGATT CCGCCTACGA AAAAAAATC GCCTGGTTAC
1151 GCCAACTTTT GGACTGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTGCGCGCGC CCTTCAAAAC CGAGCTTTT AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCCCTGCC CACAGGCGCG ACCCCCATCG
1301 ACTTCGCTTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGCTCG AAAACGGACA
1401 CGGTGTCGAA ATCATTACCG CCAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAGCCAG AAGACCTCTA CACCGCGTCT
1651 GGACAAGCGG AATTTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAACAGT
1751 CCAAAATCAA AAAAGGCGGC AAAACGGCG TGCTCATCGA CGGCGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCGACGA
1851 CATGTGCGGC TTCGTTACCC GCGATCGCGG CATTCGCTA CACGCGAAAA
1901 CCTGCCCTCT TTTCCGACAC CTCGCGGAAC ACGCGCCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGA CAAGTGTTCT CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GTCGCGGCT TTTGCGGAC GTATCCGACG
2051 CGCTCGCCCG CCACAACTC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGGAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTTACCGA
2151 CCTCCACGCG GTCCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTAGCG
2201 TTACCCGGCT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

a117-1.pep

```

1 MTAISPIQDT QSATLQELRE WFDSYCTALP NNDKKLVLA RSLAEAHYPA
51 DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLNLRTELK
251 KYNIHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPRGNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLDWR ENMAESKED
401 LAAAFTELEF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQORVE IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIRQQNADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDVKG VLSVTRL*

```

a117-1/m117-1 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFDSYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
a117-1	MTAISPIQDTQSATLQELREWFDSYCTALPNNDKKLVLAARSLAEAHYPADAATPYGEPL					
	10	20	30	40	50	60
m117-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
a117-1	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
	70	80	90	100	110	120
m117-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
a117-1	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDEVQK					
	130	140	150	160	170	180
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK					
a117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK					
	190	200	210	220	230	240
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFHQKPEKYREIALLLDEKRTERLEYIEN					
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFHQEPEKYREIALLLDEKRTERLEYIEN					
	190	200	210	220	230	240

m117-1.pep	250	260	270	280	290	300
	FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVP	ECYT				
a117-1	250	260	270	280	290	300
	FLNILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVP	ECYT				
m117-1.pep	310	320	330	340	350	360
	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
a117-1	310	320	330	340	350	360
	TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV					
m117-1.pep	370	380	390	400	410	420
	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLT	PH				
a117-1	370	380	390	400	410	420
	AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLT	PH				
m117-1.pep	430	440	450	460	470	480
	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
a117-1	430	440	450	460	470	480
	GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS					
m117-1.pep	490	500	510	520	530	540
	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
a117-1	490	500	510	520	530	540
	VNWLYEGWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKLTPKPNLQELAENLGY					
m117-1.pep	550	560	570	580	590	600
	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKI KGGKNGVLIDGED					
a117-1	550	560	570	580	590	600
	KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKI KGGKNGVLIDGED					
m117-1.pep	610	620	630	640	650	660
	GLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDA	SWAALQEG				
a117-1	610	620	630	640	650	660
	GLMTTLAKCKPAPPDDIIGFVTRDRGISVHRKTCPSFRHLAEHAPEKVLDA	SWAALQEG				
m117-1.pep	670	680	690	700	710	720
	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVAVQTQSRDLEASMRFTLEV	KQVNDLPR				
a117-1	670	680	690	700	710	720
	QVFAVDIEIRAQDRSGLLRDVSDALARHKLNVAVQTQSRDLEASMRFTLEV	KQVNDLPR				
m117-1.pep	730					
	VLASLGDVKGVLVSVTRLX					
a117-1	730					
	VLASLGDVKGVLVSVTRLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 423>:

```

g118.seq
1  ATGTGCGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGCTG GAGAATGATT TAATcgaGGT TAGGAGAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTT GAAATTAAG
251 CTTCCCCTTG GTTGCTGAT AGCGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAaCA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 424; ORF 118.ng>:

```

g118.pep
1  MCFEKDFRRN IPCFEEYDEN SFIGKWYDDG VWDDEEYWKL ENDLIEVRRK
51  YPYPM DIPRD IVIGIGTIID FLMVPNWELF EIKASPWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRFD YYNKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```
m118.seq
1  ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGTTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTCATTG GAATCGGTAC
201 CATTATTGAT TTCTTAATGG TTCCAAATTG GAAACTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```
m118.pep
1  MCEFkdIIRN VPYFEGYDEN SFIGKwyDDG VWDDEEYWL ENdLIEVRKK
51  YPYPMdIPRY VVIGIGTIID FLMVPNWKL EIKASpWLPD SVGIHERYER
101 FTTMLRYIFT EKdIVNVRFd YYNKK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```
m118/g118

          10      20      30      40      50      60
m118.pep  MCEFkdIIRNVpYFEGYDENsFIGKwyDDGvWDDEEYWLkENdLIEVRKKYPYPMdIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:
g118       MCEFkdFRRNIPCFEeYDENsFIGKwyDDGvWDDEEYWLkENdLIEVRKKYPYPMdIPRD
          10      20      30      40      50      60

          70      80      90      100     110     120
m118.pep  VVIGIGTIIDfLMVPNWKLfEIKASpWLPdSVGIHERYERfTTMLRYIfTEKdIVNVRFd
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g118       IVIGIGTIIDfLMVPNWELfEIKASpWLPdSVGIHERYERfTTMLRYIfTEKdIVNVRFd
          70      80      90      100     110     120

m118.pep  YYNKKX
          |||||
g118       YYNKKX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```
a118.seq
1  ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAATGAG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```
a118.pep
1  MCEFkdFRRN IPCFEeYDEN SFIGKwyDDG VWDDEEYWL ENdLIEVRKK
51  YPYPMdIPRD IVIGIGTIID FLMVPNWELf EIKASpWLPD SVGIHERYER
101 FTTMLRYIFT EKdIVNVRFd YYNKK*
```

m118/a118 93.6% identity in 125 aa overlap

```
m118.pep  MCEFkdIIRNVpYFEGYDENsFIGKwyDDGvWDDEEYWLkENdLIEVRKKYPYPMdIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:
a118       MCEFkdFRRNIPCFEeYDENsFIGKwyDDGvWDDEEYWLkENdLIEVRKKYPYPMdIPRD
          10      20      30      40      50      60
```

	70	80	90	100	110	120
m118.pep	VVIGIGTIIDFLMVPNWKLF EIKAS PWLPDSVGIHERYERFTT MLRYIFTEKDIVNVRFD					
a118	IVIGIGTIIDFLMVPNWELFEIKAS PWLPDSVGIHERYERFTT MLRYIFTEKDIVNVRFD					
	70	80	90	100	110	120
m118.pep	YYNKXX					
a118	YYNKXX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

```

g120.seq
1  ATGATGAAGA CTTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAAGGCTACC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGTA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAATCC GGCGGTACGG TTGTCGGCAA TACCCTGCAC CCTGCCTACT
251 ATAAAGACAT ACGCAGGGGC AAACGTGTAT CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTCA CGCTTGCCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGTCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGCC TGAATAAGGC GGGTACGGGA AAATACAGCA Taggcggcgt
501 gGAAACCGAA GTCGTCAAAT ATCGGGTGCG GC CGCGCGAC GATACGGTAA
551 CGTATTCTTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGAcgaCG GCAAAACCTA TACGCTGAAG CTCAAATCGG TGCAGATCAA
651 CGGACAGGCC GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

```

g120.pep
1  MMKTFKNIFS AAILSAAALPC AYAARLPQSA VLHYSGSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PAYYKDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DTVTYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

```

m120.seq
1  ATGATGAAGA CTTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGTA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GGCGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAACGTGTAT CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CTTACGGCAA AGCGGGCGAG AGCAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTCA CGCTTGCCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GC CGCGCGAC GATGCGGTAA
551 TGTATTCTTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG

```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

```

m120.pep
1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLXYSGSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120.pep	MMKTFKNIFS	AAILSAAALPCAYAAGLPQSAVLX	YSGSYGIPATMTFERSGNAYKIVSTIK			
g120	MMKTFKNIFS	AAILSAAALPCAYAARLPQSAVLHYSGSYGIPATMTFERSGNAYKIVSTIK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m120.pep	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTY	GKAGESKTEQSPKAM				
g120	VPLYNIRFESGGTVVGNTLHPAYYKDIRRGKLYAEAKFADGSVTY	GKAGESKTEQSPKAM				
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE	VVKYRVRRGD				
g120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETE	VVKYRVRRGD				
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA	AKP				
g120	DTVTYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQA	AKPX				
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120.seq

```

1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATTT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AACTGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTTGTTCG CGTTGCCTG GCAGTTGGCG GCAAATGACG
401 CGAAATCCC CCCGGGGCTG AAAATCACCA ACGGCAGAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGTACAGGA AAATACAGCA TAGCGGCGGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120.pep

```

1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLHYSGSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNTLH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120.pep	MMKTFKNIFS	AAILSAAALPCAYAAGLPQSAVLX	YSGSYGIPATMTFERSGNAYKIVSTIK			
a120	MMKTFKNIFS	AAILSAAALPCAYAAGLPQSAVLHYSGSYGIPATMTFERSGNAYKIVSTIK				

343

	10	20	30	40	50	60
m120.pep	70	80	90	100	110	120
	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYGKAGESKTEQSPKAM					
a120	70	80	90	100	110	120
	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYGKAGESKTEQSPKAM					
m120.pep	130	140	150	160	170	180
	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVKYRVRRGD					
a120	130	140	150	160	170	180
	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEYVKYRVRRGD					
m120.pep	190	200	210	220		
	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					
a120	190	200	210	220		
	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51  GCGGGATGCC GTGCTGGTAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCTGACC GGTTCGCGCG CAAATTGCTG
151 GATTTCAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACTGa cgcggatttT TACCGTCggc gacttcCGCA
401 GCCGCGACCT TGCTGCCGGC GGacaAGGTG CGCCGCTCGT CCCCgcCTTT
451 CACGAAGCCC TGTTCGCGCA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CGCGGGGATT GCCAACATCA GCGTACTCCC CCCCggCGCA CCCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cacTGGcagc TGCCTTACGA CAAAAacggt gcAAAGgcgg cacAAGGCAA
651 catatTGcCg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTTCTCAC
701 AACCCcacc aaAAAGCACG GGgcGCGaac TgtttgcccT AAattggctc
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgtat tgcggacgct
801 ttcccgattc accgcgcaaA ccgTttggga cgcgtctca CACGACGCGG
851 CAGATGCCCG TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATttg
1001 cgtggttggc GGCCTGTTGG ATTAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCGACCGGCG CATCCAACC GTGTATTCTG GCGCGGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM SGTSMGDADA VLVRMDGGKW LGAEGHAFTP YPDLRRLKLL
51  DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPFAP
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRF TAQTVWDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTCGCGCG CCAATTGCTG

```

```

151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCCTCC GACATTACCG CCCTCGGCTG CCACGGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxCAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTGCGAC
701 AACGCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCQNLAAPS DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL Axxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
151 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKW LGAEGHAFTPYPGRLLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDADAVLVRMDGGKW LGAEGHAFTPYPDRLLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCQNLAAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
g121	HRSRILSQELSRLYAQTAAELLCQNLAAPCDITALGCHGQTVRHAPHEGYSIQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	Axx					
g121	AELTRIFTVGDFRSRDLAAGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPFGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	xxxxxxxxxxxxxxxxxxxxxxxxxQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDAYSHAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAYSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

345

	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	:					
g121	LMADLAECFGTRVSLHSTAE LNLDPOQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
g121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATGCTG
151 GATTGTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAAGCTC AGCCGCTGTG ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTGAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCGCTCGT CCCCCTTTT
451 CACGAAGCCC TGTTCGCGCA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCCGCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCC TAAAGCAGC GGGCGCGAAC TGTTCGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTC ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGCG GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPE DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAP
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPGP NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPOQWVEA AFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	:					
a121	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	10	20	30	40	50	60
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPE DITALGCHGQTVRHAPEHGYSIQLADLPLL					
	:					
a121	HRSRILSQELSRLYAQTAAELLCSQNLAPE DITALGCHGQTVRHAPEHSYSVQLADLPLL					
	70	80	90	100	110	120

346

	130	140	150	160	170	180
m121.pep	XX					
		:	:	:	:	:
a121	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121.pep	190	200	210	220	230	240
	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
	:	:	:	:	:	:
a121	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121.pep	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRLTSLRFTAQTVCDVSHAAADARQMYICDGGIRNPV					
	:	:	:	:	:	:
a121	GRELFAINWLETYLDGGENRYDVLRLTSLRFTAQTVFDVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121.pep	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
	:	:	:	:	:	:
a121	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAXFAWMAACWVNRI PGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
	:	:	:	:	:	:
a121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCGCGCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCGCAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATT
351 GCCGCTGCTG GCGGAACGGA CGCGGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGCGCCGGC GGACAAGGCG CGCCACTCGT CCCC GCCTTT
451 CACGAAGCCC TGTTCGCGCA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGCGGGGATT GCCAACATCA GCGTACTCCC CCCC GACGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGACGCGTG GACGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTT ACCGCGCAA CCGTTTGC GA CCGCGTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLRRLQL
51  DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPENGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG QGQAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRLTSLR TAQTVCDVAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPOWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

```

m121-1.pep  METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTYPGRLRRQLLDLQDTGADEL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         METQLYIGIMSGTSMGDADAVLVRMDGGKWLGAEGHAFTYPDRLRRKLLDLQDTGTDEL
              10      20      30      40      50      60

              70      80      90      100     110     120
m121-1.pep  HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAFEPHGYSIQLADLPLL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAFEPHGYSIQLADLPLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m121-1.pep  AERTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDNRETRAVLNIGGIANISVLPDDA
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         AELTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPDGA
              130     140     150     160     170     180

              190     200     210     220     230     240
m121-1.pep  PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
              190     200     210     220     230     240

              250     260     270     280     290     300
m121-1.pep  GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICGGGIRNPV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDVASHAAADARQMYICGGGIRNPV
              250     260     270     280     290     300

              310     320     330     340     350     360
m121-1.pep  LMDLAECFGTRVSLHSTADLNLDQPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g121         LMDLAECFGTRVSLHSTAE LNLDQPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
              310     320     330     340     350     360

m121-1.pep  XAGYYYY
              |||||
g121         GAGYYYY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 443>:

```

a121-1.seq
1   ATGGAACAC  AGCTTTACAT  CGGCATCATG  TCGGGAACCA  GCATGGACGG
51  GCGCGATGCC  GTACTGATAC  GGATGGACGG  CGGCAATGG  CTGGGCGCGG
101 AAGGGCAGCG  CTTTACCCCC  TACCCCGGCA  GGTACGCGG  CAAATTGCTG
151 GATTTCAGG  ACACAGGCGC  GGACGAACTG  CACCGCAGCA  GGATGTTGTC
201 GCAAGAACTC  AGCCGCTGT  ACAGCGAAAC  CGCCGCCGAA  CTGCTGTGCA
251 GTCAAAACCT  CGCGCCGTCC  GACATTACCG  CCCTCGGCTG  CCACGGGCAA
301 ACCGTCAGAC  ACGCGCCGGA  ACACAGTTAC  AGCGTACAGC  TTGCCGATTT
351 GCCGCTGCTG  GCGGAACGGA  CTCAGATTTT  TACCGTCGGC  GACTTCCGCA
401 GCCGCGACCT  TCGCGCCGGC  GGACAAGGCG  CGCCGCTCGT  CCCCGCCTTT
451 CACGAAGCCC  TGTTCGCGA  CGACAGGGAA  ACACGCGCGG  TACTGAACAT
501 CGCGGGGATT  GCCAACATCA  GCGTACTCCC  CCCCGACGCA  CCCGCTTCG
551 GCTTCGACAC  AGGACCGGCG  AATATGCTGA  TGGACGCGTG  GATGCAGGCA
601 CACTGGCAGC  TTCCTTACGA  CAAAACGGT  GCAAAGGCGG  CACAAGGCAA
651 CATATTGCCG  CAACTGCTCG  ACAGGCTGCT  CGCCACCCG  TATTTCGCAC
701 AACCCACCC  TAAAAGCAG  GGGCGCGAAC  TGTTTGCCT  AAATTGGCTC
751 GAAACCTACC  TTGACGCGCG  CGAAAACCGA  TACGACGTAT  TCGGACGCT
801 TTCCCGATT  ACCGCGCAAA  CCGTTTTCGA  CGCGTCTCA  CACGCAGCGG
851 CAGATGCCCG  TCAAATGTAC  ATTTGCGGCG  GCGGCATCCG  CAATCCTGTT
901 TTAATGGCGG  ATTTGGCAGA  ATGTTTCGGC  ACACGCGTTT  CCCTGCACAG
951 CACCGCGGAA  CTGAACCTCG  ATCCGCAATG  GGTAGAAGCC  GCCGCGTTCG
1001 CATGGATGGC  GGCGTGTGG  GTCACCGCA  TTCCCGGTAG  TCCGCACAAA
1051 GCAACCGGCG  CATCAAACC  GTGTATTCTG  GCGCGGGAT  ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

```

a121-1.pep
1   METQLYIGIM  SGTSMDGADA  VLIRMDGGKW  LGAEGHAFTP  YPGRLRRKLL
51  DLQDTGADEL  HRSRMLSQEL  SRLYAQTAAE  LLCSQNLAPS  DITALGCHGQ
101 TVRHAFESY  SVQLADLPLL  AERTQIFTVG  DFRSRDLAAG  GQGAPLVPF
151 HEALFRDDRE  TRAVLNIGGI  ANISVLPDDA  PAFGFDTPG  NMLMDAWMQA

```

201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
 351 ATGASKPCIL GAGYYY*

m121-1/a121-1 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSM	DGADAVLIRMDGGK	WLGAEGHAFTYP	PGRLRRQLLDLQ	DTGADEL	
a121-1	METQLYIGIMSGTSM	DGADAVLIRMDGGK	WLGAEGHAFTYP	PGRLRRKLLDLQ	DTGADEL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSR	LYAQTAELLCSQ	NLAPSDITALG	CHGQTVRHAP	EHGYSIQLADL	PLLL
a121-1	HRSRILSQELSR	LYAQTAELLCSQ	NLAPSDITALG	CHGQTVRHAP	EHGYSVQLADL	PLLL
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDF	RSRDLAAGGQG	APLVPAFHEAL	FRDNRETRAV	LNIGGIANISV	LPPDA
a121-1	AERTRIFTVGDF	RSRDLAAGGQG	APLVPAFHEAL	FRDDRETRAV	LNIGGIANISV	LPPDA
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTGPGN	MLMDAWTQAHW	QLPYDKNGAKA	AQGNILPQLLD	RLLAHPYFAQ	PHPKST
a121-1	PAFGFDTGPGN	MLMDAWTQAHW	QLPYDKNGAKA	AQGNILPQLLD	RLLAHPYFAQ	PHPKST
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLE	TYLDGGENRYD	VLRTLSRFTAQ	TVCDVASHAA	ADARQMYICG	GGIRNPV
a121-1	GRELFALNWLE	TYLDGGENRYD	VLRTLSRFTAQ	TVFVDAVSHA	ADARQMYICG	GGIRNPV
	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTR	VSLSHSTADL	NLDPOWVEAAX	FAWLAACWIN	RIPGSPHKAT	GASKPCIL
a121	LMADLAECFGTR	VSLSHSTAE	LNLDPQWVEA	AAFAWMAACW	VNRIPGSPHK	ATGASKPCIL
	310	320	330	340	350	360
m121-1.pep	XAGYYYX					
a121	GAGYYYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

```

1  ATGGCTTTAC TGAGCATCCG CAAGCTGCAC AAACAATACG GCAGCGTAAC
51  CGCCATCCAA TCCTTAGACT TGGACTTGGA AAAAGGCGAA GtcatCGTAC
101 TGCTGGGCCC gTccggctgc ggCAAATCCA CCTcctgcg ctgctgcaaC
151 GGTTTGGAGC CGCACCaaag cgGCAGCATC GTGATGGACG GTgtcgGCGA
201 ATTCggcAAA GACGTTTCCT GGCAAACCGC CCGGCAAAaa gtcggtatgg
251 tctttcaaag taacgAactg Tttgccaca tgaccgtcat cgAaaacatc
301 ttcttAggcC CGGTAAagga aCAAAAcCgc gaccgtgccg aagcaGAGGC
351 gCAAGCCGGC AAactGttgg aacgcgTCGG actgctAGAC CGCAAAAACG
401 CCTATCCGCG CGAACTTTCC GCGCGTCAGA AACAGCGCAT CGCCATTGTC
451 CGCGCCCTGT GCCTGAATCC GGAAGTCATC CTGCTGGACG AAATCACC GC
501 CGCACTTGAC CCCGAAATGG TCGCGAAGT CTGGAAGTG GTTTTGG AAC
551 TCGCCCGCGA AGGGATGAGT ATGCTCATCG TAACCCACGA AATGGGGTTC
601 GCACGCAAAG TTGCCGACCG CATCGTCTTT ATGGACAAAG GCGGCATCGT
651 CGAATCGTCC GACCCGAAA CTTTTTTTC CGACCAAAA AGCGAACGCG
701 CCCGCAATT TCTGGCAGGT ATGGACTACT GA
```

This corresponds to the amino acid sequence <SEQ ID 446; ORF 122.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 447>:

m122.seq

This corresponds to the amino acid sequence <SEQ ID 448; ORF 122>:

m122.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 122 shows 47.2% identity over a 246 aa overlap with a predicted ORF (ORF 122.ng) from *N. gonorrhoeae*:

m122/g122

[illegible]

350

	180	190	200	210	220	230
	250					
m122.pep	TRRFLSQIQSTKIX					
	: : : :					
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```
a122.seq
1  GTGTGCATGA TTAAATCCG CAATATCCAT AAGACCTTCG GCAAAAATAC
51  CATTTTGC GC CATCAATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGCC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAA TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
201 GCTGAAAATC GATTTTCTA AAAAACCAAG CAAACACGAT ATTTTGGCAC
251 TGCGCCGCAA ATCAGGCATG GTGTTTCAAC AATACAACCT CTTTCCGCAC
301 AAAACCGCCT TGGAAAACGT GATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTCAG
451 CAGCAGCGCG TCGGCATTGC CCGAGCATTG GCGATTGAGC CCGAGCTGAT
501 GTTGTGTTGAC GAACCCACTT CCGCGCTTGA CCCCAGATTG GTGCAAGACG
551 TGTGTAACGC CATGAAGGAA TTGGCGCGGG AAGGTTGGAC GATGGTCGTC
601 GTTACCCACG AAATCAAGTT CGCGCTGGAA GTTGCCACGA CCGTTGTCGT
651 GATGGACGGC GCGGTTATCG TAGAGCAGGG CAGCCCAGAA GAGTTGTTTCG
701 ACCACCCCAA ACACGAACGG ACGCGGAGAT TTTTAAGCCA AATCCAATCT
751 ACCAAGATTT GA
```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```
a122.pep
1  VVMIKIRNIH KTFGKNTILR GINLDVCKGQ VVILGPSGS GKTTLRLCLN
51  ALEMPEDGQI EFDNERPLKI DFKKPSKHD ILALRRKSGM VFQQYNLFPH
101 KTALENVM EG PVAVQKPA QAREEALKLL EKVLGDKVD LYPYQLSGGQ
151 QQRVGIARAL AIQPELMLFD EPTSALDPEL VQDVNLAMKE LAREGWTMVV
201 VTHEIKFALE VATTVVVMDG GVIVEQGS PK ELFDHPKHER TRRFLSQIQS
251 TKI*
```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKTFFGENTILRGIDLVDVCKGQVVVILGPSGSGKTTFLRLCLNALEMPEDGQI					
a122	VVMIKIRNIHKTFFGENTILRGIDLVDVCKGQVVVILGPSGSGKTTFLRLCLNALEMPEDGQI					
	10	20	30	40	50	60
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSXMFQQYNLFPHKTALENVM EGPVAVQKPA					
a122	EFDNERPLKIDFSKKPSKHDILALRRKSXMFQQYNLFPHKTALENVM EGPVAVQKPA					
	70	80	90	100	110	120
m122.pep	EFDNERPLKIDFSKKPSKHDILALRRKSXMFQQYNLFPHKTALENVM EGPVAVQKPA					
a122	EFDNERPLKIDFSKKPSKHDILALRRKSXMFQQYNLFPHKTALENVM EGPVAVQKPA					
	70	80	90	100	110	120
m122.pep	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPT					
a122	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPT					
	130	140	150	160	170	180
m122.pep	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPT					
a122	QAREEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPT					
	130	140	150	160	170	180
m122.pep	VQDVLDMKELAQEGWMTMVVTHEIKFALEVATTXVMDXGVIVEQGSQDLFDHPKHER					
a122	VQDVNLAMKELAREGWTMVVTHEIKFALEVATTVVMDGGVIVEQGSQDLFDHPKHER					
	190	200	210	220	230	240
m122.pep	VQDVLDMKELAQEGWMTMVVTHEIKFALEVATTXVMDXGVIVEQGSQDLFDHPKHER					
a122	VQDVNLAMKELAREGWTMVVTHEIKFALEVATTVVMDGGVIVEQGSQDLFDHPKHER					
	190	200	210	220	230	240
	250					
m122.pep	TRRFLSQIQSTKIX					

|||||||
a122 TRRFSLSIQSTKIX
250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATTTT
51 GCGCGGCATC GATTGGATG TGGGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TGCGCTGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG
201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC
301 GTGTTGGAAA ACGTGATGGA AGGGCCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTTTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGATAAAGT GGATTTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGTGTCGGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT
501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTTGG
551 ACCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCACGCT GGAAGTTGCC ACGAACGTCG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 TCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTGCCAAG
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep
1 MIKIRNIHKT FGENTILRGI DLDVKGQV VILGPSGSGK TFLRCLNAL
51 EMPEDGQIEF DNARPLRIDF SKKTSKHDIL ALRRKSGMVF QQYNLFPHKT
101 VLENVMEGPV AVQKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT
201 HEIKFTLEVA TNVVMDGGV IVEQSGPKEL FDHLKHERTR RFLSIQSAK
251 I*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq
1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACTATTTT
51 GCGCGGCATC GATTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAATCAGG CATGGTGTTT CAACAATACA ACCTCTTCC GCACAAAACC
301 GCCTTGAAA ACGTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGACAAAGT GGATTTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGGTCGCGCA TTGCCCGCGC ATTGGCGATT CAGCCTGAAC TGATGCTGTT
501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG
551 ATACCATGAA GGAATTGGCG CAAGAAGGCT GGACCATGGT TGTGTTTACG
601 CATGAAATCA AGTTCGCCTT AGAAGTGGCA ACCACCGTCG TCGTGATGGA
651 CGGCGGCGTT ATTGTCGAAC AAGGCAGCCC GCAAGATTG TTCGACCACC
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep
1 MIKIRNIHKT FGENTILRGI DLDVCKGQV VILGPSGSGK TFLRCLNAL
51 EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENVMEGPV AVQKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDTMKELA QEGWTMVVVT
201 HEIKFALEVA TTVVMDGGV IVEQSGPQDL FDHPKHERTR RFLSIQSTK
251 I*

m122-1/g122-1 94.8% identity in 251 aa overlap

	10	20	30	40	50	60
m122-1.pep	MIKIRNIHKTFGENTILRGIDLDVCKGQVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
g122-1	MIKIRNIHKTFGENTILRGIDLDVKGQVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					

352

	10	20	30	40	50	60
m122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPFVAVQGKPAQA					
g122-1	DNERPLRIDFSKKTSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPFVAVQGKPAQA					
	70	80	90	100	110	120
m122-1.pep	130	140	150	160	170	180
	REEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMFDEPTSAIDPELVQ					
g122-1	REEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMFDEPTSAIDPELVQ					
	130	140	150	160	170	180
m122-1.pep	190	200	210	220	230	240
	DVLDTMKELAQEGWMTMVVTHEIKFALEVATTVVMDGGVIVEQGSQDLFDHPKHERTR					
g122-1	DVLDTMKELAQEGWMTMVVTHEIKFTLEVATNVVMDGGVIVEQGSQDLFDHPKHERTR					
	190	200	210	220	230	240
m122-1.pep	250					
	RFLSQIQSTKIX					
g122-1	RFLSQIQSAKIX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

```
a122-1.seq
1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTCGGCAAAA ATACCATTTT
51  GCGCGGCATC AATTGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAAAATCAGG CATGGTGTTC CAACAATACA ACCTCTTTCC GCACAAAACC
301 GCCTTGAAAA ACGTGATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAGAA GTCGGCTTGG
401 GCGACAAAGT GGATTTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGCGTCGGCA TTGCCCGAGC ATTGGCGATT CAGCCCGAGC TGATGTTGTT
501 TGACGAACCC ACTTCCGCGC TTGACCCCGA GTTGGTGCAA GACGTGTTGA
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCGCGCT GGAAGTTGCC ACGACCGTTG TCGTGATGGA
651 CGCGGCGGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 CCAAAACAGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA
```

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

```
a122-1.pep
1  MIKIRNIHKT FGKNTILRGI NLDVCKGQVV VILGPSGSGK TFLRCLNAL
51  EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENVMEGPV AVQGKPAQA REEALKLLEK VGLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMFDEP TSALDPELVQ DVLNAMKELA REGWMTMVVT
201 HEIKFALEVA TTVVMDGGV IVEQGSPEL FDHPKHERTR RFLSQIQSTK
251 I*
```

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1.pep	MIKIRNIHKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRNIHKTFGKNTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
a122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPFVAVQGKPAQA					
m122-1	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPFVAVQGKPAQA					
	70	80	90	100	110	120
a122-1.pep	130	140	150	160	170	180
	REEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMFDEPTSAIDPELVQ					
m122-1	REEALKLLEKVGLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMFDEPTSAIDPELVQ					



		130	140	150	160	170	180
a122-1.pep		190	200	210	220	230	240
	DVLNAMKELAREGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGS	KPELFDHPKHHERTR					
m122-1	::						
	DVLDTMKELAQEGWTMVVVTHEIKFALEVATTVVVMDGGVIVEQGS	PQDLFDHPKHHERTR					
		190	200	210	220	230	240
a122-1.pep	250	RFLSQIQSTKIX					
m122-1	RFLSQIQSTKIX						
	250						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 457>:

```
q125.seq
```

1	ATGTCGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCGCCGCCA	TCGGGGTGGT
51	TTGGTTCGGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCACG	GGTACGCTGC
101	TCGCCCCCTT	GGGCTGGCAG	CGCGGTCTGG	CGGCCCTGCT	TTTGGGT CAT
151	GCCGT CGGC	GCGCGCTGTT	TTTTGCGGCG	GCGTATATCG	GCGCACTGAC
201	CGGACGCAGC	TCGATGGAAA	ATATGCGCCT	GTCGTTCCGG	AAATCGGGTT
251	CAGTGCTGTT	TTCCGTGGCG	GAGTAGCTGC	AAC TGCCCGG	CTGGACGGCG
301	GTGATGATT	ACGT CGGCGC	Aacg9T CAGC	TCCGCTTTGG	CGAAAGTGTT
351	GTGGGACg9c	gaATCCTTTG	TCTGGTGGGC	ATTGGCAAAC	GGCGCACTGA
401	TCGTGCTGTG	GCTGGTTTTC	GGCGCACGCA	GAACGGGCGG	GCTGAAAACC
451	GTTTCGATGC	TGCTGATGCT	GCTTGCCGTG	TTGTGGTTGA	GCGTCGAAGT
501	GTT CGCTTCG	TCCGGCACAA	ACGCCGCGCC	CGCCGTTTCA	GACGGCATGA
551	CCTTCGGAAC	GGCAGTCGAA	CTGTCCGCGC	TCATGCCCGT	TTCTGGGCTG
601	CCGCTGGCCG	CCGACTACAC	GCGCCAAAGCA	CGCCGCCCGT	TTGCGGCAAC
651	CCTGACGGCA	ACGCTCGCCT	ATACGCTGAC	GGGCTGCTGG	ATGTATGCCT
701	TGGGTTTGGC	GGCGGCTCTG	TTTACCGGAG	AAACC GACGT	GGCGAAAATC
751	CTGTTGGGCG	CGGGCTTGGG	CATAACGGGC	ATTCTGGCAG	TCGTCCTCTC
801	CACCGTTACC	ACAACGTTTC	TCGATACCTA	TTCGCCCGGC	GCGAGTGCGA
851	ACAACATTTT	CGCGCGTTTT	GCGGAAATAC	CCGTCGCTGT	CGGCGTTACC
901	CTGATcc9ca	ccgtgccttg	cgtcatgctg	cccgttaccg	aatataaaaa
951	cttcctgctg	cttatccgct	cggatattgg	gccgatggcg	ggtggttttg
1001	attgc9caCT	TTTttgtctt	AAAACGGCGT	GA	

This corresponds to the amino acid sequence <SEQ ID 458; ORF 125.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 459>:

m125.seq

1	ATGTCGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCTCCGCCA	TCGGGGCTGAT
51	TTGGTTCCGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCAGC	GGTACGCTGC
101	TTGCGCCTTT	GGGCTGGCAG	CGCGGTCTGG	CGGCTCTACT	TTTGGGTCAT
151	GCCGTCGGCG	GCGCGCTGTT	TTTTCGGCGG	GCGTATATCG	GCGCACTGAC
201	CGGACGCGAGC	TCCGATGGAAA	GCTTGCGCCT	TCGTGTCGGC	AAACGCGGTT
251	CAGTGCTGTT	TTCCGTGGCG	AATATGCTGC	AACGTGGCCG	CTGGACGCGC
301	GTGATGATTT	ACGCCGGCGC	AACGGTCAGC	TCCGCTTTGG	GCAAAGTGTT
351	GTGGGACGCG	GAATCTTTTG	TCTGGTGGGC	ATTGGCAAAC	GGCGCGCTGA
401	TTGTGCTGTG	GCTGGTTTTG	GGCGCACGCA	AAACAGGCGG	GCTGAAAACC
451	GTTTCGATGC	TGCTGATGCT	TTGGCGGTT	CTGTGGCTGA	GTGCCGAAGT
501	CTTTTCCACG	GACGACAGCA	CGCCGCGACA	GGTTTCAGAC	GGCATGAGTT
551	TCGGAACGCG	AGTCGAGCTG	TCCGCCGTGA	TGCCGCTTTC	CTGGCTGCCG
601	CTTGCCGCCG	ACTACACGCG	CCACGCGCGC	CGCCCGTTTG	CGGCAACCCCT
651	GACGGCAACG	CTCGCTTACA	CGCTGACCGG	CTGCTGGATG	TATGCCTTGG
701	GTTTGGCAGC	GGCGTTGTTC	AGCCAGAGAA	CCGACGTGGC	AAAAATCCTG
751	CTGGGCGCgAr	GTTTgGTGC	GCGGCGATT	TTGGCGGTGC	TCCTCTCCAC
801	CGTTACCACA	ACGTTTCTCG	ATGCCTATTG	CGCGCGCGCG	AGTGCGCAAC



m125.pep

analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m125/q125

10 20 30 40 50 60

a125.seq

1	ATGTCGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCGCCGCCA	TCGGGCTGAT
51	TTGGTTCGGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCACG	GGTACACTGC
101	TTGCGCCTTT	GGGCTGGCAG	CGCGGTCTGG	CGGCTCTGCT	TTTGGGTCTAT

```

151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGCGCCT GTCGTTCCGGC AAACGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GGCGCGCTGA
401 TTGTGCTGTG GCTGGTTTTC GGCGCAGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGGCTGA GTGCCGAAGT
501 CTTTTCCACG GCAGGCAGCA CCGCCGCACA GGTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTGA TGCCCGTTTC TTGGCTGCCG
601 CTGGCCGCGC ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCCT
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTTGGCAGC GGCCTTGTTT ACCGGAGAAA CCGACGTGGC AAAAATCCTG
751 CTGGGCGCAG GTTTGGGTGC GGCAGGCATT TTGGCGGTGC TCCTGTCCAG
801 CGTTACCACC ACTTTTCTCG ATGCCTACTC CGCCGGCGTA AGTGCCAACA
851 ATATTTCGCG CAAACTTTCG GAAATACCCA TCGCCGTTCG CGTCGCCGTT
901 GTCGGCACAC TGCTTGCCGT CCTCCTGCCC GTTACCGAAT ATGAAAACCT
951 CCTGCTGCTT ATCGGCTCGG TATTTCGCGC GATGGCG.GC GGTTTTGATT
1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 462; ORF 125.a>:

```

a125.pep
1  MSGNASSPSS SAAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
51  AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLSVA NMLQLAGWTA
101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
201 LAADYTRHAR RFFAATLTAT LAYTLTGCMW YALGLAAALF TGETDVAKIL
251 LGAGLGAAGI LAVVLSTVTT TFLDAYSAGV SANNISAKLS EIPIAVAVAV
301 VGTLLAVLLP VTEYENFLLL IGSVFAPMAX GFDCRLFRLE TA*

```

m125/a125 95.6% identity in 342 aa overlap

```

          10      20      30      40      50      60
m125.pep  MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA
          |||||
a125      MSGNASSPSSSSAIGLIWFGAAVSIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA
          10      20      30      40      50      60

          70      80      90      100     110     120
m125.pep  AYIGALTGRSSMESVRLSFGKRGSVLSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
          |||||
a125      AYIGALTGRSSMESVRLSFGKRGSVLSVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
          70      80      90      100     110     120

          130     140     150     160     170     180
m125.pep  ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD
          |||||
a125      ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQVSD
          130     140     150     160     170     180

          190     200     210     220     230     240
m125.pep  GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAAALF
          |||||
a125      GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCMWYALGLAAALF
          190     200     210     220     230     240

          250     260     270     280     290     300
m125.pep  TGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVTL
          |||||
a125      TGETDVAKILLGAGLGAAGILAVVLSTVTTTFLDAYSAGVSANNISAKLSEIPIAVAVAV
          250     260     270     280     290     300

          310     320     330     340
m125.pep  IGTVLAVMLPVTEYENFLLLIGSVFAPMAGGFDCRLFRLETAX
          :||:||||:|||||
a125      VGTLLAVLLPVTEYENFLLLIGSVFAPMAXGFDCRLFRLETAX

```

310 320 330 340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

g126.seq

```

1   AtgccgtcTG AAaccCcaaa ggcACGCCGC CGGCTTTCAG ACGGCATCGC
51  GTCCGACAAC CATACCAAAG AATCCATCAT GCTCACCctg tacggcGAAA
101 CTTTCCCTTC GCGGCTGCTg ctcggcacgG cggcctacCC GACCCCTGAA
151 ATCCTCAAAC AATCCGTCCG AACGCCCGG CCCGCGATGA ttaccGTCTC
201 GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTGGT
251 CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301 CAAAGCGTGC AGGAAGCGGT AACGACGGCG CAAATGGCGC GCGAAGTGTT
351 TGAAACCGAT TGGATAAAAT TGGAATCAT CGGCGACGAC GACACCTTGC
401 AGCCGGACGT GTTCCAATC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451 GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CTGCGCCCG
501 CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551 GCACGGGTTT GGGGGCGGTT CACGCCTATG CGCTCAAAAT CCTGCGCGAA
601 CGCCTGCCCG ACACGCCGT GATTATCGAC GCGGGCTTGG GTTTGCCTTC
651 CCAAGCGGCA CAAGTGATGG AATGGGGTTT TGACGGCGTA TTGTTAAACA
701 CCGCCGTTTC CCGCAGCGGC GACCCCGTCA ACATGGCGCG CGCCTTCGCA
751 CTCGCCGTCG AATCCGGACG GCTGGCATTG GAAGCCGGGC CGGTCGAAGC
801 GCGAACCAAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTGGC
851 ATTCGGCGGA ATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

g126.pep

```

1   MPSETPKARR RLSDGIASDN HTKESIMLTL YGETFPSRL LGTAAYPTPE
51  ILKQSVRTAR PAMITVSLRR TCGGGEAHGQ GFWSLLQETG VPVLPNTAGC
101 QSVQEAVTTA QMAREVFETD WIKLELIGDD DTLQPDVFQL VEAELLIKD
151 GFKVLPYCTE DLIACRRLLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201 RLPDTPLIID AGLGLPSQAA QVMEWGFQDV LLNTAVSRSG DPNMARAFA
251 LAVESGRLAF EAGPVEARTK AQASTPTVGQ PFWHSABEY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

m126.seq (partial)

```

1   ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACCTTTCCC
51  CTCGCGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCC GAAATCCTCA
101 AACAAATCCAT CCAAACCGCC CAGCCTGCGA TGATTACCGT CTCGCTGCGC
151 CGCGCGGGAA GCGGCGGCGA GGCGCACGGT CAGGGGTTTT GGTGCTGCT
201 TCAAGAAACC GCGGTTCCCG TCCTGCCGAA CACGGCAGGC TGCCAAAGCG
251 TGCAGGAAGC GGAACGACG GCGCAAATGG CCGCGGAAGT GTTTGAAACC
301 GATTGGATAA AATTGGAAC CATCGGAGAT GACGACACCT TGCAGCCGGA
351 TGTGTTCCAG CTGTGCGAAG CGGCGGAAAT CCTGATTAAA GACGGCTTCA
401 AAGTGCTGCC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCCTGCTC
451 GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCCGA TCGGCACGGG
501 TTTGGGCGCG GTTACGCCT ACGCGTTGAA CGTCTGCGC GAACGCCTGC
551 CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601 GCACAAGTGA TGAATGGGG CTTTGACGCG GTGCTTTTGA ATACTGCCGT
651 TTCCCGCAGC GGCATCCCG TCAATATGCG ACGCGCCTTC GCACTCGCCG
701 TCGAATCCGG ACGGCTGGCA TTTGAAGCCG GACCGGTCGA AGCACGCGAC
751 AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTTT GGCATTGCGC
801 GGAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

m126.pep (partial)

```

1   ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP EILKQSIQTA QPAMITVSLR
51  RAGSGGEAHG QGFWSLLQET GVPVLPNTAG QSVQEAVTT AQMAREVFET

```

```

101 DWIKLELIGD DDTLQPDVFQ LVEAAEILIK DGFKVLPYCT EDLIACRRL
151 DAGCQALMPW AAPIGTGLGA VHAYALNVLR ERLPDTPLII DAGLGLPSQA
201 AQVMEWGFDG VLLNTAVSRS GDPVNMARAF ALAVESGRLA FEAGPVEARD
251 KAQASTPTVG QPFWHSAEY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 126 shows 95.9% identity over a 269 aa overlap with a predicted ORF (ORF 126.ng) from *N. gonorrhoeae*:

m126/g126

```

                                10      20      30      40
m126.pep      .  HYTKPEIMLTLYGETFPSSRLLLGTAAAYPTPEILKQSIQTAQ
                  ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      MPSETPKARRRLSDGIASDNHTKESIMLTLYGETFPSSRLLLGTAAAYPTPEILKQSVRTAR
                  10      20      30      40      50      60

                                50      60      70      80      90     100
m126.pep      PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      PAMITVSLRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  70      80      90     100     110     120

                                110     120     130     140     150     160
m126.pep      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  130     140     150     160     170     180

                                170     180     190     200     210     220
m126.pep      APIGTGLGAVHAYALNVLRERLPDTPPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      APIGTGLGAVHAYALKILRERLPDTPPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                  190     200     210     220     230     240

                                230     240     250     260     270
m126.pep      DPVNMARAFALAVESGRLA FEAGPVEARDKAQASTPTVGQPFWHSAEYX
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      DPVNMARAFALAVESGRLA FEAGPVEARTKAQASTPTVGQPFWHSAEYX
                  250     260     270     280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 467>:

```

a126.seq
1  TTGTTAATCC ACTATACAAA GGAACCCATT ATGCTCACCC TGTACAGCGA
51  AACTTTCCCT TCGCGGCTGC TGCTCGGCAC AGCCGCCTAC CCGACCCCTG
101 AAATCCTCAA ACAATCCGTC CGAACC GCCCGCGAT GATTACCGTC
151 TCGCTGCGCC GCGCGGGATG CGGCGGCGAG GCGCACGTC AGGGGTTTGT
201 GTCGCTGCTT CAAGAAACCG GCGTTCCCGT CCTGCCGAAC ACGGCAGGCT
251 GCCAAAGCGT GCAGGAAGCG GTAACGACGG CGCAAATGGC GCGCGAAGTG
301 TTTGAAACCG ATTGGATTAA ACTCGAACTC ATCGGCGACG ACGACACCTT
351 GCAGCCGAT GTGTTCCAAC TTGTCGAAGC GCGCGAAATC CTGATTAAAG
401 ACGGCTTCAA AGTGCTGCCT TATTGCACCG AAGACCTGAT TGCCTGCCGC
451 CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG ATGCCGTGGG CGGCCCCGAT
501 CGGCACGGGT TTGGGCGCGG TTCACGCCTA CGCGTTGAAC GTCCTGCGCG
551 AACGCCTGCC CGACACGCCG CTGATTATCG ACGCGGGCTT GGGTTTGCCC
601 TCACAGGCGG CACAAGTGAT GGAATGGGGC TTTGACGGCG TGCTTTTGAA
651 TACTGCCGTT TCCCGCAGCG GCGATCCGGT CAATATGGCA CGCGCCTTCG
701 CACTCGCCGT CGAATCCGGA CGGCTGGCAT TTGAAGCCGG ACCGGTCGAA
751 GCACGCGACA AAGCGCAAGC CAGCACGCCG ACAGTCGGAC AACCGTTTGT
801 GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
  1  LLIHYTKPEI MLTYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV
 51  SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101  FETDWIKLEL IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR
151  RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201  SQAAQVMEWG FDGVLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251  ARDKAQASTP TVGQPFWWSA EY*
```

m126/a126 98.1% identity in 269 aa overlap

	10	20	30	40	50	
m126.pep	HYTKPEIMLTLYGETFP SRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGE					
a126	LLIHYTKPEIMLTLYSETFP SRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGE					
	10	20	30	40	50	60
	60	70	80	90	100	110
m126.pep	AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPD					
a126	AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPD					
	70	80	90	100	110	120
	120	130	140	150	160	170
m126.pep	VFQLVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN					
a126	VFQLVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN					
	130	140	150	160	170	180
	180	190	200	210	220	230
m126.pep	VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLNTAVSRSGDPVNMA RAFALAVESG					
a126	VLRERLPDTP LIIDAGLGLPSQAAQVMEWGF DGVLNTAVSRSGDPVNMA RAFALAVESG					
	190	200	210	220	230	240
	240	250	260	270		
m126.pep	RLAFEAGPVEARDKAQASTPTVGQPFWWSAEYX					
a126	RLAFEAGPVEARDKAQASTPTVGQPFWWSAEYX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
  1  ATGCTCAGCC TGTACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
 51  GGCCGCGTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCAGCC
101  GGCCGCGGAT GATTACCGTC TCGCTGCGCC GCACGGGATG CGGCGGCGAG
151  GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201  CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251  CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAATC
301  ATCGGCGGACG ACGACACCTT GCAGCCGGAC GTGTTCCAAC TCGTCGAAGC
351  GGCGGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCTT TATTGCACCG
401  AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ATGCGGGCTG TCAGGCGTTG
451  ATGCCGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCCTA
501  TCGGCTCAAA ATCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551  ACGCGGGGCTT GGGTTTGCTT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601  TTTGACGGCG TATTGTAAAT CACCGCCGTT TCCGCGAGCG GCGACCCCGT
651  CAACATGGCG CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701  TTGAAGCCGG GCCGGTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751  ACAGTCGGAC AACCGTTTTG GCATTGCGCG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
  1  MLTYGETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
```

```

51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSQDPVNMA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWHSA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

m126-1.seq

```

1 ATGCTCACCC TATACGGCGA AACTTTCCCC TCGCGGCTGC TGCTCGGCAC
51 GGCTGCCTAC CCGACCCCGG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAAGTC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTGTTCCAGC TTGTCGAAGC
351 GGCGGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGCG
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCAGCCCG
751 ACASTCGGAC AACCGTTTTG GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

m126-1.pep

```

1 MLTYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSQDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWHSA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTYGETFP	SRLLLGTAAY	PTPEILKQSI	QTAQPAMITV	SLRRAGSGGE	AHGQGFWSLL
g126-1	MLTYGETFP	SRLLLGTAAY	PTPEILKQSV	RTARPAMITV	SLRRAGSGGE	AHGQGFWSLL
	10	20	30	40	50	60
m126-1.pep	QETGVPVLP	NTAGCQSVQEA	VTTAQMAREV	FETDWIKLEL	IGDDDTLQPD	VFQLVEAAEI
g126-1	QETGVPVLP	NTAGCQSVQEA	VTTAQMAREV	FETDWIKLEL	IGDDDTLQPD	VFQLVEAAEI
	70	80	90	100	110	120
m126-1.pep	LIKDGFKVLP	YCTEDLIACR	RLLDAGCQAL	MPWAAPIGTG	LGAVHAYALN	VLRERLPDTP
g126-1	LIKDGFKVLP	YCTEDLIACR	RLLDAGCQAL	MPWAAPIGTG	LGAVHAYALK	ILRERLPDTP
	130	140	150	160	170	180
m126-1.pep	LIIDAGLGLP	SQAAQVMEWG	FDGVLLNTAV	SRSQDPVNMA	RAFALAVESG	RLAFEAGPVE
g126-1	LIIDAGLGLP	SQAAQVMEWG	FDGVLLNTAV	SRSQDPVNMA	RAFALAVESG	RLAFEAGPVE
	190	200	210	220	230	240
m126-1.pep	ARDKAQASTP	TVGQPFWHS	AEYX			
g126-1	ARTKAQASTP	TVGQPFWHS	AEYX			
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

a126-1.seq

```

1 ATGCTCACCC TGTACAGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51 AGCCGCCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GGCCCGCAT GATTACCGTC TCGCTGCGCC GCGCGGGATG CGGCGGCGAG

```

360

```

151 GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAAGAAACCG GCGTTCCTCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATTAA ACTCGAACTC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAT GTGTTCCAAC TTGTGCAAGC
351 GGCGGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTCG CACTCGCGCT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTGT GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

a126-1.pep

```

1 MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
51 AHQGGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDLQPD VFQLVEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAQVMWEG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

a126-1/m126-1 98.1% identity in 262 aa overlap

a126-1.pep	10	20	30	40	50	60
	MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE AHQGGFWSLL					
m126-1	MLTLYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE AHQGGFWSLL					
	10	20	30	40	50	60
a126-1.pep	70	80	90	100	110	120
	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDLQPD VFQLVEAAEI					
m126-1	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDLQPD VFQLVEAAEI					
	70	80	90	100	110	120
a126-1.pep	130	140	150	160	170	180
	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP					
m126-1	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP					
	130	140	150	160	170	180
a126-1.pep	190	200	210	220	230	240
	LIIDAGLGLP SQAQVMWEG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
m126-1	LIIDAGLGLP SQAQVMWEG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
a126-1.pep	250	260				
	ARDKAQASTP TVGQPFWWSA EYX					
m126-1	ARDKAQASTP TVGQPFWWSA EYX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

g127.seq

```

1 ATGGAAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCGATACG
51 CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGTTTTTT GGTGCGCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GGCAGCAATT CAAACGCTGG
251 CTTTGTCGAT GTTTGCGGTG GCGGCGGCGG TCGTCTGTGC GACAAAAGAA
301 CTGATTATGT GTCTGTGCGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTGTT
501 GAGCCACCCC GTGCGCGCGG ACAATATTTT GGGCGACTAT GTCATCCATA

```

```

551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 TCAGCGGTAT TTGGAACG TGCAGGCGGA AAAACTGTTT ATCAGGCCCG
701 CCGCCAGGCC GCGCGTTACC CGCGTACCGT ACGACGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGCGCGTACA ATACCGCCTG TTAAATCATC
851 CCGCCGgctc cgAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

```

g127.pep
1  MEIWNMLNTW PDAVPIRAEA AESVAAVAAL LLARALLNI HFRRHPDFGI
51  ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAADVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNLLLLSHV VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVs KRLEIQQAVM DEFLRVQYRL LNHYPAGSETL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

```

m127.seq
1  ATGGAAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCGATACG
51  TGCGGAGGCG GTCGAATCCG TGGCGGCGGT TCGCGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGTTTTTT GGTGCGCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCGAAATC CAAACGCTGG
251 CTTTGTTCGAT GTTTCGGGTG GCGGCGGCGG TCGTCGTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTGCGG CAGTATTTTA AGGTCTGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTCCGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCGCGC ACAATATTTT GGGCGACTAT GTCATCCATA
551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCCGGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 CCAACGGSAT TTGGAACG TGCAGGCGGA AAAACTGTTT ATCAGGCCCG
701 CCGCCAGACC GCGCGTTACC CGCGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCTTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TGCGCGTACA ATACCGCCTG TTAAATCACC
851 CCGCCGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

```

m127.pep
1  MEIWNMLDTW LGAVPIRAEA VESVAAVAAL LLARALLNI HFKRHPDFGI
51  ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAADVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNLLLLSHV VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVs KRLEIQQAVM DEFLRVQYRL LNHYPAGSETL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng) from *N. gonorrhoeae*:

```

m127/g127
          10      20      30      40      50      60
m127.pep MEIWNMLDTWLGAVPIRAEAVESVAAVAALLARALLNIHFKRHPDFGIESKRRFLVAS
          |||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g127      MEIWNMLNTWPDVPIRAEAAESVAAVAALLARALLNIHFRRHPDFGIESKRRFLVAS
          10      20      30      40      50      60

          70      80      90     100     110     120
m127.pep RNITLLLVLFSLAFIWSAQIQTALSMFAVAAADVATKELIMCLSGSILRSATQQYSVG
          |||:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g127      RNITLLLVLFSLAFIWSAQIQTALSMFAVAAADVATKELIMCLSGSILRSATQQYSVG

```

362

	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSDEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

a127.seq	1	ATGGAATAT	GGAATATGTT	GGACACTTGG	CTCGGTGCCG	TCCCGATACG
	51	TGCGGAGGCG	GTCGAATCCG	TGGCGGTGGT	CGCGGCTTTG	CTGCTGGCGC
	101	GCGCCCTTCT	GTTGAATATC	CACTTCAAAC	GGCATCCGGA	TTTCGGCATC
	151	GAAAGCAAGC	GGCGGTTTTT	GGTTGCCAGC	CGCAATATAA	CGCTGCTTTT
	201	GGTGCTGTTT	TCGCTGGCAT	TTATCTGGTC	GGCGCAAATC	CAAACGCTGG
	251	CTTTGTCGAT	GTTTGCGGTG	GCGGCGGCGG	TCGTCGTGGC	GACGAAGGAA
	301	CTGATTATGT	GTCTGTCGGG	CAGCATTTTA	AGGTCTGCCA	CCCAGCAATA
	351	CTCGGTCGGC	GACTATATCG	AAATCAACGG	CCTGCGCGGG	CGCGTGGTCG
	401	ACATCAACCT	GTTGAACACG	CTGATGATGC	AGGTGCGGTC	GAACCCCTTG
	451	GTCGGACAGC	TGCGGGAAC	CACCGTTTCT	TTCCCAACA	GCCTGTTGTT
	501	GAGCCACCCC	GTGCGCGCG	ACAATATTTT	GGGCGACTAC	GTCATCCATA
	551	CGGTGAAAT	CCCGTTCCC	ATCCATTGG	ATTCGGATGA	AGCCGTATGC
	601	CGTCTGAAAG	CGTACTCGA	GCCCTTGTC	GCGCCCTACA	TCCCGGCCAT
	651	CCAACGGCAT	TTGAAAACG	TGCAGGCGGA	AAACTGTTT	ATCACGCCCG
	701	CCGCCAAACC	GCGCGTTACC	CGCGTGCCGT	ACGATGACAA	GGCATACCGC
	751	ATCATCGTCC	GCTTCGCCTC	CCCCGTTTCA	AAGCGGCTGG	AAATCCAACA
	801	GGCGGTATG	GACGAATTTT	TGCGCGTACA	ATACCGCTG	TTAAATTACC
	851	CCGCCGGCTC	CGAAACACTT	TAA		

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

a127.pep	1	MEIWNMLDTW	LGAVPIRAEA	VESVAVVAAL	LLARALLNI	HFKRHPDFGI
	51	ESKRRLVAS	RNITLLLVLF	SLAFIWSAQI	QTLALSMFAV	AAAVVVATKE
	101	LIMCLSGSIL	RSATQQYSVG	DYIEINGLRG	RVVDINLLNT	LMMQVGNPL
	151	VGQLAGTTVS	FPNSLLLSHP	VRRDNILGDY	VIHTVEIPVP	IHLDSDEAVC
	201	RLKAVLEPLC	APYIPAIQRH	LENVQAEKLF	ITPAKPRVT	RVPYDDKAYR
	251	IIVRFASPV	KRLEIQQAVM	DEFLRVQYRL	LNYPAGSETL	*

m127/a127 98.6% identity in 290 aa overlap

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRLVAS					
a127	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALALSMFAVAAVVVATKELIMCLSGSILRSATQQYSVG					
a127	RNITLLLVLFSLAFIWSAQIQTALALSMFAVAAVVVATKELIMCLSGSILRSATQQYSVG					
	70	80	90	100	110	120

363

	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
a127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRHLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVYRLLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVYRLLNYPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

1	atgattgaca	acgCActgct	ccacttgggc	gaagaaccCC	GTTTaatca
51	aatccaaacc	gaagACAtca	AACCCGCCGT	CCAAACCGCC	ATCGCCGAAG
101	CGCGCGGACA	AATCGCCGCC	GTCAAAGCGC	AAACGCACAC	CGGCTGGGCG
151	AACACCGTCG	AGCGTCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTGT
201	GGGCGTCGTG	TCCCATCTCA	ACTCCGTCGT	CGACACGCCC	GAACTGCGCG
251	CCGTCTATAA	CGAACTGATG	CCTGAAATCA	CCGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TGGAAGTGA	CAACCGCTTC	AAAACCATCA	AAAATTCCCC
351	CGAATTGCA	ACGCTTTCCC	CCGCACAAAA	AACCAAGCTC	GATCACGACC
401	TGCGCGATTT	CGTATTGAGC	GGCGCGGAAC	TGCCGCCCGA	ACGGCAGGCA
451	GAACTGGCAA	AACTGCAAAC	CGAAGGCGCG	CAACTTTCCG	CCAAATTCTC
501	CCAAAACGTC	CTAGACGCGA	CCGACGCGTT	CGGCATTAC	TTTGACGATG
551	CCGCACCGCT	TGCCGGCATT	CCCGAAGACG	CGCTCGCCAT	GTTTGCCGCC
601	GCCGCGCAAA	GCGAAGGCAA	AACAGGTTAC	AAAATCGGCT	TGCAGATTCC
651	GCACTACCTT	GCCGTTATCC	AATACGCGCG	CAACCGCGAA	CTGCGCGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGTGCCA	GCGAACTTTC	AAACGACGGC
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCATTGAA
801	AACCGccaaa	cTGCTCGGCT	TTAAAAATTA	CGCCGAATTG	TCGCTGGCAA
851	CCAAAATGGC	GGACACGCCC	GAACAGGTTT	TAAACTTCCT	GCACGACCTC
901	GCCCGCGCGC	CCAAACCCTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAGC
951	CTTCGCCCGC	GAACACCTCG	GTCTCGCCGA	CCCGCAGCCG	TGGGACTTGA
1001	GCTACGCCGG	CGAAAACTG	CGCGAAGCCA	AATACGCATT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTTCTGGCAG	GCCTGTTCCG
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	CGCCGAAAAA	ACCGTTCCCG
1151	TCTGGCACAA	AGACGTGCGC	TATTTTGAAT	TGCAACAAAA	CGGCAAAACC
1201	ATCGGCGGCG	TTTATATGGA	TTGTACGCA	CGCGAAGGCA	AACGCGGCGG
1251	CGCGTGGATG	AACGActaca	AAGGCCGCGG	CCGCTTTGCC	GACGgcacGC
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	GCCCGTCGGC
1351	GGCAAAGAAG	CGCGTTTAAG	CCACGACGAA	ATCCTCACCC	TCTTCCACGA
1401	AacCGGCCAC	GGACTGCACC	ACCTGCTTAC	CCAAGTGGAC	GAACTGGGCG
1451	TGTCCGCAT	CAAcggcgtA	GAATGGGACG	CGGTGCAACT	GCCCAGCCAG
1501	TTTATGGAAA	ACTTCGTTTG	GGAATACAAT	GTATTGGCAC	AAATGTCCGC
1551	CCACGAAGAA	AccgGCGAGC	CCCTGCCGAA	AGAACTCTTC	GACAAAATGC
1601	TcgcGCCCAA	AAACTTCCAG	CGCGGTATGT	TCCTCGTCCG	GCAAATGGAG
1651	TTCGCCCTCT	TCGATATGAT	GATTTACAGT	GAAAGCGACG	AATGCCGTCT
1701	GAAAAACTGG	CAGCAGGTTT	TAGACAGCGT	GCGCAAAGAA	GTcGCCGTCA
1751	TCCAACCGCC	CGAATACAAC	CGCTTCGCCA	ACAGCTTCGG	CCacatctTC
1801	GCcggcGGCT	ATTCCGCAGG	CTATTACAGC	TACGCATGGG	CCGAAGTCCT
1851	cAGCACCGAT	GCCTACGCCG	CCTTTGAAGA	AAGcGACGac	gtcGCCGCCA
1901	CAGGCAAACG	CTTCTGGCAA	GAAAtccttg	ccgtcggcgg	ctCCCCGAGC
1951	gcgGCGGAAT	CCTTCAAAGC	CTTCGCGGGA	CGCGAACCGA	GCATAGACGC

2001 ACTGCTGCGC CAAagcggT TCGACAACGC gGcttgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

g128.pep

```

1  MIDNALLHLG  EEPFRNQIQT  EDIKPAVQTA  IAEARGQIAA  VKAQHTTGWA
51  NTVERLTGIT  ERVGRWGVV  SHLNSVVDTP  ELRAVYNELM  PEITVFFTEI
101 GQDIELYNRF  KTIKNSPEFA  TLSPAQKTKL  DHDLRDFVLS  GAELPPERQA
151 ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201 AAQSEGKTGY  KIGLQIPHYL  AVIQYAGNRE  LREQIYRAYV  TRASELSNDG
251 KFDNTANIDR  TLENALKTAK  LLGFKNYAE  SLATKMADTP  EQVLNPLHDL
301 ARRAKPYAEK  DLAEVKAFAR  EHLGLADPQP  WDSL YAGEKL  REAKYAFSET
351 EVKKYFPVGK  VLAGLFAQIK  KLYGIGFAEK  TVPVVHKDVR  YFELQONGKT
401 IGVVYMDLYA  REGKRGGAWM  NDYKGRRRFA  DGTQLQLPTAY  LVCNFAPPVG
451 GKEARLSHDE  ILTLFHETGH  GLHLLTQVD  ELGVSGINGV  EWDAVELPSQ
501 FMENFVWEYN  VLAQMSAHEE  TGEPLPKELF  DKMLAAKNFQ  RGMFLVRQME
551 FALFDMMIYS  ESEDECRKNW  QQVLDSVRKE  VAVIQPPEYN  RFANSFGHIF
601 AGGYSAGYYS  YAWAEVLSTD  AYAFAEESDD  VAATGKRFWQ  EILAVGGSRS
651 AAESFKAFRG  REPSIDALLR  QSGFDNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

m128.seq (partial)

```

1  ATGACTGACA  ACGCACTGCT  CCATTTGGGC  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AACC CGCCCT  GCAAACCGCC  ATCGCCGAAG
101 CGCGCGAACA  AATCGCCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTCT  AACCCTGTAC  CGGCATCACC  GAACGCGTCG  GCAGGATTTG
201 GGGCGTGGTG  TCGCACCTCA  ACTGCGTCCG  CGACACGCC  GAACGCGCG
251 CCGTCTATAA  CGAACTGATG  CCCGAAATCA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CAACCGCTTC  AAAACCATCA  AAAATTCCCC
351 CGAATTCGAC  ACCCTCTCCC  CCGCACAAA  AACCAAATC  AACCAAC
1  TACGCCAGCG  AAAAAGTCCG  CGAAGCCAAA  TACGCGTTCA  GCGAAACCGA
51 wGTCAAAAAA  TAyTTCcCyG  TCGGCAAwGT  ATTAACCGGA  CTGTTCCGCC
101 AAmTCAAAAA  ACTmTACGGC  ATCGGATTTA  CCGAAAAAAC  yGTCCCGCTC
151 TGGCACAAG  ACGTGCCTA  TTkTGAATTG  CAACAAAACG  GCGAaCCAT
201 AGGCGGCGTT  TATATGGATT  TGTACGCACG  CGAAGGCAAA  CGCGGCGGCG
251 CGTGGATGAA  CGACTACAAA  GGCCGCCGCC  GTTTTTCAGA  CGGCACGCTG
301 CAAYTGCCCA  CCGCCTACCT  CGTCTGCAAC  TTCGCCCCAC  CCGTCGGCGG
351 CAGGGAAGCC  CGCyTGAGCC  ACGACGAAAT  CCTCATCTC  TTCCACGAAA
401 CCGGACACGG  GCTGCACCAC  CTGCTTACC  AAGTGGACGA  ACTGGGCGTA
451 TCCGGCATCA  ACGGCGTAK  ATGGGACGCG  GTCGAACTGC  CCAGCCAGTT
501 TATGGAATA  TTCGTTTGGG  AATACAATGT  CTTGGCACAA  mTGTGAGCCC
551 ACGAAGAAAC  CGGcgTTCCC  yTGCCGAAAG  AACTCTTtGA  CAAAwTGCTC
601 GCCGCCAAA  ACTTCCAAaG  CGGCATGTT  yTsGTCCGGC  AAwTGGAGTT
651 CGCCTCTTT  GATATGATGA  TTTACAGCGA  AGACGACGAA  GGCGTCTGA
701 AAAACTGGCA  ACAGGTTT  GACAGCGTGC  GCAAAAAAGT  CGCCGTCTC
751 CAGCCGCCCG  AATACAACCG  CTTGCCTTG  AGCTTCGGCC  ACATCTTCGC
801 AGGCGGCTAT  TCCGAGCTn  ATTACAGCTA  CGCGTGGGCG  GAAGTATTGA
851 GCGCGGACGC  ATACGCGGCC  TTTGAAGAAA  GCGACGATGT  CGCCGCCACA
901 GGCAAACGCT  TTTGGCAGGA  AATCCTCGCC  GTCGGGnAT  CGCGCAGCGG
951 nGCAGAATCC  TTCAAAGCCT  TCCGCGGCCG  CGAACCGAGC  ATAGACGCAC
1001 TCTTGCGCCA  CAGCGTTTC  GACAACGCGG  TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

m128.pep (partial)

```

1  MTDNALLHLG  EEPFRDQIKT  EDIKPALQTA  IAEAREQIAA  IKAQHTTGWA
51  NTVEPLTGIT  ERVGRWGVV  SHLNCVADTP  ELRAVYNELM  PEITVFFTEI
101 GQDIELYNRF  KTIKNSPEFD  TLSPAQKTKL  NH

//

1  YASEKLREAK  YAFSETXVKK  YFPVGXVLNG  LFAQXKKLYG  IGFTEKTVPV
51  WHKDVRXYEL  QQNGEXIGV  YMDLYAREGK  RGGAWMNDYK  GRRRFSDBGTL
101 QLPTAYLVCN  FAPPVGGREA  RLSDHEILIL  FHETGHGLHH  LLTQVDELGV
151 SGINGVXWDA  VELPSQFMEN  FVWEYNVLAQ  XSAHEETGVP  LPKELXDKXL
201 AAKNFQXGMF  XVRQXEFALF  DMIIYSEDE  GRLKNWQQVL  DSVRKKVAVI
251 QPPEYNRFAL  SFGHIFAGGY  SAAXYSYAWA  EVLSADAYAA  FEESDDVAAT

```

301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHS GF DNAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
				340	350	360
g128.pep	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
m128	YASEKLREAKYAFSETXVKKYFPVGKVLNG					
				10	20	30
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQKKKLYGIGFTEKTVPVWHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSESDCELRKNWQQVLDSVRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDDDEGRKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAFRGREPS					
	280	290	300	310	320	330

```

          670      679
g128.pep  IDALLRQSGFDNAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```

a128.seq
1  ATGACTGACA  ACGCACTGCT  CCATTGGGC  GAAGAACCCC  GTTTTGATCA
51  AATCAAAACC  GAAGACATCA  AACCCGCCCT  GCAAACCGCC  ATTGCCGAAG
101 CGCGCGAACA  AATCGCCGCC  ATCAAAGCCC  AAACGCACAC  CGGCTGGGCA
151 AACACTGTCTG  AACCCCTGAC  CGGCATCACC  GAACGCGTCG  CGAGGATTTG
201 GGGCGTGGTG  TCGCACCTCA  ACTCCGTCAC  CGACACGCCC  GAACTGCGCG
251 CCGCTACAA  TGAATTAATG  CCCGAAATTA  CCGTCTTCTT  CACCGAAATC
301 GGACAAGACA  TCGAGCTGTA  CAACCGCTTC  AAAACCATCA  AAAATCCCCC
351 CGAGTTCGAC  ACCCTCTCCC  ACGCGCAAAA  AACCAAACTC  AACCACGATC
401 TGCGCGATTT  CGTCCTCAGC  GGCGCGGAAC  TGCCGCCCGA  ACAGCAGGCA
451 GAATTGGCAA  AACTGCAAAC  CGAAGGCGCG  CAACTTTCGG  CCAAATTCTC
501 CCAAAACGTC  CTAGACGCGA  CCGACGCGTT  CGGCATTTAC  TTTGACGATG
551 CCGCACCGCT  TGCCGGCATT  CCCGAAGACG  CGCTCGCCAT  GTTGGCCGCT
601 GCCGCGCAAA  GCGAAGGCAA  AACAGGCTAC  AAAATCGGTT  TGCAGATTCC
651 GCACTACCTC  GCCGTCATCC  AATACGCCGA  CAACCGCAAA  CTGCGCGAAC
701 AAATCTACCG  CGCCTACGTT  ACCGCGGCCA  GCGAGCTTTC  AGACGACGGC
751 AAATTCGACA  ACACCGCCAA  CATCGACCGC  ACGCTCGAAA  ACGCCCTGCA
801 AACCGCCAAA  CTGCTCGGCT  TCAAAAATA  CGCCGAATTG  TCGCTGGCAA
851 CCAAATGGC  GGACACCCCC  GAACAAGTTT  TAAACTTCCT  GCACGACCTC
901 GCCCGCCGCG  CCAAACCCTA  CGCCGAAAAA  GACCTCGCCG  AAGTCAAAGC
951 CTTGCCCCGC  GAAAGCCTCG  GCCTCGCCGA  TTTGCAACCG  TGGGACTTGG
1001 GCTACGCCGG  CGAAAAACTG  CGCGAAGCCA  AATACGCATT  CAGCGAAACC
1051 GAAGTCAAAA  AATACTTCCC  CGTCGGCAAA  GTATTAAACG  GACTGTTCGC
1101 CCAAATCAAA  AAATCTACG  GCATCGGATT  TACCGAAAAA  ACCGTCCCCG
1151 TCTGGCACAA  AGACGTGCGC  TATTTTGAAT  TGCAACAAA  CGGCGAAACC
1201 ATAGGCGGCG  TTTATATGGA  TTTGTACGCA  CGCGAAGGCA  AACGCGGCGG
1251 CGCGTGGATG  AACGACTACA  AAGGCCGCCG  CCGTTTTTCA  GACGGCACGC
1301 TGCAACTGCC  CACCGCTTAC  CTCGTCTGCA  ACTTACCCCC  GCCCGTCGGC
1351 GGCAAAGAAG  CCCGCTTGAG  CCATGACGAA  ATCCTCACCC  TCTTCCACGA
1401 AACCGGACAC  GGCCTGCACC  ACCTGCTTAC  CCAAGTCGAC  GAACTGGGCG
1451 TATCCGGCAT  CAACGGCGTA  GAATGGGACG  CAGTCGAACT  GCCCAGTCAG
1501 TTTATGGA  ATTTCTGTTG  GGAATACAAT  GTCTTGGCGC  AAATGTCCGC
1551 CCACGAAGAA  ACCGGCGTTC  CCCTGCCGAA  AGAATCTTTC  GACAAAATGC
1601 TCGCGCCAA  AAATTTCCAA  CGCGAATGT  TCCTCGTCCG  CCAAATGGAG
1651 TTCGCCCTCT  TTGATATGAT  GATTTACAGC  GAAGACGACG  AAGGCCGTCT
1701 GAAAACTGG  CAACAGGTTT  TAGACAGCGT  GCGCAAAGAA  GTCGCCGTCG
1751 TCCGACCGCC  CGAATACAAC  CGCTTCGCCA  ACAGCTTCGG  CCACATCTTC
1801 GCAGGCGGCT  ATTCCGCAGG  CTATTACAGC  TACGCGTGGG  CGGAAGTATT
1851 GAGCGCGGAC  GCATACGCCG  CCTTTGAAGA  AAGCGACGAT  GTCGCCGCCA
1901 CAGGCAAACG  CTTTGGCAG  GAAATCCTCG  CCGTCGGCGG  ATCGCGCAGC
1951 GCGGCAGAAT  CCTTCAAAGC  CTTCCGCGGA  CGCGAACCGA  GCATAGACGC
2001 ACTCTTGCGC  CACAGCGGCT  TCGACAACGC  GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG  EEPFRDQIKT  EDIKPALQTA  IAEAREQIAA  IKAQHTGWA
51  NTVEPLTGIT  ERVGRWGVV  SHLNSVTDTP  ELRAAYNELM  PEITVFTEI
101 GQDIELYNRF  KTIKNSPEFD  TLSHAQKTKL  NHDLRDFVLS  GAELPPEQQA
151 ELAKLQTEGA  QLSAKFSQNV  LDATDAFGIY  FDDAAPLAGI  PEDALAMFAA
201 AAQSEKGTGY  KIGLQIPHYL  AVIQYADNRK  LREQIYRAYV  TRASELSDDG
251 KFDNTANIDR  TLENALQTAK  LLGFKNYAEL  SLATKMADTP  EQVLNLFHDL
301 ARRAKPYAEK  DLAEVKAFAR  ESLGLADLQP  WDLGYAGEKL  REAKYAFSET
351 EVKKYFPVGK  VLNGLFAQIK  KLYGIGFTEK  TVPVWHKDVR  YFELQONGET
401 IGGVYMDLYA  REGKRGGAWM  NDYKGRRRFS  DGTLLQLPTAY  LVCNFTPPVG
451 GKEARLSHDE  ILTLFHETGH  GLHLLTQVD  ELGVSGINGV  EWDAVELPSQ
501 FMENFVWEYN  VLAQMSAHEE  TGVPLPKELF  DKMLAAKNFQ  RGMFLVRQME

```

551 FALFDMMIYS EDDEGRILKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
 651 AAESFKAFRG REPSIDALLR HSGFDNAA*

m128/a128 66.0% identity in 677 aa overlap

	10	20	30	40	50	60
m128.pep	MTDNALLHLGEEPFRDQIKTEDIKPALQTAIAEAREQIAAIKAQTHGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPFRDQIKTEDIKPALQTAIAEAREQIAAIKAQTHGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m128.pep	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130					
m128.pep	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL					
	250	260	270	280	290	300
				140	150	
m128.pep	-----YASEKLREAKYAFSETXVKKYFPVVGX					
	:					
a128	ARRAKPYAEKDLAEVKAFARESGLADLQPWDLGAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
	160	170	180	190	200	210
m128.pep	VLNGLFAQXKKLYGIGFTEKTVPVWHKDVRYXELQQNGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	220	230	240	250	260	270
m128.pep	NDYKGRRRFSDGTLQLPTAYLVCNFPVVGGEARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	280	290	300	310	320	330
m128.pep	ELGVSGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
	340	350	360	370	380	390
m128.pep	XGMFXVRQXEFALFDMMIYSEDDEGRILKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGRILKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600



```

      400      410      420      430      440      450
m128.pep  AGGYSAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAESFKAFRG
          610      620      630      640      650      660

      460      470
m128.pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 487>:

g128-1.seq (partial)

1	ATGATTGACA	ACGCAGTGCT	CCACTTGGGC	GAAGAACCCC	GTTTAAATCA
51	AATCAAAACC	GAAGACATCA	AATCCGCGCT	CCAAACCCGC	ATCGCCGGAAG
101	CGCGCGGACA	AATGCGCGCC	GTCAAAGCGC	AAACGCACAC	CGGCTGGGCG
151	AACACCGTCG	AGCGTCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTCTGT	TCCCATCTCA	ACTCCGTGCT	CGACACGCCCT	GAACCTGCGCG
251	CCGTCTATAA	CGAAGTATG	CACTGAAATCA	CCGTCTTCCC	CACCGAAATC
301	GGACAAATCA	TCGAACTGTA	CAGCCGCTTC	AAACCATCA	AAATTTCCCC
351	CGAATTTGCA	ACGCTTTCCC	CCGCACAAAA	AACCAAGCTC	GATCACGACC
401	TGCGCGATT	CGTATTGAGC	GGCGCGGAAC	TGCGCGCCGA	ACGGCAGGCA
451	GAACGTGGCA	AATGTCAAAC	CGAAGGCGCG	CAACTTTCCG	CCAAATTTCTC
501	CCAAAAAGTC	CTAGACGGCA	CCGACGCGTT	CGGATTTTAC	TTTGACGATG
551	CCGCACCGCT	TGCCGGCATT	CCCGAAGACG	CGCTCGCCAT	GTTTGGCCGCC
601	GCGCGCAAAA	GCGAAGGCAA	AACAGGTTAC	AAAATCGGCT	TGCAGATTCC
651	GCACTACCTT	CGCGTTATCC	AATACGCGCG	CAACCGCGAA	CTGCGCGCAAC
701	AAATCTACCG	GCCCTAGCTT	ACCGTGCCCA	CGCAACTTTC	ATAGCAGCGGC
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCATTGAA
801	AACCGCCAAA	CTGCTCGGCT	TTAAAAATTA	CGCGGAATTG	TCGCTGGCAA
851	CCAAAATGGC	GGACACGCC	GAACAGGTTT	TAAACTTCTC	GCACGACCTC
901	GCCCGCCGCG	CCAAACCCCTA	CGCGCAAAAA	GAACTCGCCG	AAGTCAAAAGC
951	CTTCGCCCGC	GAACACCTCG	GTCTCGCCGA	CCCGCAGCCG	TGGGACTTGA
1001	GCTACGCCGG	CGAAAAATCG	CGCGAAGCCA	AATACGCAT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGGCAA	GTTCTGGCAG	CCCTGTTCCG
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	CGCGAAAAAA	ACCGTTCCCG
1151	TCTGGCACAA	AGAGCTGGCG	TATTTTGAAT	TGCAACAAAA	CGGCAAAACC
1201	ATCGCGCGCG	TTTATATGGA	TTGTACGCA	CGCGAAGCA	AACCGCGCGG
1251	CGCGTGGATG	AACAGTACA	AAAGCGCCGC	CGGTTTGGCC	GACGCGACGC
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	GCCCGTGGCG
1351	GGCAAGAAG	CGCGTTTAAG	CCACGACGAA	ATCTCACCCC	TCTTCCACGA
1401	AACCGGCCAC	GGACTGCACC	ACCTGCTTAC	CCAAGTGGAC	GAACCTGGCG
1451	TGTCGCGCAT	CACCGCGGTA	AAA		

This corresponds to the amino acid sequence <SEQ ID 488; ORF 128-1.ng>:

g128-1.pep (partial)		g128-2.pep (partial)				g128-3.pep (partial)			
1	MIDNALHLHG	EPRFNQIKT	EDIKPAVQTA	IAEARGQIAA	VKAQTHTQWA				
51	NTVERLTGIT	EVERGRINGVV	SHLSNVVDTP	ELRAVYINAA	PEITVFTTTE				
101	GQDIELYNRF	KTIKNSPEFA	TLSPAQKTKL	DHDLRDFVLS	GAELPPERQA				
151	ELAKLQTEGA	QLSAKFSQNV	LDATDAFGIY	FDDAAPLAGI	PEDALAMFAA				
201	AAQSEKGTGY	KIGLQIPHYL	AVIQYAGNRE	LREQIYRAYV	TRASELSNDG				
251	KFDNTANIDR	TLENALKTAK	LLGFKNYAEL	SLATKMADTP	EQVLNLFHDL				
301	ARRAKPYAEK	DLAEVKAFAR	EHLGLADPQP	WDLSYAGEKL	REAKYFASFD				
351	EVKKYFPVGK	VLAGLFAFAK	KLYGIGFAEK	TVPVWHKDVR	YFELQQNGKT				
401	IGGVYMDLYA	REGKRGGAWM	NDYKGRRRFA	DGTIQLPLTA	LVCNFAPPVG				
451	GKEARLSHDE	ILTLFHETGH	GLHHLLTOVD	ELGVSGINGV	K				

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 489>:

m128-1.seq

```
1 ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTTGATCA
51 AATCAAACC GAAGACATCA AACCGCCCT GCAAAACGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGC AACCCCTGAC CGGCATCACC GAACGCGTCG CAGGATTTTG
```

```

201 GGGCGTGGTG TCGCACCTCA ACTCCGTCGC CGACACGCCC GAACGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAAA AACCAAACTC AACACGATC
401 TGCGCGATT TCGTCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATGGCAA AACTGCAAC CGAAGGCGCG CAACTTTCG CCAAATTCCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTC TTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 AACTACCTC GCCGTCATCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAAGTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTC TCGCTGGCAA
851 CCAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 CCCC GCCG CCAAACCTA CGCCGAAAAA GACCTCGCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTGA ACCTCGCCGA TTGCAACCG TGGGACTTGG
1001 GGTACGCCAG CGAAAACTG CGCGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCCGCAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGCGC TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTTCA GACGCGACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCGCCCC ACCCGTCGGC
1351 GGCAGGGAAG CCCGCTGAG CCACGACGAA ATCCTCATCC TCTTCCACGA
1401 AACCGGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACGCGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CGGTGGAAT GCCAGCCAG
1501 TTTATGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCAC AAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCGGCCAA AAATCTCAA CGCGCATGT TCCTCGTCCG GCAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAAAA GTCGCCGTC
1751 TCCAGCGGCC CGAATACAAC CGCTTCGCTT TGAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAAG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAACG CTTTGGGAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGC GCGAACCAG GCATAGACGC
2001 ACTCTGCGC CACAGCGGTT TCGACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pep.

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA
51 NTVEPLTGIT ERVGRWGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLQP WDLGYASEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHHLTQVD ELGVSGINGV EWDDELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRKKNW QQVLDVSRKK VAVIQPPEYN RFALSFHGIF
601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

```

m128-1/g128-1 94.5% identity in 491 aa overlap

```

          10      20      30      40      50      60
g128-1.pep MIDNALLHLGEEPRFNQIKTEDIKPAVQTAAEARGQIAAVKAQHTGTGWANTVERLTGIT
          |||
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90     100     110     120
g128-1.pep ERVGRWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
          |||
m128-1      ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

```

370

	130	140	150	160	170	180
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
	190	200	210	220	230	240
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV					
	190	200	210	220	230	240
	250	260	270	280	290	300
g128-1.pep	TRASELSNDGKFDNTANIDRTLLENALKTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL					
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMDTPEQVLNFLHDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDLSYAGEKLREAKYAFSETEVKKYFPVGK					
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPQWDLGVAEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
	370	380	390	400	410	420
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQQNGKTIGGVYMDLYAREGKRGGAWM					
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
	490					
g128-1.pep	ELGVSGINGVK					
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

```

1   ATGACTGACA ACGCACTGCT CCATTGGGCG GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCG GAACTGCGCG
251 CCGCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCCAGATC
401 TGC GCGATT TCGTCTCAGC GCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAA CGAAGGCGCG CAACTTTCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACGCAAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCAAAA CTGCTCGGCT TCAAAAATA CGCCGAATG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCGC CCAAACCTTA CGCCGAAAAA GACCTCGCGG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAAATG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCGC
1101 CCAAAATCAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCAGAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACCGGCGCG

```

```
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACGCGCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAACCTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCCGTG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCAGCGCAG
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGC GC CACAGCGGCT TCGACAACGC GGCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

a128-1.pep

```
1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWGA
51 NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKYPFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQQNGET
401 IGGVYMDLYA REGKRGGAWM NDYKRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELP SQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDDMMIYS EDDEGRLEKNW QQVLDVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAFAESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*
```

m128-1/a128-1 97.8% identity in 677 aa overlap

```
10 20 30 40 50 60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
|||||
m128-1 MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
10 20 30 40 50 60

70 80 90 100 110 120
a128-1.pep ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
|||||
m128-1 ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
70 80 90 100 110 120

130 140 150 160 170 180
a128-1.pep TLSHAQTKL NHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
|||||
m128-1 TLSPAQTKL NHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
130 140 150 160 170 180

190 200 210 220 230 240
a128-1.pep FDDAAPLAGI PEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV
|||||
m128-1 FDDAAPLAGI PEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
190 200 210 220 230 240

250 260 270 280 290 300
a128-1.pep TRASELSDDGKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
|||||
m128-1 TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
250 260 270 280 290 300

310 320 330 340 350 360
a128-1.pep ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKYFPVGK
|||||
```

```
m128-1      ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
              310      320      330      340      350      360

              370      380      390      400      410      420
a128-1.pep   VLNGLFAQIKKLYGIGFTEKTPVWVKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
              |||
m128-1       VLNGLFAQIKKLYGIGFTEKTPVWVKDVRYFELQQNGETIGGVYMDLYAREGKRGGAWM
              370      380      390      400      410      420

              430      440      450      460      470      480
a128-1.pep   NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
              |||
m128-1       NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILTLFHETGHLHLLTQVD
              430      440      450      460      470      480

              490      500      510      520      530      540
a128-1.pep   ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              |||
m128-1       ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
              490      500      510      520      530      540

              550      560      570      580      590      600
a128-1.pep   RGMFLVRQMEFALFDMMIYSEDDGRLKNWQQVLDVRKEVAVVRPPEYNRFANSFGHIF
              |||
m128-1       RGMFLVRQMEFALFDMMIYSEDDGRLKNWQQVLDVRKKVAVIQPPEYNRFALSFGHIF
              550      560      570      580      590      600

              610      620      630      640      650      660
a128-1.pep   AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              |||
m128-1       AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
              610      620      630      640      650      660

              670      679
a128-1.pep   REPSIDALLRHSGFDNAAX
              |||
m128-1       REPSIDALLRHSGFDNAVX
              670
```

a128-1/ P44573

sp|P44573|OPDA_HAEM OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlc) homolog
- Haemophilus influenzae (strain Rd KW20)
>gi|1573174 (U32706) oligopeptidase A (prlc) [Haemophilus influenzae Rd] Length = 681
Score = 591 bits (1507), Expect = e-168
Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)

Query: 4 NALLHLGEBEPRFDQIKTEDIKPALQTXXXXXXXXXXXXXTHTGWANTVEPLTGITERV 63
N LL++ P F QIK E I+PA++ H W N + PLT +R+
Sbjct: 5 NPLLNIQGLPPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHFTWENFILPLTETNDRL 64

Query: 64 GRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFTIKNSPEFDTLS 123
R W VSHLNSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S
Sbjct: 65 NRAWSPVSHLNSVKNSTELREAYQTCLPLLSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

Query: 124 HAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183
AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++
Sbjct: 125 IAQKKAIENSLRDFELSGIGLSEKQQRYSGEIVARLSELNSQFSNNVLDATMGWEKLIEN 184

Query: 184 AAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHVLAVIQYADNRKLRQIYRAYVTRA 243
A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE++YRAY TRA
Sbjct: 185 EAELAGLPESALQAAQSAESKGLKGYRFTLEIPSYLPVMTYCENRALREEMYRAYATRA 244

Query: 244 SELSDD-GKFDNTANIDRTLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDLAR 302
SE + GK+DN+ ++ L ++ AKLLGF Y ELSLATKMA+ P+QVL+FL LA
Sbjct: 245 SEQGPNGAKWDNSKVMEEILTLRVELAKLLGFNTYTELSLATKMAENPQQVLDLFLDLAE 304

Query: 303 RAKPYAEKDLAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGKVL 362
RAKP EK+L E+K + + G+ +L PWD+G+ EK ++ YA ++ E++ YFP +V+
Sbjct: 305 RAKPQGEKELQELKGYCEKEFGVTELPWDIGFYSEKQKQHLAYAINDEELRPYPENRVI 364

Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QQNETIGGVYMDLYAREGKRGAWM 420
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGAWM
 Sbjct: 365 SGLFELIKRIFNIRAVERKGVDTWHKDVRFFDLIDENDQLRGSFYLDLYAREHKRGAWM 424

Query: 421 NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEIXXXXXXXXXXXXXXQVD 480
 +D GR+R DG+++ P AYL CNF P+G K A +H+E+ Q+D
 Sbjct: 425 DDCIGRKRKLDGSIETPVAYLTCNFNAPIGNKPALFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSGINGVENDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ 540
 V+GINGV WDAVELPSQFMEN+ WE LA +S H ETG PLPKE ++L AKNFQ
 Sbjct: 485 VSDVAGINGVPWDAVELPSQFMENWCWEEALAFISGHYETGEPLPKEKLTQLLKAKNFQ 544

Query: 541 RGMFLVRQMEFALFDMMIYSEDDEGRLEKNWQQVLDVSRKEVAVVRPPEYNRFANSFGHIF 600
 MF++RQ+EF +FD ++ D + L SV+ +VAV++ ++ R +SF HIF
 Sbjct: 545 AAMFILRQLEFGIFDFRLHHTFDAEKTNQILDTLKSVKSQVAVIKGVWDWARAPHFSFHF 604

Query: 601 XXXXXXXXXXXXXWAEVLSADAYAAFEESDDV-AATGKRFWQEILAVGGSRSAAESFKAFR 659
 WAEVLSADAY+ FEE TKG F EIL GGS E FK FR
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYSRFEEGIFNPITGKSFLDEILTRGGSSEPMELFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676
 GREP +DALLRH G N
 Sbjct: 665 GREQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq
 1 ATGCTTTCAC CTCCTCGGCG TAAACGGCG GCACATCAAT CAAGCCGTCT
 51 TTCATTTGCG TCGGAAAAA ATGCGGCGTG TTGCCGTGAT CAAAATCAAT
 101 ATCGTGCAGC ATCCAGCCCA AATCGCGGTT TGCCTCGCTT TCCGATAACG
 151 CCGACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTCGCC ATTTGCCCTT
 201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GCGGTCGAA TCCTGTTTCA
 251 TCCGGACAAA CGCGTTGGCA GTCGAAAAAT CCGGCCGGCC GTGTCAAATA
 301 ATGCGTTACT TTGGCCGGGT CTTGTCCTTT GTAAGCGGCG GTCTTTTTTT
 351 GCGCGCCATC CGCATCTGTT TGGGCGCATG GCAAACGGCG GCTGCCGTAC
 401 AATCAAAATG TTTGGCGATT TCATGCAGAC AGGCATCCGG ATGCCGCCCG
 451 ACATATCGAG CCGGTTTTTG CCTATCCGAT TTGGCGGCAT TTAGGCCGGT
 501 AACTTGA

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep
 1 MLSPPRRKA AHQSSRLSFA CGKNAACCRD QNQYRAASSP NRGLPRFPIT
 51 PTAAAVHPYP RFRHLPFQAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI
 101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP
 151 TYRAGFCLSD LAAFRPVT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)
 1 ..TATCTGCGCT TTTACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA
 51 ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG
 101 GAAAATTCGG CCGGCTGTGT CAAATAATGC GTTACTTTGG CCGGTCCTTG
 151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCG GTTATCCCA TCTGTTTGAG
 201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTTAT
 251 GCAGATAGGC ATCCGGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCGCTA
 301 TCCGATTTGA CGGCATTTAG ACCGTAAC TGA

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)
 1 ..YLRPHYLPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL
 51 FFFVSGGLFLR VIPICLSAXQ MVAAVQSKCL AISCRXASGC CPTYXAGFCL
 101 SDLTAFRPVT *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 129 shows 79.1% identity over a 110 aa overlap with a predicted ORF (ORF 129.ng) from *N. gonorrhoeae*:

m129/g129

						10	20	30
m129.pep						YLRFHYPFQAAGIGTEQVAVKSCFIQINT		
						:		
g129	RDQNQYRAASSPNRGLPRFPIPTAAAVHPYPRFRHL	PFQAAGIGAEQA	AVESCFIRTNA					
	30	40	50	60	70	80		
		40	50	60	70	80	90	
m129.pep	LVVGKFGRLCQIMRYFGRVLFVSGGLFLRVIPICLSAXQMVA	AVQSKCLAISCRXASGC						
g129	LAVGKSGRPCQIMRYFGRVLSFVSGGLFLRAIRICLGAWQTAA	AVQSKCLAISCRQASGC						
	90	100	110	120	130	140		
		100	110					
m129.pep	CPTYXAGFCLSDLTAFRPVTX							
g129	RPTYRAGFCLSDLA	AFRPVTX						
	150	160						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

a129.seq (partial)

1	TATCTGCGCT	TTC	ACTATTT	GCCCTTTCAG	GCTGCGGGCA	TAGGGACGGA
51	ACAGGTAGCG	GTCAAATCCT	GTTTCATCCA	AATAAACACG	TTGGTAGTCG	
101	GAAAATTCGG	CCAGCTGTGT	CAAATAATGC	GTTACTTTGG	CCGGGTCTTG	
151	TTCTTTGTAA	GTGGTGGTCT	TTTTTTGCGC	GTTATCCCCA	TCTGTTTGAG	
201	TGCATAGCAA	ATGGTGGCTG	CCGTACAATC	AAAATGTTTG	GCGATTTCAT	
251	GCAGATAGGC	ATCCTGGTGT	TGCCCAACAT	ATTGAGCCGG	TTTTTGCCTA	
301	TCCGATTGTA	CGGCATTAG	ACCGGTAAC	TGA		

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

a129.pep (partial)

1	YLRFHYPFQ	AAGIGTEQVA	VKSCFIQINT	LVVGKFGQLC	QIMRYFGRVL
51	FFVSGGLFLR	VIPICLSA*Q	MVA	AVQSKCL	AISCR*ASWC
101	SDLTAFRPVT	*			

m129/a129 98.2% identity in 110 aa overlap

						10	20	30	40	50	60
m129.pep	YLRFHYPFQAAGIGTEQVAVKSCFIQINTLVVGKFGRLCQIMRYFGRVLFVSGGLFLR										
a129	YLRFHYPFQAAGIGTEQVAVKSCFIQINTLVVGKFGQLCQIMRYFGRVLFVSGGLFLR										
	10	20	30	40	50	60					
		70	80	90	100	110					
m129.pep	VIPICLSAXQMVA	AVQSKCLAISCRXASGCCPTYXAGFCLSDLTAFRPVTX									
a129	VIPICLSAXQMVA	AVQSKCLAISCRXASWCCPTYXAGFCLSDLTAFRPVTX									
	70	80	90	100	110						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

g130.seq

1	ATGAAACAAC	TCCGCGACAA	CAAAGCCCAA	GGCTCTGCAC	TGTTTACCCT
51	TGTGAGCGGT	ATCGTTATTG	TTATTGCAGT	CCTTTATTTC	CTGATTAAGC
101	TGGCGGGCAG	TGGATCGTTC	GGCGATGTCG	ATGCCACTAC	GGAAGCGGCA
151	ACGCAGACCC	GCATCCAGCC	TGTCGGACAA	TTGACGATGG	GTGACGGCAT
201	CCCCGTGCGC	GAACGCCAAG	GCGAACAGAT	TTTCGGCAAA	ATCTGTATCC

```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGCGGACT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCGA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAAGCTC AAACGGGCGA TTACCTACAT GGCGAATAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAGGTG TGCCACGGCG GTTCGATTCC
651 CCGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGCAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
  1 MKQLRDNKAQ GSALFTLVSG IVIVIAVLVF LIKLAGSGSF GDVDATTEAA
 51 TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAADLTDQEL KRAITYMANK
151 SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAAPAVGVGD
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
  1 ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CGGCGGACAG
 51 CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACCGC
101 GTATCGGCAA GGCTTCGATA CCTTGTTCGA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAAGCTT
201 AAACGGGCGA TTACTTACAT GGCGAACAAA AGCGGCGGTT CTTTCCCGAA
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACCCC TGCGGTCGGC GTTGACGGTA AAAAAGTCTT CGAAGCAACC
401 TGTCAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCG GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGCACA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAAG CGGCAATGCA
551 GGTTTGAGCG ATGACGAAGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
  1 ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQGFDL LFOHALNGFN
 51 AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAPAEAE KAEDKGAAPA VGVDGKKVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPKXG NAGLSDEVK AAVDYMANKS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng) from *N. gonorrhoeae*:

```

m130/g130
          10      20      30
m130.pep          GEQIFGKICIQCHAADSNVPNAPKLEHNGD
                  |||
g130      DATTEAATQTRIQPVGQLTMDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
          50      60      70      80      90     100

          40      50      60      70      80      89
m130.pep      XAPRI-QGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
                  |||
g130      WAPRIAQGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFPNPDEAAP
          110     120     130     140     150     160

```

376

```

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||||||
g130      ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDEVKAAVDYMANQSGAKFX
          |||||||
g130      KKDDWAPRIKKGKETLHKHALEGFNAMPKGGNAGLSDEVKAAVDYMANQSGAKFX
          230      240      250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130.seq
1  ATGAAACAAC  TCCGCGACAA  CAAAGCCCAA  GGCTCTGCAC  TGTTTACCCT
51  TGTGAGCGGT  ATCGTTATTG  TTATTGCAGT  CCTTTATTTC  CTGATTAAAG
101 TGGCGGGCAG  CGGCTCGTTC  GGCATGTCTG  ATGCCACTAC  GGAAGCAGCA
151 ACGCAGACCC  GTATCCAGCC  TGTCGGACAA  TTGACGATGG  GCGACGGCAT
201 CCCCCTCGGC  GAACGCCAAG  GCGAACAGAT  TTTCCGGCAA  ATCTGTATCC
251 AATGCCACGC  GCGGCAGAGC  AATGTGCCGA  ACGCTCCGAA  ACTGGAACAC
301 AACGGCGATT  GGGCGCGCG  TATCGCGCAA  GGCTTCGATA  CCTTGTTCCT
351 ACACGCGCTG  AACGGCTTTA  ACGCCATGCC  TGCCAAAGGC  GGTGCGGTAG
401 ACCTGACCGA  TCAGGAACCT  AAACGGGCGA  TTAATTACAT  GGCGAACAAA
451 AGCGGCGGTT  CTTTCCCGAA  TCCTGATGAG  GCTGCGCCTG  CCGACAATGC
501 CGCTTCAGGA  ACAGCTTCTG  CTCCTGCCGA  TAGTGAGCT  CCGGCAGAAG
551 CGAAGGCAGA  AGACAAGGGT  GCGGCAGCCC  CTGCGGTCGG  CGTTGACGGT
601 AAAAAAGTCT  TCGAAGCAAC  CTGTCAGGTG  TGCCACGGCG  GTTCGATTCC
651 CCGTATTCCC  GGCATAGGCA  AAAAAGACGA  TTGGGCACCG  CGTATCAAAA
701 AAGGCAAAGA  AACCTTGCAC  AAACACGCC  TTGAAGGCTT  TAACGCGATG
751 CCTGCCAAG  GCGGCAATGC  AGGTTTGAGC  GATGACGAAG  TCAAAGCGGC
801 TGTGACTAT  ATGGCAAACC  AATCCGGTGC  AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130.pep
1  MKQLRDNKAQ  GSALFTLVSG  IVIVIAVLYF  LIKLAGSGSF  GDVDATTEAA
51  TQTRIQPVGQ  LTMGDGIPVG  ERQGEQIFGK  ICIQCHAADS  NVPNAPKLEH
101 NGDWAPRIAQ  GFDTLFQHAL  NGFNAMPAKG  GAVDLTDQEL  KRAITYMANK
151 SSGSFNPDE  AAPADNAASG  TASAPADSAA  PAEAKAEDKG  AAAPAVGVDG
201 KKVFEATCQV  CHGGSIPGIP  GIGKKDDWAP  RIKKGKETLH  KHALEGFNAM
251 PAKGNAGLS  DDEVKAAVDY  MANQSGAKF*

```

m130/a130 97.6% identity in 206 aa overlap

```

          10      20      30
m130.pep  GEQIFGKICIQCHAADSNVPNAPKLEHNGD
          |||||||
a130      DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
          50      60      70      80      90      100

          40      50      60      70      80      89
m130.pep  XAPRI-QGFDTLFQHALNGFNAMPAKGGADLTDQELKRAITYMANKSGGSFNPDEAAP
          |||||
a130      WAPRIAQGFDTLQHALNGFNAMPAKGGAVDLTDQELKRAITYMANKSGGSFNPDEAAP
          110      120      130      140      150      160

          90      100      110      120      130      140
m130.pep  ADNAASGTASAPADSAAPEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||||||
a130      ADNAASGTASAPADSAAPEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130.pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDEVKAAVDYMANQSGAKFX

```

a130
KKDDWAPRIKKGKETLHKHALEGFNAMPAGGNGAGLSDDVEKAAVDYMANQSGAKFX
230 240 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 505>:

```
g132.seq
1  ATGGAAGCCT TCAAAACCTT AATTGGATT ATTAATATTA TTTCCGCTTT
51  GGCCAGTCATT GTGTTAGTAT TGTCTCAACA CGGCAAAAGGC GCGGATGCCG
101 GCGCGACCTTC CGGATCGGGA AGCGCGACGC CGCAAGCGCT ATTTCGGTCT
151 GCCGCGCAACG CCAACTTcct CAgccGCTCG AccGccGTTG CAGCAACAtt
201 tttcttTGca acctgcAtgg gctatggTgt atattcacac CCACACGACA
251 AAACACGGTT TGGACTtcag caacataCGA CAGACTCAGC AagcACCCAA
301 ACCcgtAAGC AATACCGCAc CTTTCGCCCC TGTCCTCAG CAGCAGAAAT
351 AACAgTTTTT CAAATgccga caTGtgta
```

This corresponds to the amino acid sequence <SEQ ID 506; ORF 132.ng>:

g132.pep

```
1  MEAFKTLIWI INIISALAVI VLVLLQHKGK ADAGATFGSG SGSAQGVFGS
51 AGNANFLSRS TAAVATFFFA TCMGYGVYSH PHDKTRFGLQ QHTTDSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 507>:

```
m132.seq (partial)
      1 ATGGAACCTT TCAAAACCTT AATTGGATT GTTAATTTAA TTTCCGCTTT
     51 GGCCGTCTTC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
    101 GCGCGACTTT CGGA...
```

This corresponds to the amino acid sequence <SEQ ID 508; ORF 132>:

```
m132.pep (partial)
      1 MEPFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 132 shows 89.5% identity over a 38 aa overlap with a predicted ORF (ORF 132.ng) from *N. gonorrhoeae*:

m132/g132

10 20 30

m132.pep MEPFKTLIWIIVNLISALAVFVLVLLQHGKGADAGATFG

|| |||||:|:|||||:|:|||||

g132 MEAFKTLIWIINIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS

10 20 30 40 50 60

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 509>:

```

a132.seq
  1  ATGGAAGCCT  TCAAAACCCT  AATTGGATT  GTTAATATAA  TTCCGCTTT
51  GGCGTCATC  GTGTTAGTAT  TGCTCCAACA  CGGCAAAGGC  GCGGATGCCG
101 GCGCGACTTT  CGGATCGGGA  AGCGGCAGCG  CGCAAGCGGT  ATTCGGTCTT
151 GCCGGCAACG  CTAACTTCCT  CAGCCGCTCG  ACCGCGGTG  CAGCAACATT
201 TTTCTTTGCA  ACCTGCATGg  GCTATGGTGT  ATATTCACAC  CCACACGACA
251 AAACACGGTT  TGGACTTCAG  CAACGTACAA  CAAACTCAGC  AAGCACCCAA
301 ACCCGTAAGC  AATACCGAAC  CTTCTGCCCC  TGTTCTCAG  CAGCAGAAAT
351 AACAGTTTTT  CAAATGCCGA  CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 510; ORF 132.a>:

a132.pep
1 MEAFKTLIWI VNIISALAVI VLVLQHGKG ADAGATFGSG SGSAQGVFGS
51 AGNANFLSRS TAVAAFFFA TCMGYGVYSH PHDKTRFGLQ QRTTNSASTQ
101 TRKOYRTFCP CSSAAEITVF QMPTW*

m132/a132 92.1% identity in 38 aa overlap

	10	20	30	
m132.pep	MEPFKTLIWIIVNLISALAVFVLVLLQHGKGADAGATFG			
	: :			
a132	MEAFKTLIWIIVNIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

g134.seq

```

1  ATGTCCCAAG AAATCCTCGA CCAAGTGC GC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCCGATGCGG GTAAAACCA C GCTGACCGAA AACTGCTGC
101 TGTTCGCGG  CGCGATTCAA AGCGCAGGCA CGGTGAAAGG TAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTGCA CTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CAGTGGACAG CGCCTTGATG GTCATCGACG CGGCAAAGG
351 CGTGGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCGATA
401 CGCCGATTGT TACCTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCT
451 TTGGAACCTT TGGACGAAGT GGAAGACATC CTGCAAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTCAAGGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCCTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATAAAC AATCCCGAAT TGGAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAAG
701 CGGCTTCCAA CGAATTTAAT CTCGacgaAT TTCTCGccgG CGAACTCACG
751 CCAGTGTCTT TCGGCTCTGC GATTAACAAC TTCGGCATTC AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CACCCGCACC GAAACCGCGC GACGCGACCA
851 TGCGCATGGT CGGGCCGGAC GAGCCGAAAT TTTCCGATT TATCTTTAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATCG CCTTCTTGCG
951 CGTCTGTCTC GGTAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTAG TAACCTTCAT GTCGCACGAC
1051 CGCGAACTGG CGGAAGAAGC CTACGCCGGC GACATCATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGG
1151 CGTTTACCGG CATCCCATTC TTCGCGCCCG AACTGTTCCG CAGCGTCCGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAAC TG CAAAAGGTT TGCAACAAC T
1251 CGGCGAAGAA GGTGCGGTT C AAGTATTCAA ACCGATGAGC GGC GCGGATT
1301 TGATTTTGGG TCGGTCGCG GTGTGTCAGT TTGAAGTCGT AACCTCACGC
1351 CTGCGCAACG AATACGGCGT GGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAATG GCGGAATTG
1451 AAAAAGCCAA CGCAGGCAAC CTCGCCATG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTTGGG TTGACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCAACA TTCGGTCAAA CTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

g134.pep

```

1  MSQEILDQVR RRRTFAIISH PDAGKTLTE KLLLFSGAIQ SAGTVKGKKT
51  GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLDTTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDPPIVTFM NKYDREVRDS
151 LELLDEVEDI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGIN NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATMRMVGPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELAEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL OKGLQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

m134.seq

```

1  ATGTCCCAAG AAATCCTCGA CCAAGTGC GC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCTGACGCAG GTAAAACCA C GTTGAAGTGA AACTCTTG
101 TGTTCGCGG  CGCGATTCAA AGCGCGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACTTCCGA CTGGATGGAA ATCGAGAAGC AGCGCGGCAT

```

```

201 TTCCGTGGCA TCAAGTGTGA TGCAGTTCGA TTACAAAGAC CACACCGTCA
251 ACCTCTTGGA CACGCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CCGTGGACAG CGCATTAATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAGCG CAAACCATCA AGCTCTTAAA CGTCTGCCGC CTGCGCGATA
401 CACCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAAC TTT TGGACGAAGT GGAAAACATT TTA AAAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA TGA AATTTAT CTCTTTGAAG CTGGCGGCGA ACGCCTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCTGAAT TGGAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTTAAT CTCGACGAAT TCCTCGCCGG CGAACTCACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CGCCCGCGCC GAAACCGCGC GACGCGACCG
851 TACGTATGGT CGAGCCGGAC GAGCCGAAGT TTTCCGGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CTTTCTTGCG
951 CGCTGCTCC GGCAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TTACCTTCAT GTCGCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAAC TGG
1151 CGTTCACCGG CATCCCATTC TTCGCACCCG AACTGTTCCG CAGCGTACGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAAC TCAAAAAGGCT TGCAACAGCT
1251 CGGCGAAGAA GGCGCGGTGC AGGTGTTCAA ACCGATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTGTCAGT TTGAAGTCGT TACCTCGCGC
1351 CTCGCCAAGC AATACGGCGT AGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAAGT GCTGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACGCGT GAATTGGA CTCACGCAAG AACGTTGGCC
1551 GGACATCGTG TTCCACGAAA CACGCGAACA TTCGGTCAAA CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

m134.pep

```

1 MSQEILDQVR RRRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWME IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSED TYR
101 VLTAVDSALM VIDAAGVEA OTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151 LELLDEVENI LKIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKID NPELEQRFPL EIQQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLOFEVVTSR
451 LANEYGVAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng) from *N. gonorrhoeae*:

m134/g134

```

          10      20      30      40      50      60
m134.pep MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
          10      20      30      40      50      60
g134      MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD
          70      80      90      100     110     120
m134.pep IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSED TYRVLTA VDSALMVIDAAKGVEA
          70      80      90      100     110     120
g134      IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSED TYRVLTA VDSALMVIDAAKGVEA
          130     140     150     160     170     180

```

380

m134.pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPIGMGKNFKG
g134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVEDILQIRCAPVTWPIGMGKNFKG
	130 140 150 160 170 180
m134.pep	VYHILNDEIYLFEGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLFEGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134.pep	LDEFLAGELTPVFFGSAINNFGIOEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIOEILNSLIDWAPAPKPRDATMRMVGPEPKFSGFIFK
	250 260 270 280 290 300
m134.pep	IQANMDPKHRDRIAFRLVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELVEEAYAG
g134	IQANMDPKHRDRIAFRLVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELAEAYAG
	310 320 330 340 350 360
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE
	370 380 390 400 410 420
m134.pep	GAVQVFKPMSGADLILGAVGVLFQFEVVTSLRANEYGVAVFDSASIWSARWVSCDDKKKL
g134	GAVQVFKPMSGADLILGAVGVLFQFEVVTSLRANEYGVAVFDSASIWSARWVSCDDKKKL
	430 440 450 460 470 480
m134.pep	AEFEKANAGNLAI DAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNLAI DAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

```

a134.seq
1  ATGTCCAAG AAATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC CCGTACGCAG GTAAAACCAC GTTGACTGAA AAACCTCTGC
101 TGTTCAGG TGCGATTCAA AGCGCGGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTCGA CTATAAAGAC CACACCGTCA
251 ACCTTTTGA CACGCCGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTGACCG CCGTCGATAG TGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCAATA
401 CGCCGATTGT TACGTTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAATTGC TGGACGAAGT GGAAAACATC CTGCAATCC GCTGCGCGCC
501 CGTAACCTGG CCGATCGGCA TGGGCAAAAA CTTCAAAGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCTTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCCGAAT TGGAACACG
651 CTTTCCGTTA GAAATACAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTCAAT CTCGACGAAT TCCTCGCCGG CGAACTACG
751 CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGAATGGG CGCCCGCGCC GAAACCACGC GATGCGACCG
851 TCGTATGGT CGAGCCGGAC GAGCCGAAGT TTTCCGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG

```

```

951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCCACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GTATCCCAAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGA
1151 CGTTTACCGG CATCCCATTG TTCGCGCCCG AACTGTTCCG CAGCGTTCGC
1201 ATCAAAAACC CGCTGAAAAT CAAGCAACTG CAAAAAGGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTTCAA ACCAATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCACT TTGAAGTCGT TACCTCGCGC
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAACTG GCGGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACCGCGT GAATCTGGGA CTCACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAAA CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```

a134.pep
1 MSQEILDQVR RRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGGVEA QTIKLLNVCR LRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGID NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLTFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGVEAV FDNASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

m134/a134 98.9% identity in 531 aa overlap

	10	20	30	40	50	60
m134.pep	MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME					
a134	MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD					
	10	20	30	40	50	60
m134.pep	70	80	90	100	110	120
	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGGVEA					
a134	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGGVEA					
	70	80	90	100	110	120
m134.pep	130	140	150	160	170	180
	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILKIRCAPVTWPIMGKNFKG					
a134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLDEVENILQIRCAPVTWPIMGKNFKG					
	130	140	150	160	170	180
m134.pep	190	200	210	220	230	240
	VYHILNDEIYLFEGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
a134	VYHILNDEIYLFEGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
	190	200	210	220	230	240
m134.pep	250	260	270	280	290	300
	LDEFLAGELTPVFFGSAINNFGIQLNSLIDWAPAPKPRDATVRMVEPDPEPKFSGFIFK					
a134	LDEFLAGELTPVFFGSAINNFGIQLNSLIEWAPAPKPRDATVRMVEPDPEPKFSGFIFK					
	250	260	270	280	290	300
m134.pep	310	320	330	340	350	360
	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELVEEAYAG					
a134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFMSHDRELVEEAYAG					
	310	320	330	340	350	360

382

	370	380	390	400	410	420
m134.pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134.pep	GAVQVFKPMSGADLILGAVGLQFEVVTSRLANEYGVEAVFDSASIWSARWVSCDDKKKL					
a134	GAVQVFKPMSGADLILGAVGLQFEVVTSRLANEYGVEAVFDNASIWSARWVSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134.pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
a134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

g135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51  TTCGGACgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTCGG CGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAAATATAC GGCAAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GTGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTCGGTT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACG GGCGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTcggaaa gcggGGgcag cgttTatgtg gacgaaagtg
851 cggaacacgc tTgtccgaa caagggaaaag cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

g135.pep

```

1  MKYKRIVFKV GTSSITRSDG SLSRGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDS LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESGGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

m135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAAATATAC GGCAAAACCTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

```

```

501  GACCGACATA GACGGTCTTT ACACGGGCAA CCCGAACAGC AATCCCGATG
551  CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601  GCGGGCGGCT CGGGTTCGGC AACCGGCACG GCGGGTATGC TGACCAAAAT
651  CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701  CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CTGCCGAACA TCAGGCGGAC
751  GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801  GCTGGCGTTC TATTCGAAA GCCGGGGCAG CGTTTATGTG GACGAAGGTG
851  CGGAACACGC TTTGTCCGAA CAGGGGAAAA GCCTGCTGAT GTCGGGCATT
901  GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGACAG
951  CAAGGCAACC AACAGCCCC TGGGCAAAGG GCGCGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATCGCGTA AGGCGAAAGG CGTGTTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 520; ORF 135>:

```

m135.pep
1   MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TCQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRRAVP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHNHEIEM
201 AGGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDA LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGSVYV DEGAEHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KSRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 135 shows 97.6% identity over a 294 aa overlap with a predicted ORF (ORF 135.ng) from *N. gonorrhoeae*:

```

m135/g135
      10      20      30      40      50      60
m135.pep  MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      MKYKRIVFKVGTSSITRSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG
          10      20      30      40      50      60

      70      80      90      100     110     120
m135.pep  FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL
          70      80      90      100     110     120

      130     140     150     160     170     180
m135.pep  SVLLQRRRAPIINENDTVSVVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      SVLLQRRRAPIINENDTVSVVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS
          130     140     150     160     170     180

      190     200     210     220     230     240
m135.pep  NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      NPDAVRLDKIEHNHEIEMAGGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDS
          190     200     210     220     230     240

      250     260     270     280     290     300
m135.pep  LAEAAEHQADGSFFVPRAKGLRRTQKQWLAFYSESRGSVYVDEGAEHALSEQGKSLLMSGI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g135      LAEAAEHQADGSFFVPRAKGLRRTQKQWLAFYSESGSVYVDESAEHALSEQGKACX
          250     260     270     280     290

      310     320     330     340     350     360

```

m135.pep AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGSAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

```
a135.seq
1 ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51 TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTCGGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGCTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACA GCGGGTATGC TGAATAAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTGCGGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCCGAAA GCAGGGGCGG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCTT TGGGCAAAGG GCGAGTCTTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATTGCGTA AGGCGAAAGG CGTGTTTCATC
1051 CATCGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTAG
```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

```
a135.pep
1 MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TRQLAALHHA GHELVLVSSG
51 AVAAGFGALG FKKRPVKIAD KQASAAVGQG LMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHNHEIIE
201 AGGSGSANGT GGMLTKIKAA TIATESGVPV YICSSLKPPA LAEADNQAD
251 GSFFVPRAGK LRTQKQWLAF YSESRGGVYV DEGAEHALSE QKSLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLLTEF*
```

m135/a135 98.4% identity in 369 aa overlap

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
a135	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS					
a135	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHNHEIIEAGGSGSANGTGGMLTKIKAATIAESGVVPVYICSSLKPPA					
a135	NPDAVRLDKIEHNHEIIEAGGSGSANGTGGMLTKIKAATIAESGVVPVYICSSLKPPA					
	190	200	210	220	230	240

385

	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRSVYVDEGAEHALSEQGKSLMSGI					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSESRRGVYVDEGAEHALSEQGKSLMSGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGAAEDLLKSRKAGVFIHRDDWISITP					
a135	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGAAEDLLKLRKAGVFIHRDDWISITP					
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLTEFX					
a135	EIRLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

g136.seq

1	ATGGAAATCC	GGTTTCAGAC	AGCATTTT	CGTTTGTTTC	AGatgaAAAC
51	AAACGCTtca	aTTCTtaccg	caACACGCCT	TGTATTTCCT	GccgCTGCCG
101	CACGGACAGG	GATCGTTCCT	GCCGgtTTTT	TCCCCCTCCC	TGCGGACGGT
151	TTGCGGTTTG	TTGATGACCG	CCTGCCAGTA	GCGGTAGATG	Tctgccagcg
201	cgTAAGGCag	tTCGGAcgca	agttccgcca	gctcgccttc	ggTGAATTGC
251	AGgcgataa	cgccgtttTC	CTCTTCGTCg	taaagtccgc	ccactgccat
301	cacgGGGTAA	AACAGCTCTT	CAAACGCTTC	ATCATCGGCG	GCTTCAAACC
351	AATCGGTCGG	CACAATGTCC	AAACCGTAAA	GATAGGCGTT	GCACCAAGTG
401	TAAAAATCGC	TGCCGCCCTC	GCCGTCGTCG	TAGAGCCACA	AATCGGGCAG
451	CTTTTATCC	GACATCGCGG	CGGTTGTTC	CATCGCCATT	GCCAAAACCA
501	GCCGTTTCGAT	TTCGGAACGT	TCGGCGGCGG	TAAATGCGA	TCGTCGCCCC
551	AACACTTCGG	GCAGCCAGTC	GAGCGGTGCC	AATTTGTCCG	GCCCGCTCAA
601	CAGCGCCGTC	ATAAAACCTT	GAACCTCGTC	GCAACGCATC	GTGTTGCCTT
651	GTTCGCTTTT	GGCATCCAAT	AA		

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

g136.pep

1	MEIRFQTAFL	RLVQMKTNAS	ILTATRLVFP	AAAARTGIVP	AGFFFPFPADG
51	LRFVDDRLPV	AVDVCQRVRQ	FGRKFRQLAF	GELQADNAVF	LFVVNAAHCH
101	HGVKQLFKRF	IIGGFKPIGR	HNVTQVKIGV	APSVKIAAAL	AVVVEPQIGQ
151	LFIRHRGGCF	HRHCQNQPF	FGTFGGGKLR	FVAQHFGQPV	ERCQFVRPAQ
201	QRRHKTLNLV	ATHRVALFAF	GIQ*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

m136.seq

1	ATGGAAACAA	ACGCTTCAAT	TCTTACCGCA	ACACGCCTTG	TATTTTCTGC
51	CGCTGCCGCA	CGGACAGGGA	TCGTTCCCTGC	CTGTTTTTTC	GCCTTCCCTG
101	CGGACGGTTT	GCGGTTTGTT	GATGACTGCC	TGCCAGTAGC	GGTAGATATC
151	CGCCAATGCA	TAAGGCAACT	CGGATTCCAG	TCCCGCCAGC	TCGCCTTCTG
201	TGAATTGCAG	ACGGATAGCG	CCGTTTTCTT	CTTCGTCGTA	AATACCGCCC
251	AATGCCATGA	TGGGATAAAA	CAACTCTTCA	AACGCTTCAT	CATCGACGGC
301	TTCAAACCAA	TCGGTCGGCA	CAATATCCAA	ACCGTAAAGA	TAAGCATTGC
351	ACCATGTGTA	AAAATCGCTG	CCGCCGTCTT	CGTTTTTCATA	CAGCCACAAA
401	TCGGGCAGTT	TTTTATCCGA	CATCGCGGCG	GTTGTTTCCA	TCGCCATTGC
451	CAAAACCAGC	CGTTCGATTT	CGGAACGTTC	GGCGGCGGTA	AATTGCGATT
501	CGTCGCCCAA	CACTTCGGGC	AGCCAGTCGA	GCGGTGTCAA	TTGTCCGGC
551	CCGCTCAACA	GCGCCGTCAT	AAAACCTTGA	ACCTCGTCGC	AACGCATCGT
601	GTTGCCTTGT	TCGCTTTTGG	CATCCAACAA	TTCGCTCAAC	CGCCGTTTGG
651	ATGCTTCGGT	AAATTTTCGG	GAATCCATCA	TTTTCCTTTT	CAAATGGGTT
701	TTGCGCCCTA	TTATCGCCGC	AATGCCGTCT	GA	

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:



1	METNASILTA	TRLVFSAAAA	RTGIVPACFF	AFPADGLRFV	DDCLPVAVDI
51	RQCIRQLGFO	FRQLAFCELQ	TDSAVFLFVV	NTAQCHDGIK	QLFKRFIIDG
101	FKPIGRHNIQ	TVKISIAFVC	KIAAAVVFVI	QPQIQGFFIR	HRGGCGFHRHC
151	QNQPFDFGTF	GGGKLRFPVQ	HFGQPVVERC	FVRPAQQRHR	KTNLNVATHR
201	VALFAFGIOQ	FAQPPFGCFG	KFSGIHHPFF	QMGFAPYYRR	NAV*

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 136 shows 85.6% identity over a 209 aa overlap with a predicted ORF (ORF 136.ng) from *N. gonorrhoeae*:

m136/q136

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 527>:

```

a136.seq
1  ATGGAACAA  ACGCTTCAAT  TCTTACCGCA  ACACGCCTTG  TATTTTCTGC
51  CGCTGCCGCA  CGGACAGGGA  TCGTTCCTGC  CTGTTTTTTC  GCCTTCCCTG
101 CGGACGGTTC  GTCGCTTGTT  GTGACCGCC  TGCCATAGTC  GGTAGATATC
151 CGCCAATGCA  TAAGGCAACT  CGGATTCCAG  TTCCGCCAGC  TCGCCTTCTG
201 TGAATTGCAG  ACGGATAGTG  CCGTTGTCCT  CTTCGTCGTA  AATACCGCCC
251 AATGCCATGA  TGGGATAAAA  CAACTCTTCA  AACGCTTCAT  CATCGACGGC
301 TTCAAACCAA  TCGGTCGGCA  CAATATCCAA  ACCGTAAGA  TAAGCATTGC
351 ACCATGTGTA  AAAATCGCTG  CGGCGTCTT  CGTTTTCATG  CAGCCACAAA
401 TCGGGCAGTT  TTTTATCCGA  CATCGCGGCG  GTTGTTTCCA  TCGCCATTGC
451 CAAAACGAGC  CGTTCGATTT  CGGAACGTT  GCGGCGGGTA  AATTGCGATT
501 CGTCGCCCAA  CACTTCGGGG  AGCCAGTCGA  GCGGTGTCAA  TTTGTCGGCG
551 CCGCTCAACA  GCGCGTCAT  AAAACCTTGA  ACCTCGTCGC  AACCCATCGT
601 GTTGCCCTGT  TCGCTTTTGG  CATCCAAACA  TTCGCTCAAC  CGCGGTTTGG
651 ATGCTTCGGT  AAATTTTCGG  GAATCCATCA  TTTTCCTTTT  CCAATGGGTT
701 TTGCGCCCTA  TTATAGTGA  TTAAGATTAA  ATCAGGACAA  GGCGACGAAG
751 CCGCAGACAG  TACAAATAGT  ACGGCAAGG  GAGGCAACGC  CGTACTGGTT
801 TAAATTTAAT  CCACATATAT  GCGCAATGC  CGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 528; ORF 136.a>:

a136.pep

```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFVV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQQRH  KTLNLVATHR
201 VALFAFGIQQ  FAQPPFGCFG  KFSGIHHFPF  PMGFAPYYS  LNLNQDKATK
251 PQTQIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

```

m136.pep      10      20      30      40      50      60
METNASILTATRLVFSAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ
|||||
a136          10      20      30      40      50      60
METNASILTATRLVFSAAAARTGIVPACFFAFPADGLRLVDRLPVAVDIRQCIRQLGFQ

m136.pep      70      80      90      100     110     120
FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
|||||
a136          70      80      90      100     110     120
FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV

m136.pep     130     140     150     160     170     180
KIAAAVFVFIQPIQIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ
|||||
a136         130     140     150     160     170     180
KIAAAVFVFIQPIQIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ

m136.pep     190     200     210     220     230     240
FVRPAQQRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPFQMGFAPYYRR
|||||
a136         190     200     210     220     230     240
FVRPAQQRHKT LNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIHHFPFPMGFAPYYSG

m136.pep      NAVX
a136          LNLNQDKATKPQTQIVRQGEATPYWFKFNPLYRRNAVX
                250      260      270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

```

g137.seq
1  ATGATTATCC  ATCACcaatt  CGATCCCGTC  CTCATCAGTA  TCGGCCCGCT
51  TGCCGTCCGC  TGGTATGCCT  TAAGCTACAT  CCTCGGATTT  ATTCTTTTAA
101 CCTTTCTCGG  CAGAAGGCGC  ATCGCGCAAG  GCTTGTCCGT  TTTTACCAAA
151 GAATCGCTCG  ACGACTTCCT  GACATGGGGC  ATTTTGGGCG  TGATTTTGGG
201 CGGACGCTTG  GGCTATGTCC  TGTTTTACAA  ATTCTCCGAC  TACCTCGCCC
251 ATCCGCTTGA  TATTTTCAAG  GTATGGGAAG  GCGGAATGTC  GTTCCACGGC
301 GGCTTTTGGG  GTGTAGTTAT  TGCCATATGG  TTGTTTCAGCC  GCAAGCACGG
351 CATCGGCTTC  CTCAAAGTGA  TGGACACGGT  CGCGCCGCTC  GTTCCGCTGG
401 GTCTCGCTTC  GGGACGTATC  GGCAACTTTA  TCAACGGCGA  ACTTTGGGGA
451 CGCATTACCG  ACATTAACGC  ATTTTGGGCA  ATGGGCTTCC  CGCAAGCGCA
501 TTACGAAGAT  GCCGAAGCCG  CCGGCACAAA  TCCGCTTTGG  GCAGAATGGC
551 TGCAACAATA  CGGTATGCTG  CCGCGTCATC  CCTCGCAGCT  TTATCAGTTT
601 GCCCTTGAAG  GCATCTGCCT  GTTCGCCGTC  GTTTGGCTGT  TTTCCAAAAA
651 ACCGCGCCCG  ACCGGGCAGA  CTGCGCGCT  TTTTCTCGGC  GGCTACGGCG
701 TGTTCGCTT  TATTGCCGAA  TTTGCGCGCC  AACCAGACGA  CTATCTCGGG
751 CTGCTGACCT  TGGGGCTGTC  GATGGGGCAA  TGGTTGAGCG  TCCCGATGAT
801 TGTTTTGGGT  ATCGTCGGCT  TTGTCCGGTT  CGGCATGAAA  AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 530; ORF 137.ng>:

g137.pep

```

1  MIIHHQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSY YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RITDINAFWA MGFPQAHYED AEAHAHNPLW AEWLQQYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSKKPRP TGQTAALFLG GYGVFRFIAE FARQPDYDLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 531>:

```

m137.seq
1  ATGATTACCC ATCCCAATT CGATCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATTT ATTCTTTTAA
101 CCTTTCTCGG CAGAAGGCGC ATCGCGCAAG GCTTGTCCGT TTTTACCAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTGGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGGG GTGTAGTTAT TGCCATACGG TTGTTCGGCC GCAAACACGG
351 CATCGGCTTC CTCAAAGTGA TGGATACGGT CGCACCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAT GCCGAAGCCG CCGCGCACAA TCCGCTTGGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTACCGGTC ATTTGGCTGT TCTCTAAAAA
651 ACAGCGGTCG ACCGGACAAG TCGCCTCGCT CTTCTCTGGC GGCTACGGCA
701 TATTCGCTT CATTGCCGAA TTCGCACGCC AACCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 532; ORF 137>:

```

m137.pep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSY YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIR LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RVTDINAFWA MGFPQARYED AEAHAHNPLW AEWLQQYGML PRHPSQLYQF
201 ALEGICLFTV IWLFSKKQRS TGQVASLFLG GYGVFRFIAE FARQPDYDLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 137 shows 95.4% identity over a 283 aa overlap with a predicted ORF (ORF 137.ng) from *N. gonorrhoeae*:

```

m137/g137
      10      20      30      40      50      60
m137.pep  MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
          |||||
g137      MIIHHQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW
          10      20      30      40      50      60

      70      80      90     100     110     120
m137.pep  ILGVILGGRLGYVLFYKFSYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRLFGRKHGIGF
          |||||
g137      ILGVILGGRLGYVLFYKFSYLAHPLDIFKVWEGGMSFHGGFLGVVIAIWLFSRKHGIGF
          70      80      90     100     110     120

      130     140     150     160     170     180
m137.pep  LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDAEAAHNPLW
          |||||
g137      LKLMDTVAPLVPLGLASGRIGNFINGELWGRITDINAFWAMGFPQAHYEDAEAAHNPLW
          130     140     150     160     170     180

      190     200     210     220     230     240
m137.pep  AEWLQQYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGFIRFIAE

```

	: : : : :
g137	A E W L Q Q Y G M L P R H P S Q L Y Q F A L E G I C L F A V V W L F S K K P R P T G Q T A A L F L G G Y G V F R F I A E
	190 200 210 220 230 240
	250 260 270 280
m137.pep	F A R Q P D D Y L G L L T L G L S M G Q W L S V P M I V L G I V G F V R F G M K K Q H X
g137	F A R Q P D D Y L G L L T L G L S M G Q W L S V P M I V L G I V G F V R F G M K K Q H X
	250 260 270 280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 533>:

```

al37.seq
1  ATGATTACCC ATCCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCGCC TGGTATGCCC TAAGTCACAT CCTCGGATTT ATTCTTTTTA
101 CTTTCTCGCG CAGAAGCGCG ATCGCGCAAG GCTTGTCCGT TTAATCAAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TTTATTTTGG
201 CGGGCGTTTG GGTTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTTCG GTGTAGTTAT TGCCATATGG TTGTTCCGTC GCAAACACGG
351 CATCGGCTTC CTCAAACTGA TGGACACGGT CGCACCGCTC GTTCCACTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAC CTCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTCGCGCTC GTTTGGCTGT TCTCTAAAAA
651 ACAGCGGCCG ACCGGACAAG TCGCCTCACT CTTCTCGGC GGTACGGCA
701 TATTCCGCTT CATTGCCGAA TTTGCACGCC AACCAGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCGGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 534; ORF 137.a>:

```

a137.pep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTWG ILGVILGGRL GYVLFYKFSD YLAHPLDIFK VWEGGMSFHG
101 GLGVVIAIW LFGRKHGIGF LKLMOTVAPL VPGLASGRI GNFINBELWG
151 RVTDINAFWA MGFPQARYED LEAAAHNPWL AEWLQYQYGL PRHPSQLYQF
201 ALEGICLFAV VWLFSSKKQRP TGQVASLFLG GYGIFRFIAE FARQPDYDLG
251 LLTLGLSMGQ WLSVPMIVLG IVGVFRFGMK KQH*

```

m137/a137 98.2% identity in 283 aa overlap

	10	20	30	40	50	60
m137.pep	MITHPQDFPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFTKESLDDFLT	WG			
a137	MITHPQDFPVLISIGPLAVRWYALS	YILGFILFTFLGRRRIAQGLSVFTKESLDDFLT	WG			
	10	20	30	40	50	60
m137.pep	ILGVILGGRLGYVLFYKFS	DYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRL	FGRKHGIGF			
a137	ILGVILGGRLGYVLFYKFS	DYLAHPLDIFKVWEGGMSFHGGFLGVVIAIW	LFGRKHGIGF			
	70	80	90	100	110	120
m137.pep	LKLMDTVAPLVLPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDAEAAAHNPLW					
a137	LKLMDTVAPLVLPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDLEAAAHNPLW					
	130	140	150	160	170	180
m137.pep	AEWLQQYGMLPRHPSQLYQFALEGICLFTVIWLFSKQ	RSTGQVASLFLGGYGIFR	ETAE			
a137	AEWLQQYGMLPRHPSQLYQFALEGICLFAVVWLFSKQ	RPTGQVASLFLGGYGIFR	ETAE			
	190	200	210	220	230	240

390

	190	200	210	220	230	240
	250	260	270	280		
m137.pep	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFMGKKQHX					
a137	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFMGKKQHX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

g138.seq

```
1  ATGGAGTTTG AAAACATTAT TTCCGCCGCC gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACatcc gccgGTTTTT CCGTTCCGGT GCCGTCATCA
101 AGTATGGCGG CAACGCGATG ACCGAACCTG CTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGAC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGGCACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGGTCGATA CGCCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGGCT GCATCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT GGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACTC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCcgccgtc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGGTCGATG ATTTTAGGCA GAGGGAAGA TGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

g138.pep

```
1  MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKETMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LVDTPEQNSV
151 DIGQVGTVES IDTGLVKGLI ERGCIPVVP VGVGEKGAEF NINADLVAGK
201 LAEELNAEKL LMTNIAAGVM DKTGNLLTKL TPKRIDGLIA DGTLYGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGRGEDA*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

m138.seq

```
1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGTTTTTC CCGTTCCGGT GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACTC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTCGATG ATTTTGGGCG GTGGGAAGA TGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

m138.pep

```
1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
```

51 RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAMDI
 101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
 151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
 201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
 251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGGGEDA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 138 shows 98.0% identity over a 298 aa overlap with a predicted ORF (ORF 138.ng)
 from *N. gonorrhoeae*:

m138/g138

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
g138	MEFENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAMDIVEMVLGGHVNKEIVSMINTY					
g138	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKETMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
g138	GGHAVGVSGRDDHFIKAKKLLVDTPEQNSVDIGQVGTVESIDTGLVKGLIERGCI PVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
g138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAGVMDKTGNLLTKLTPKRIDGLIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
g138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGRGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 539>:

a138.seq

```

1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51 CGAAGCGCTG CCTTACATCC GCCGTTTTC CGGTTCCGTC GCCGTCATCA
101 AATACGGCGG CAACCGCATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGCGCGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAGAGAGC GATGGATATT
301 GTCGAAATGG TGTTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAAACTT TTGATCGATA CGCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAAGC ATCGATACCG GTTTGGTTAA
501 AGGCGTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 GTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 TTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAACTC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCCGTC AACGGCGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGGTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGTAT CGGTTGATG ATTTTGGGCG GTGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
  1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
 51  RDVVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI
101  VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151  DIGQVGTVES IDTGLVKGLI ERGCIPVVAP VGVGEKGEAF NINADLVAGK
201  LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251  KIASAVEAAV NGVKATHIID GRVFNALLLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
a138	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
a138	IHPVIVHGGGPQINAMLEKVGKKGEFVQGM RVTDKAEMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
a138	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLMMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
a138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRFPNALLLEIFTDAGIGSMILGGGEDAX					
a138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRFPNALLLEIFTDAGIGSMILGGGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
  1  ATGCGAACCA CCTCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
 51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAagg ggcggcggag
101  gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
151  AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
201  AAAAAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTCGGGATG
251  ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
301  ATACCGGAGA CTTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
351  CCTCAAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
401  GTATCGTCGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCCGAAGTG
451  TATGGCAGAA AAGAACACGG CTATAACGAA AATTACAAAA ACAAATTACA
501  AAAACTATAC GGCGTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
  1  MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
 51  NSRATIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
101  IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPPEL
151  YGRKEHGYNE NYKNKLQKLY GVYAEGSA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 543>:

```
m139.seq
      1  ATGCGAACGA  CCCCAACCTT  CCCTACAAAA  ACTTTCAAAC  CGACTGCCAT
     51  GCGGTTAGCT  GTTGCAACAA  CACTTTCTGC  CTGCTTAGGC  GCGGCGCGAG
    101  GCGGCACTTC  TGCGCCCGAC  TTCAATGCAG  GCGGTACCGG  TATCGGCAGC
    151  AACAGCAGAG  CAACAACAGC  GAAATCAGCA  GCAGTATCTT  ACGCCGGTAT
    201  CAAGAACGAA  ATGTGCAAAG  AAGAAGCATG  CACTGTGTGC  GGTGCGGATG
    251  ACGTTGCGGT  TACAGACAGG  GATGCCAAAA  TCAATGCCCC  CCCCCGAATC
    301  TGCATACCGG  AGACTTTCCA  AATCCAAATG  ACGCATtACA  AGAATTTGAT
    351  CAACCTCAAA  CCTGCAATTG  AAGCAGGCTA  TACAGGACGC  GGGGTAGAGG
    401  TAGGTATCGT  GCACACAGGC  GAATCCGTGC  GCAGCATATC  CTTTCCCGAA
    451  CTGTATGGCA  GAAAAGAA  CCGCTATAAC  GAAAATTACG  AAAAACTATA
    501  CGCGGTATAT  GCGGAAGGAA  GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 544; ORF 138>:

```
m139.pep
  1  MRTTPTFPTK TFKPTAMALA VATTLSACLG GGGGGSAPD FNAGGTGIGS
51  NSRATTAKSA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETFQTQM THYKNLNLK PAIEAGYTG R GVEVGIVDTG ESVGSISFPE
151 LYGRKEHGYN ENYEKLYGVY AEGSA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

m139/q139

	10	20	30	40	50	60
m139.pep	MRTTPTFTPKTKFKPTAMALAVATTLSACLGGGGGGTSAPDFNAGGTGIGSNSRATTAKSA					
g139	MRTTSTFTPKTKFKPAAMALAVATTLSACLGGGGGGTSAPDFNAGGTGIGSNSRATIAESA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGRDDVAVTTDRDAKINAPPRICIPETFQTMTHYKNLINLK					
g139	AVSYAGIKNEMCKDRSMLCAGRDDVAVTTDRDAKIP-RICIPETFQTMNKNMINLK					
	70	80	90	100	110	
	130	140	150	160	170	
m139.pep	PAIEAGYTRGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENY----EKLYGVYAEGSAX					
g139	PAIEAGYTRGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENYKNKLQKLYGVYAEGSAX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 545>:

```

a139.seq
1  ATGCGAACGA  CCCCAACCTT  CCCTACAAAA  ACTTTCAAAC  CGGCTGCCAT
51  GGGCTTAGCT  GTTGCAACAA  CACTTTCGTC  CTGCTTAGGC  GGCGCGGGAG
101 GCGGCAGCTT  TGGCGCCGAC  TTCAATGCAG  GCGGCACCGG  TACTCGGCAGC
151 AACAGCAGGG  CAACAACAGC  GAAATCAGCA  GCAATATCTT  ACGCCGGTAT
201 CAAGACAGAA  ATGTGCAAA  ACAGAAGCAT  GCTCTGTGCC  GGTCTGGGATG
251 ACGTTGCGGT  TACAGACAGG  GATGCCAAAT  TCAATGCCCC  CCCCAGAAATC
301 TGCATACCGG  AGACTTTACA  AACCCAAATG  ACGCAT  A.  AGAATTTGAT
351 CAACCTCAA  CCTGCAATTG  AAGCAGGCTA  TACAGGACGC  GGGGTAGAGG
401 TAGGTATCGT  CGACACAGGC  GAAATCCGTG  GCAGCATATC  CTTTCCCGAA
451 CTGTATGGCA  GAAAAGAAC  CGGCTATAAC  GAAAATTAC.  AAAAATATA
501 CCGCGTATAT  GCGGAAGGAA  GCGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 546; ORF 139.a>:

a139.pep
1 MRTTPTEFTK TFKPAAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS

51 NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
 101 CIPETLQTQM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSISFPE
 151 LYGRKEHGYN ENYXKLYGVY AEGSA*

m139/a139 97.1% identity in 175 aa overlap

	10	20	30	40	50	60
m139.pep	MRTTPTFP	TKFTKPTAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA
a139	MRTTPTFP	TKFTKPAAMALAVAT	TL	SACLG	GGGGG	TSAPDFNAGGTGIGSNSRATTAKSA
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGR	DDVAVTDRDAKINAPPRI	CIPET	FQTQM	THXKNLINLK	
a139	AISYAGIKNEMCKDRSMLCAGR	DDVAVTDRDAKINAPPRI	CIPET	LQTQM	THXKNLINLK	
	70	80	90	100	110	120
	130	140	150	160	170	
m139.pep	PAIEAGYTGRGVEVGIVDTG	ESVGSISFPELYGRKEHGYN	ENYKLYGVY	AEGSAX		
a139	PAIEAGYTGRGVEVGIVDTG	ESVGSISFPELYGRKEHGYN	ENYXKLYGVY	AEGSAX		
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 547>:

g140.seq

1	Atgtcggcac	gCGCAAGGG	GGCAGgctat	ctcAACAGTA	CCGGACGACa
51	TGTTCCCTTC	CTGAGTGCCG	CCAAAATCGG	GCAGGATTAT	TCTTTCTTCA
101	AAAATATCAA	AACCGACGGC	GGTCTGCTGG	CTTCCCTCGA	CAGCGTCGAA
151	AAAACAGCGG	GCAGTGAAGG	CGACACGCCG	TCCTATTATG	TCCGTCGCGG
201	CAATGCGGCA	CGGACTGCTT	CGGCAGCGGC	ACAATCCGCG	CCCGCCGGTC
251	TGAAACACGC	CGTAGAACAG	GGCGGCAGCA	ATCTGGA AAA	CCTGATGGTC
301	GAGCTGGATG	CCTCCGAATC	ATCCGCAACA	CCCAGACGCG	TTGAAACTGC
351	GGTCGCCGAC	CGCACAGATA	TGCCGGGCAT	CCGCCTACGG	CGCACAACTT
401	TCCGCACAGC	GGCAGCCGTA	CAGCATGCGA	ATACCGCCGA	CGGCGTACGc
451	aTCTTcaaCA	GTCTCGCCGC	TAccgTCTAt	GccgACAGTG	CCGCGCCCA
501	TGccgATATG	CAGGGACGCC	GCCTGAAAGC	CGTATCGGAC	GGGTTGGACC
551	ACAACGGTAC	GGGTCTGCGC	GTCATCGCGC	AAACCCAACA	GGACGGTGGA
601	ACGTGGGAAC	AGGGCGGTGT	CGAAGGCAAA	ATGCGCGGCA	GTACCCAAAC
651	TATCGGCATT	GCCGCGAAAA	CCGGCGAAAA	TACGACAGCA	GCCGCCACAC
701	TGGGCATAGG	ACGAGCACA	TGGAGCGAAA	ACAGTGCAAA	TGCAAAAACC
751	GACAGCATTa	GTCTGTTTGC	AGGCATACGG	CACGATGTGG	GCGATATCGG
801	CTATCTCAAA	GGCCTGTTCT	CctaCGGACG	CTACAAAAAC	AGCATCAGCC
851	GCAGCACCGG	TGCGGATGAA	TATGCGGAAG	GCAGCGTCAA	CGGCACGCTG
901	ATGCAGCTGG	GCGCACTGGG	TGGTGTC AAC	GTTCCGTTTG	CCGCAACGGG
951	AGATTGACG	GTTGAAGGCG	GTCTGCGCCA	CGACCTGCTC	AAACAGGATG
1001	CATTTCGCCA	AAAAGGCagt	GCTTTGGGCT	GGAGCGGCAA	CAGCCTCACT
1051	GAAGGCACAC	TGGTCGGACT	CGCGGGTCTG	AAACTGTCTG	AACCTTTGAG
1101	CGATAAAGCC	GTCTGTCTG	CGACGGCGGG	CGTGGAACGC	GACCTGAACG
1151	GACGCGACTa	CGCGGTAACG	GGCGGCTTTA	CCGGCGCGGC	TGCAGCAACC
1201	GGCAAGACGG	GTGCACGCAA	TATGCCGCAC	ACCCGCCGGG	TTGCCGGTCT
1251	GGGGGTGGAT	GTGCAATTCTG	GCAACGGCTG	GAACGGCTTG	GCACGTTACA
1301	GCTACACCGG	TTCCAAACAG	TACGGCAACC	ACAGCGGACA	AATCGGCGTA
1351	GGCTACCGGT	TCTGA			

This corresponds to the amino acid sequence <SEQ ID 548; ORF 140.ng>:

g140.pep

1	MSARGKGAGY	LNSTGRHVPF	LSAAKIGQDY	SFFKNIKTDG	GLLASLDSVE
51	KTAGSEGDTP	SYVVRGNAA	RTASAAHSA	PAGLKHAVEQ	GGSNLENLMV
101	ELDASESAT	PETVETAVAD	RTDMPGIRLR	RTTFRTAAAV	QHANTADGVR
151	IFNSLAATVY	ADSAAAHADM	QGRRLKAVSD	GLDHNGTGLR	VIAQTQQDGG
201	TWEQGGVEGK	MRGSTQTIGI	AAKTGENTTA	AATLGIGRST	WSENSANAKT

395

251 DSISLFAGIR HDVGDIGYLK GLFSYGRYKN SISRSTGADE YAEGSVNGTL
 301 MQLGALGGVN VPFAATGDLT VEGGLRHDL LKQDAFAEKGS ALGWSGNSLT
 351 EGTLVGLAGL KLSQPLSDKA VLSATAGVER DLNGRDYAVT GGFTGAAAAT
 401 GKTGARNMPH TRRVAGLGVD VEFNGWNGL ARYSYTGSKQ YGNHSGQIGV
 451 GYRF*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 549>:

m140.seq
 1 ATGTCGGCAC GCGGCAAGGG GGCAGGCTAT CTCAACAGTA CCGGACGACG
 51 TGTTCCTTC CTGAGTGCCG CCAAATCGG GCAGGATTAT TCTTTCTTCA
 101 CAAACATCGA AACCGACGGC GGCCTGCTGG CTTCCCTCGA CAGCGTGGAA
 151 AAAACAGCGG GCAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
 201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCGGTC
 251 TGAAACACGC CGTAGAACAG GGCAGCAGCA ATCTGGAAAA CCTGATGGTC
 301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
 351 GGCAGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCCTAC GGCAGCACTT
 401 TCCGCGCAGC GGCAGCCGTA CAGCATGCCA ATGCCGCCGA CGGTGTACGC
 451 ATCTTCAACA GTCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCGCCCA
 501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
 551 ACAACGGCAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA
 601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
 651 CGTCGGCATT GCCGCGAAAA CCGCGGAAAA TACGACAGCA GCCGCCACAC
 701 TGGGCATGGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
 751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
 801 CTATCTCAA GGCCTGTTCT CCTACGGACG CTACAAAAC AGCATCAGCC
 851 GCAGCACCGG TCGGACGAA CATGCGGAAG GCAGCGTCAA CCGCACGCTG
 901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG
 951 AGATTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
 1001 CATTGCGCGA AAAAGGCAGT GCTTGGGCT GGAGCGGCAA CAGCCTCACT
 1051 GAAGGCACGC TGGTCGGACT CGCGGTCTG AAGCTGTGCG AACCTTGAG
 1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGGAAACG GACCTGAACG
 1151 GACGCGACTA CACGGTAACG GCGCGCTTTA CCGCGCGGAC TGCAGCAACC
 1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGTCTGG TTGCCGGCCT
 1251 GGGCGCGGAT GTCGAATTCT GCAACGGCTG GAACGGCTTG GCACGTTACA
 1301 GCTACGCCGG TTCCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
 1351 GGCTACCGGT TCTGA

This corresponds to the amino acid sequence <SEQ ID 550; ORF 140>:

m140.pep
 1 MSARGKGAGY LNSTGRRVPF LSAKIGQDY SFFTNIETDG GLLASLDSVE
 51 KTAGSEGDITL SYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
 101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
 151 IFNSLAATVY ADSTAAHADM QGRRLKAVSD GLDHNGTGLR VIAQTQDGG
 201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGRST WSENSANAKT
 251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
 301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSLT
 351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
 401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
 451 GYRF*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 140 shows 94.5% identity over a 454 aa overlap with a predicted ORF (ORF 140.ng) from *N. gonorrhoeae*:

m140/g140

	10	20	30	40	50	60
m140.pep	MSARGKGAGYLNSTGRRVPFLSAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
g140	MSARGKGAGYLNSTGRHVPFLSAKIGQDYSFFKNIKTDGGLLASLDSVEKTAGSEGDTF					
	10	20	30	40	50	60
	70	80	90	100	110	120

m140.pep	SYYYVRRGNAARTASAAAH SAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAAAD
g140	SYYYVRRGNAARTASAAAH SAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAVAD
	70 80 90 100 110 120
m140.pep	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLSLAATVYADSTAAHADMQGRRLLKAVSD
g140	RTDMPGIRLRRTTFRATAAVQHANTADGVRIFNLSLAATVYADSAAAHADMQGRRLLKAVSD
	130 140 150 160 170 180
m140.pep	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST
g140	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTIGIAAKTGENTTAAATLGI GRST
	190 200 210 220 230 240
m140.pep	WSENSANAKTDSISL FAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
g140	WSENSANAKTDSISL FAGIRHDVGDIGYLKGLFSYGRYKNSISRSTGADEYAEGSVNGTL
	250 260 270 280 290 300
m140.pep	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
g140	MQLGALGGVNVFPAATGDLTVEGGLRHDLLKQDAFAEKGSALGWSGNSLTEGTLVGLAGL
	310 320 330 340 350 360
m140.pep	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD
g140	KLSQPLSDKAVLSATAGVERDLNGRDYAVTGGFTGAAAATGKTGARNMPHTRRVAGLGVD
	370 380 390 400 410 420
m140.pep	VEFGNGWNGLARYSYAGSKQYGNHSGRVGVGYRFX
g140	VEFGNGWNGLARYSYTGSKQYGNHSGQIGVGYRFX
	430 440 450

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140.seq
1  ATGTCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCTTC CTGAGTGCCG CCAAAATCGG GCGGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTCCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GCGGCAGCA ATCTGGAAAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTTAC GGCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGCTAC GGGTCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAC
651 CGTCGGCATT GCCGCAAAA CCGCGAAAA TACGACAGCA CGCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTA GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAC AGCATCAGCC
851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG

```

```

951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTCGCCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCATCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGGTCTG AAGCTGTCGC AACCTTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGCTTTA CCGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGCTGG TTGCGGGTCT
1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTT GCACGTTACA
1301 GCTACGCCG TTCCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 552; ORF 140.a>:

```

a140.pep
  1 MSAGGKGAGY LNRTGQRVPF LSAAKIGRDY SFFTNIETDG GLLASLDSVE
 51 KTAGSEGDITL SYYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNNLAATVY ADSTAAHADM QGRRKAVSD GLDHNATGLR VIAQTQODGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGHST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSIT
351 EGTLVLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

m140/a140 98.2% identity in 454 aa overlap

	10	20	30	40	50	60
m140.pep	MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
a140	MSAGGKGAGYLNRTGQRVPFLLSAAKIGRDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m140.pep	SYYVRRGNAAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
a140	SYYVRRGNAAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m140.pep	RTDMPGIRPYGATFRAAAVQHANAADGVRIFFNLAATVYADSTAAHADMQGRRKAVSD					
a140	RTDMPGIRPYGATFRAAAVQHANAADGVRIFFNLAATVYADSTAAHADMQGRRKAVSD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m140.pep	GLDHNATGLRVIAQTQODGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST					
a140	GLDHNATGLRVIAQTQODGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGHST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m140.pep	WSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
a140	WSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m140.pep	MQLGALGGVNVFFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVLAGL					
a140	MQLGALGGVNVFFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVLAGL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m140.pep	KLSQPLSDKAVLFLATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					
a140	KLSQPLSDKAVLFLATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					

398

	370	380	390	400	410	420
	430	440	450			
m140.pép	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYREFX					
a140	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYREFX					
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

g141.seq

```

1  atgagcttca aAAccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGC GGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTCG GCGTGAAAGG CGGCGCGGCA GCGGCGGGCT ACGCGCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGCGAC TTCCACGCCA
401 TCGGTGCGGC GAATAACCTC CTCGCCGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GGCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTtga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTGa tggcgGTATT CTGCCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTTtt gGCAATATTC TCGTCGCCTA CGCCAAAGAC GGCAGCCCGC
701 TTTACGCCAA AGATTGGAAG GCACACGGCG CGATGGCGGC ATTGCTAAAA
751 GATGCGATTA AGCCCAATTT GGTGCAAACC ATCGAAGGCA CTCCGGCCTT
801 TGTACACGGC GGCCCCTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG TGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCGCGC
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAC
1051 CTCGAAGCCT TGGCAAAGG TTTGCCCAAC CTGTTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTCGGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GCGGCGGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA TGCCATCGAC AACCAACCTA
1301 ATAACCTCGG TTTCGCCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCAAAAAGT GTACGGCGCG GAAGATGTCG ATTTAGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTGAGCGA CAACGCCAAA
1501 CTCTTTGGCT GCCCGAAGG CTTCCGCATC GCCGTACGCG GTATCACTGT
1551 TTCCGCGGCG GCGGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGGGCCT GCCGAAAGT CCGGCTGCCG AGAAAAATCGA TGTGGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

g141.pép

```

1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFVGKGGAA GGGYAQVLPD EDINLHFTGD PHAIGAANNL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNID GMGKPDVGM RPDGFDITVA
201 SEVMVAFCLA KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNNG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVVNAID NQPNNFGFAY DVELGIKDKI
451 RAIQKQVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCEPGFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDE
551 HGVHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1  ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGTCAT TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGGGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTGC
251 GCCACATCGG CAAAGATGCC GTGATTGCCG TGCGCGAACC TTCTCTGGGG
301 CCGGTGTTCC GCGTGAAAGG CGGCGCGGCA GCGGCGGCT ATGCCCAAGT
351 AGAGCGTTTG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GGCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCCGTTGA CGGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCGCTA CGCCAAAGAC GGCAGCCCGG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCGCGCTT
801 CGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CTTTCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGAAAAGG TTTGCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACGC CGATGCCGAG TTGGCGATGA TTGAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CCGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACTTCGG TTTGCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT CCGGAAATCG CTTCCTGGA AAAACTGGG TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCGCGATC GCGGTGCGCG GCATCACCCT
1551 TTCCGAGGCG GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCTT GCCCAAAGT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1  MSFKTDAEIA QSSTMRPIGE IAAKLGLNAD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFVGKGGAA GGGYAQVLPD EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNID GMGKPDVGVN RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDADAE LAMIEKACAE
401 HGVEVSLTEV WGKGGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVHGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

	10	20	30	40	50	60
m141.pep	MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL					
g141	MSFKTDAETAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL					
	10	20	30	40	50	60

400

m141.pep	70	80	90	100	110	120
	TAINPTPAGEGKTTVTITGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLP					
g141	TAINPTPAGEGKTTVTITGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLP					
	70	80	90	100	110	120
m141.pep	130	140	150	160	170	180
	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVVDMDNRQLRNIID					
g141	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVVDMDNRQLRNIID					
	130	140	150	160	170	180
m141.pep	190	200	210	220	230	240
	GMGKPDGVMPDGFDTIVASEVMAVFLAKDISDLKERLGNILVAYAKDGSVPYAKDLK					
g141	GMGKPDGVMPDGFDTIVASEVMAVFLAKDISDLKERFGNILVAYAKDGSVPYAKDLK					
	190	200	210	220	230	240
m141.pep	250	260	270	280	290	300
	ANGAMAALLKDAIKPNLVQTIETGPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
g141	AHGAMAALLKDAIKPNLVQTIETGPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	310	320	330	340	350	360
	GFGADLGAEKFCDIKRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
g141	GFGADLGAEKFCDIKRLAGLKPDAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
	310	320	330	340	350	360
m141.pep	370	380	390	400	410	420
	LLKHISNLKNVFGLPVVVALNRFVSDADAEIAMIEKACAEHGVESLSEVWGKGGAGGAD					
g141	LLKHISNLKNVFGLPVVVALNRFVSDSDAEIAMIEKACAEHGVESLSEVWGKGGAGGAD					
	370	380	390	400	410	420
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
g141	LARKVVNAIDNQPNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
g141	LDKMPICMAKTQYSLSDNAKLLGCPGEGFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
g141	PAAEKIDVDEHGVHGLFX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

a141.seq

```

1   ATGAGTTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAAC TG
151 CCGCAAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC

```

```

201 GGC GGCGCGGAA GGTAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTTC GCGTGAAAGG CGGCGCGGCA GCGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GCGGCGGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTTGA CGGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTTTG GGCAACATCC TTGTGCTCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAAAC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAA
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCGTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAATTTCGG TTTCGCTTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCAAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGAGGCG GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCGT GCCCAAAGTT CCGGCTGCCG AGAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

```

a141.pep
1 MSFKTDAEIA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGAA GGGYAQVLPM EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPDGVM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKRLAG LKPDAAVVVA TVRALKYNNG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRVSDSDAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVHGLF*

```

m141/a141 99.5% identity in 558 aa overlap

```

          10      20      30      40      50      60
m141.pep MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL PQKQGRILIV
          |||||
a141      MSFKTDAEIAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL PQKQGRILIV
          10      20      30      40      50      60

          70      80      90      100     110     120
m141.pep TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLPM
          |||||
a141      TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLPM
          70      80      90      100     110     120

          130     140     150     160     170     180
m141.pep EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVVDNDRQLRNIID
          |||||
a141      EDINLHFTGDFHAIGAANLLAAMLNDHIYQGNELNIDPKRVLWRRVVDNDRQLRNIID
          130     140     150     160     170     180

```

m141.pep	190	200	210	220	230	240
	GMGKPV DGVMR PDGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
a141	GMGKPV DGVMR PDGFDITVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
m141.pep	250	260	270	280	290	300
	ANGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAALLKDAIKPNLVQTIIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	310	320	330	340	350	360
	GFGADLGA EKFC DIKCR LAGLKPDA AVV VATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGA EKFC DIKCR LAGLKPDA AVV VATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
m141.pep	370	380	390	400	410	420
	LLKHISNLKNV FGLPVVVALNR FVSDADAELAMIEKACAEHGVEVSLTEVWGKGAGGAD					
a141	LLKHISNLKNV FGLPVVVALNR FVSDADAELAMIEKACAEHGVEVSLTEVWGKGAGGAD					
	370	380	390	400	410	420
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAI AQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
a141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

```

g142.seq
1  ATGCGTGCCG  ATTCATGTT  TGCCGACAAT  ATGCCCGTGC  AGGTGCGCCA
51  ACGCGCCTTC  TATTTCAAGT  TGTCCCGTTT  TGCCGCGATG  CCAAATATGG
101 TAGGCAAAACC  GCTCTTCGGG  CGACAGGCCG  GTCAGCCCGG  CAAAATGTTT
151 GGCAACATCC  TGATGTTTCG  CCGCCAGCAT  ATTGATGCAG  AGgCTGCCGT
201 TTCCGACAG  GATcggaATG  AttcgCGCAC  TCCGGTTTAT  GCACAGCATC
251 ACGGTCGGCG  GCTCGTCGGT  AACCGGCGCA  ACCGCCGTCA  TTGTAATGCC
301 GTAACGCCCT  GCCGCACCGT  CTGTCGTGAT  GACATGAACG  CCTGCCGCAC
351 AGGATGCCAT  CGCATCACGG  AACGAAGTTT  GAAAAGTTT  CTGCAAATCC
401 GCCATTTTTC  CCCTTTAAAC  CGTCCCTTAT  ATAAGAATGC  TGCACACAAG
451 GCATCCCCC  ATGTGCAGCA  GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

```

g142.pep
1  MRADFMFADN  MPVQVRQRAF  YFKLSRFAAM  PNMVGKPLFG  RQAGQPGKMF
51  GNILMFVRQH  IDAEAAVFRQ  DRNDSRTPVY  AQHHGRRLVG  NRRNRHRCNA
101 VTPCRTVCRD  DMNACRTGCH  RITERSLKSF  LQIRHFSPLN  RPLYKNAAHK
151 ASPHVQQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 561>:

```
m142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCTGC AGGTGCGCCA
51  ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTT
151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCG ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AAGATGCCAT CGCATCACGG AACGAAGTTT GAAAATTTT CTGCAAATCC
401 GCCATTTTTC CCTTTTAAAC TGCCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCcC ATGTGCAGCA GTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 562; ORF 142>:

```
m142.pep
1  MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
51  GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVG NRRDRRHCA
101 VTPCRTVCRD DMNACRARCH RITERSLKIF LQIRHFSPLN CPLYKNAAHK
151 ASPHVQOF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 142 shows 93.7% identity over a 158 aa overlap with a predicted ORF (ORF 142.ng) from *N. gonorrhoeae*:

```
m142/g142
10      20      30      40      50      60
m142.pep MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNLMFVRQR
|||
g142      MRADFMFADNMPVQVRQAFYFKLSRFAAMPNMVGKPLFGRQAGQPGKMFNLMFVRQH
|||
10      20      30      40      50      60

70      80      90      100     110     120
m142.pep IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRHCAVTPCRTVCRDDMNACRARCH
|||
g142      IDAEAAVFRQDRNDSRTPVYAQHHGRRLVGNRRNRHCAVTPCRTVCRDDMNACRTGCH
|||
70      80      90      100     110     120

130     140     150     159
m142.pep RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX
|||
g142      RITERSLKSLQIRHFSPLNRPPLYKNAAHKASPHVQQFX
|||
130     140     150
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 563>:

```
a142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCTGC AGGTGCGCCA
51  ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTT
151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTCGCGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCTTTTAAAC TGCCCCCTAT ATAAGAATGC TGCACACAAG
451 GCACCCCCCA TGTGCAGCAG TTCTGATTCA AAAAGCCGTC GGTCCGACAT
501 TTCCGCGCGT TACGGCGTAT TACGAGTTCA ACGCATCCTC GATTTTGCCA
551 AGTTCTGCCA ACAGGTCTTT AAGCAGCAGC ATTTTCTCGC GGGCCAGCAC
601 TTCCTCGATA GCGTCGTAAC GTCGTCCAC TTCTTCGCGG ATTTCCTCAT
651 ACAGCTTCTC GCCCTCGGCA GTCAGCTTCA GAAAAACAG TCGTTGGTGC
701 TTGGAAGGTT TCAGGCGGAC AACCAAACCC GCTTTTTCAG GCGGGTCAG
751 GATACCGGTC AGGCTGGGGC GCAAAATGCA CGCCTGATTC GCCAAATCTT
```

801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC
 851 TGATCGGTAA TATTCGCCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG
 901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

a142.pep
 1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVR NRRNRHCNA
 101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAAHK
 151 APPMCSSSDS KSRRSDISAR YGVLVRQIL DFGKFCQOVF KQQHFLAAQH
 201 FLDSVVTLVH FFADFLIQLL ALGSQLOKNT SLVVGRFQAD NQTRFFKAGQ
 251 DTGQAGAQNA RLIRQILKVQ RAVFRQKTDN PELLIGNIRL IQNRPELGHQ
 301 GFPCLYQTDI DRRMF*

m142/a142 96.1% identity in 153 aa overlap

	10	20	30	40	50	60
m142.pep	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF	GNILMFVRQR				
a142	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF	GNILMFVRQR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m142.pep	IDAEAAVFRQDRNDSRTPVDAQHHGRRLVGNRRDRRHCNAVTPCRTVCRDDMNACRARCH					
a142	IDAEAAVFRQDRNDSRTPVDAQHHGRRLVNRNRNRHCNAVTPCRTVCRDDMNACRTGCH					
	70	80	90	100	110	120
	130	140	150	159		
m142.pep	RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX					
a142	RITERSLKSFQIRHFSPLNCPPLYKNAAHKAPPMCSSSDSKSRRSDISARYGVLVRQIL					
	130	140	150	160	170	180
a142	DFGKFCQOVFKQQHFLAAQHFLDSVVTLVHFFADFLIQLLALGSQLOKNTSLVVGRFQAD					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

g143.seq
 1 ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
 51 CTCGCAGATG AGCGCAGATT TTCAAACGCT AGGCGCAGAC CCGCACAAAT
 101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTTCAGCCG
 151 ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCCG
 201 CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCCTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTCGTCGAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGATATG GTCAACGAGG
 401 AGCAGAAAAG CTACGCCTAC GGGATTCAAA GTTCTTAGC GAATACGGAC
 451 GCGGTTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC
 501 GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCGTGGTC GTAGCATTCT
 551 ATGTGGGTGC GCGGTTACTG ATTATTACCA GTGCGTTTAC AATCTCCAAA
 601 GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACCGCGC
 701 CTAAAGTGTT TTGGACGGTT ACTCCGGTAC AGTTTTCTG CTGGTTCGCC
 751 TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGCAG AAAACGCTG
 801 GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCAACCGGT
 851 ACGGCGTTTT GGCGGCGGTG TAGTCGGTTG CGGCGGTGAT TTGTCGTTT
 901 ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGGCGGGTT ATTTCGGCTG
 951 TTTGGCTTTG GGCGCGCTCG GTTCTTCTC TATCTTCTC ATCTACAATC
 1001 AATACGCACT CATCCTGTCT TATATCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGGCC AACGCTTTGT CGGGCAAACA
 1101 CATGGATACT TATTTGGGCC TGTttaacgg ctctgtCTGT ATGCcgcaaa
 1151 tcgTcgctTC GctgttgAGT TTCGTGCTTT TCCCAGTGCT GGGCGGCCAT

1201 CAGGCAACCA TGTCTTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT
 1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep
 1 MLSFGYLGVO TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGYSDRTW KPRLGRRRLP YLLYGTLIAV IVMILMPNSG SFGFGYASLA
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKSYAY GIOSFLANTD
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSAFTISK
 201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFVTV TPVQFFCWFA
 251 FRYMWTYSAG AIAENVWHTT DASSVGHQEA GNRYGVLAHV *SVAVICSF
 301 ILAKVPNKYH KAGYFGCLAL GALGFFSIFV IYNQYALILS YILIGIAWAG
 351 IITYPLTIVA NALSGKHMGT YLGLFNGSVC MPQIVASLLS FVLFPMLGGH
 401 QATMFLVAGA VLLLGAFSVC LIKEIHGGV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq
 1 ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
 51 CTCGCAAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT
 101 TGGGCTGGTT TTTCATCCTG CCGCGCTGG CGGGGATGCT GGTGCAGCCG
 151 ATTGTGCGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG
 201 CCGTCTGCGG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
 301 GCTTTGTCTG TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAAA
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCACAGAGG
 401 AGCAGAAAGG CTACGCCTAC GGGATTCAAA GTTCTTAGC AAATACGGGC
 451 GCGGTCGTGG CCGCGATTCT GCCGTTTGTG TTTGCGTATA TCGGTTTGGC
 501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGGTC GTGGCGTTTT
 551 ATGTGGGTGC GCGTTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA
 601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
 651 CGCGCGAAT CAGGAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCGC
 701 CTAAGGCGTT TTGGACGTT ACTTTGGTGC AATTCTTCTG CTGGTTCGCC
 751 TTCCAATATA TGTGACTTA CTCGGCAGGC GCGATTGCGG AAAACGCTCTG
 801 GCACACCAAC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACTGGT
 851 ACGGCGTTTT GCGGCGGTG CAGTCGGTTG CCGCGGTGAT TTGTTGTTTT
 901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGCGGGTT ATTTGCGCTG
 951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTTCTTC ATCGGCAACC
 1001 AATACGCGCT GGTGTTGCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
 1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CCGGCAAGCA
 1101 TATGGGCACT TACTTGGGCT TGTTAACGG CTCTATCTGT ATGCCTCAA
 1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCTATGCT GGGCGGCTTG
 1201 CAGGCCACTA TGTCTTGGT AGGGGCGCTC GTCTGCTGC TGGGCGCGTT
 1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep
 1 MLSFGFLGVQ TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP
 51 IVGHYSRTW KPRLGRRRLP YLLYGTLIAV IVMILMPNSG SFGFGYASLA
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKGYAY GIOSFLANTG
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
 201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFVTV TLVQFFCWFA
 251 FQYMWTSYAG AIAENVWHTT DASSVGYQEA GNWYGVLAHV QSVAAVICSF
 301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
 351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGL
 401 QATMFLVGGV VLLLGAFSVF LIKETHGGV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10 20 30 40 50 60

m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
g143	MLSFGYLGVTAFQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGYYSDRTW
	10 20 30 40 50 60
m143.pep	70 80 90 100 110 120
	KPRLGRRRLPYLLYGTLIIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
g143	KPRLGRRRLPYLLYGTLIIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
	70 80 90 100 110 120
m143.pep	130 140 150 160 170 180
	QPFKMMVGDVNEEQKGYAYGQSFLANTGAVVAAILPFVFAYIGLANTAEGVVPQTVV
g143	QPFKMMVGDVNEEQKSYAYGQSFLANTDAVVAAILPFVFAYIGLANTAEGVVPQTVV
	130 140 150 160 170 180
m143.pep	190 200 210 220 230 240
	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV
g143	VAFYVGAALLIITSFTISKVKEYDPETYARYHGIDVAANQEKANWFELLKTAPKVFWTV
	190 200 210 220 230 240
m143.pep	250 260 270 280 290 300
	TLVQFFCWFQYMWYTSAGAIAENVWHTDASSVGYQEAGNWWYGVLAQVQSVAAVICSF
g143	TPVQFFCWFQYMWYTSAGAIAENVWHTDASSVGHQEAGNRYGVLAQVXSVAAVICSF
	250 260 270 280 290 300
m143.pep	310 320 330 340 350 360
	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
g143	ILAKVPNKYHKAGYFGCLALGALGFFSIFFIYNQYALILSYILIGIAWAGIITYPLTIVA
	310 320 330 340 350 360
m143.pep	370 380 390 400 410 420
	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVVLGAFSVF
g143	NALSGKHMDTYLGLFNGSVCMQIVASLLSFVLPMLGGHQATMFLVAGAVLLGAFSVC
	370 380 390 400 410 420
m143.pep	430
	LIKETHGGVX
g143	LIKEIHGGVX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 569>:

```

a143.seq
1  ATGCTCAGTT  TCGGCTTTCT  CGGCGTTCAG  ACGGCCTTTA  CCCTGCAAAG
51  CTCGCAGATG  AGCCGCATCT  TCCAGACGCT  CGGTGCCGAT  CCGCACAGCC
101 TCGGCTGGTT  CTTTATCCTG  CCGCCGCTGG  CGGGGATGCT  GGTGCAGCCG
151 ATTGTCGGCC  ATTACTCCGA  CCGCACTTGG  AAGCCGCGTT  TGGGCGGCCG
201 CCGTCTGCCG  TATCTGCTTT  ATGGCACGCT  GATTGCGGTT  ATTGTGATGA
251 TTTTGATGCC  GAACTCGGGC  AGCTTCGGTT  TCGGCTATGC  GTCGCTGGCG
301 GCTTTGTCGT  TCGGCGCGCT  GATGATTGCG  CTGTTAGACG  TGTCGTCAAA
351 TATGGCGATG  CAGCCGTTTA  AGATGATGGT  CGGCGACATG  GTCAACGAGG
401 AGCAGAAAGG  CTACGCCTAC  GGGATTCAAA  GTTCTTAGC  GAATACGGGC
451 GCGGTCTGG  CGGCGATTCT  GCCGTTTGTG  TTTGCGTATA  TCGGTTTGGC
501 GAACACCGCC  GAGAAAGGCG  TTGTGCCGCA  GACCGTGGTC  GTGGCGTTTT
551 ATGTGGGTGC  GCGGTTGCTG  GTGATTACCA  GCGCGTTCAC  GATTTTCAAA
601 GTGAAGGAAT  ACAATCCGGA  AACCTACGCC  CGTTACCACG  GCATCGATGT
651 CGCCGCGAAT  CAGGAAAAAG  CCAACTGGAT  CGAACTCTTG  AAAACCGCGC
701 CTAAGCGGTT  TTGGACGGTT  ACTTTGGTGC  AATTCTTCTG  CTGGTTCGCC

```

```

751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACCTGGT
851 ACGGCGTTTT GCGGCGGGTG CAGTCGGTTG CCGCGGTGAT TTGTTCTGTTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTTCGGCTG
951 TTTGGCTTTG GCGGCGCTCG GCTTTTCTC CGTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTTAACGG CTCTATCTGT ATGCCGCAAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTC CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
1  MLSFGLGVQ TAFTLQSSQM SRIFQTLGAD PHSLGWFFIL PPLAGMLVQP
51  IVGHYSDRTW KPRLGGRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA
101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDV VNEEQKGYAY GIQSFLANTG
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201 VKEYNPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FQYMWYSAG AIAENVHHTT DASSVGYQEA GNWYGVLAIV QSVAAVICSF
301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGL
401 QATMFLVGGV VLLLGAFSVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

	10	20	30	40	50	60
m143.pep	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
a143	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
	10	20	30	40	50	60
m143.pep	70	80	90	100	110	120
a143	KPRLGGRRLPYLLYGTLIIVIMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
	70	80	90	100	110	120
m143.pep	130	140	150	160	170	180
a143	QPFKMMVGDVNEEQKGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVPQTVV					
	130	140	150	160	170	180
m143.pep	190	200	210	220	230	240
a143	VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
	190	200	210	220	230	240
m143.pep	250	260	270	280	290	300
a143	TLVQFFCWFAFQYMWYSAGAIENVHHTTDASSVGYQEAAGNWYGVLAIVQSVAAVICSF					
	250	260	270	280	290	300
m143.pep	310	320	330	340	350	360
a143	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT					
	310	320	330	340	350	360
m143.pep	370	380	390	400	410	420
a143	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMLGGLQATMFLVGGVVLLLGAFSVF					

```

|||||
a143      NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMLGGLQATMFLVGGVVLLGAFSVF
              370      380      390      400      410      420

              430
m143.pep   LIKETHGGVX
              |||||
a143      LIKETHGGVX
              430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTTCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC CCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGTAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGCAC GGGCTGGCCG TTACCGgtTT
351 CAACGCGGTG GCGGCAGACG Gccgacggtt atCCCAACGA TTTGGatAtT
401 TCctaccgCT TGGACGAGGA CGGCCGGCTT ACCGTtacct ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGGCGGACAT
551 ATTCCGCGCG ATGCCGAAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFSVLADGV
51  RENPVVSFDD AASYADNPFO INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FGYFLPLGRG RPAYRYLSRH
151 RARRHGVRPD AAHLAAGRG PARCGSAYSA GRYSGRCRK TARLNGFRFP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGATGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAAC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTTCGGT GGTGCTGCGC AGCCGCGTg
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGG ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TAcCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFSVLADGV
51  RENLVVSFDD AASYADNPFO INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRL SQRFGEFYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHL AAGRGPARG SAYSAGR TYA
201 GRCRKTARLN GFRRPRSI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
g144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEFSVLADGVRENPFVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
g144	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m144.pep	AADGRSVVLRSLATVGRRLSQRFQYFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL					
g144	AAD-----GRLSQRFQ--YFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL					
		130	140	150	160	
	190	200	210	219		
m144.pep	AAGRGPARCGSAYSAGRTYAGRCRKRTARLNGFRFRPSIX					
g144	AAGRGPARCGSAYSAGRTYSGRCRKRTARLNGFRFRPSIX					
	170	180	190	200		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

```

a144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGTGACACG CGGTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTGCGT GGTGCTGCGC AGCCGCCTG.
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGCG ATATTTCCTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TACCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATTCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 576; ORF 144.a>:

```

a144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFSVLADGV
51  RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLXTVGRR L SQRFQGYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHLL AAGRGPARCG SAYSAGRTYS
201 GRCKRTARLN GFRFRPSI*

```

m144/a144 99.1% identity in 218 aa overlap

	10	20	30	40	50	60
m144.pep	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
a144	MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFSVLADGVRENLVVSFDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m144.pep	AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV					

410

```

a144      |||||
          AASYADNPFOINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
          70      80      90      100     110     120

          130     140     150     160     170     180
m144.pep  AADGRSVVLRSLATVGRRLSQRFGFYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL
          |||||
a144      AADGRSVVLRSLATVGRRLSQRFGFYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL
          130     140     150     160     170     180

          190     200     210     219
m144.pep  AAGRGPARGCSAYSAGRTYAGRCRKRTARLNGFRRPRSIX
          |||||
a144      AAGRGPARGCSAYSAGRTYSGRCRKRTARLNGFRRPRSIX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

gl46.seq
1  ATGAAGCAAA TCCCCCTCCG CCTTCTCCAG GTCGTCATTG ACCACGACAA
51 AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCTT CGACAGCCTC
101 CTTTGGATAa ctTCCCGACT GTCCGTCCCG CGCctTTGA GGCGCGCGGC
151 AAGCACGTCTG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCCGGCA
201 GCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGTCTG CGTATTCCAA AAAAGCCTCC TGCGCGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTATGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGGAC ACCCTATTTT
601 ATATTGCGG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

gl46.pep
1  MKQIPLRLQ VVIDHDKVEQ YGLFDEMPC L RQPPLDNFPT VRPAPEARG
51 KHVERRRQDK DTDSEFRQVA NLRRLNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCVFQ KSLLRDKRFK LFFGNKVIMY AVCFAFTRRA RMRHGNNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1  ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51 AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCTT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTCCGTCCCG CGTCCGTTGA GGCGCGCGGC
151 AAGTACGTCTG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCCGGCA
201 GCGCGTTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAGCCTG CCGCCGCCAA CGCATTACAG CCCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGTCTG CGTATTCCAA AAAAGCTTCC TGCGCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGGGCG CGTCGTGTGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTG CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTGCGG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.pep
1  MAQILLRSRQ VVIDHDKVKQ YGLLDEMPC L RQPPLDNFPT VRPASVEARG
51 KYVERRRQDK DADGFGQVA NLRRLNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYVGVFQ KSLFLDKRLK LFFGNKVIMY AVCFAFTRRA RVRHGNNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
g146	10	20	30	40	50	60
	MKQIPLRLQVVVIDHDKVEQYGLDFMPCLRQPPLDNFPTVRPAPFEARGKHVERRRQDK					
m146.pep	70	80	90	100	110	120
	DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFRLDKRLK					
g146	70	80	90	100	110	120
	DTDSFRQRVANLRRALNVDFQNHVIACRRQRIHALRACAVIVAEYVCVFQKSLLRDKRKF					
m146.pep	130	140	150	160	170	180
	LFFGNKVIMYAVCFATRRARRVRHGNATVMVCQQPRHQRFARAGSGRNDKDVAFSIS					
g146	130	140	150	160	170	180
	LFFGNKVIMYAVCFATRRARRMRHGNATVMVCQQPRHQRFARAGSGRNDKDVAFSIS					
m146.pep	190	200	210			
	GHIFYLYIFQPIVSQWTPSFLFADAHILPLLF					
g146	190	200	210			
	GHIFYLYIFQPIVSQRTPYFIFADAHILPLLF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

```

a146.seq
1  ATGGCGCAAA TCCTCCTCCG CCCGCGCCAA GTCATCATTG ACCACGACAA
51  AATCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCCT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTCCGTCCCG CGTCCGTTGA GACGCGCAGC
151 AAGCACATCG AAAGACGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCATCTCG AACCTGAGCC GCGCCCTGAA CGTCGATTTC CAAAATCACG
251 TCATAACCTG CCGCCGCCAA CGCATTCACA CCCTCCGCGC TTGTGCCGTA
301 ATAGTTGCCG AACACGTCCG CGTATTCCAA AAAAGCCTCC TCGCGGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGCGGACG CGTCGTGTGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATT
551 TTTACCTGTA TATTTCCAG CCGATTGTAT CACAACGGAC ACCCGGTTTC
601 CTATTTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

```

a146.pep
1  MAQILLRPRQ VIIDHDKIEQ YGLDFMPCL RQPPLDNFPT VRPASVETR
51  KHIERRRQDK DADGFGQRIS NLSRALNVDF QNHVITCRRQ RIHTLRACAV
101 IVAEHVRVFQ KSLLRDKRLK LFFGNKVIMY AVCFAFTRRT RVRHGNAT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPGF
201 LFADAHILPL LF*

```

m146/a146 90.6% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
a146	10	20	30	40	50	60
	MAQILLRPRQVIIDHDKIEQYGLDFMPCLRQPPLDNFPTVRPASVETRSKHIERRRQDK					
	70	80	90	100	110	120

```

m146.pep  DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK
          |||||::|| |||||::|| |||||::|| |||||::|| |||||::|| |||||::||
a146      DADGFGQRI SNLSRALNVDFQNHVITCRRQRIHTLRACAVIVA EHV RVFQKSLLRDKRLK
          70          80          90          100         110         120

          130         140         150         160         170         180
m146.pep  LFFGNKVIMYAVCFATRRRARRVRHGNATVMVCQQPRHQRFARAGSGRNDKDVAFSIS
          |||||::|| |||||::|| |||||::|| |||||::|| |||||::|| |||||::||
a146      LFFGNKVIMYAVCFATRRRARRVRHGNATVMVCQQPRHQRFARAGSGRNDKDVAFSIS
          130         140         150         160         170         180

          190         200         210
m146.pep  GHIFYLYIFQPIVSQWTPSFLFADAHILPLLFX
          |||||::|| |||||::|| |||||::|| |||||::|| |||||::||
a146      GHIFYLYIFQPIVSQRTPGFLFADAHILPLLFX
          190         200         210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```

g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC ACACTCAAAC CCATTGTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CGCCCAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCGACTT CGGGGCTGCT GCACACTTCG ACCGCCTCCG ACAAATCAT
201 CTCCGGCGAT ACTTTGCGCC AAAAAGCCGT CAACTTGGGC GACGCTTTGG
251 ACGGCGTACC GGGCATCCAC GCTTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAAGTAT TGAACCATCA
351 CGGCGAAACG GGGATATGG CGGACTTTTC TCCGATCAC GCCATTATGG
401 TAGATACCGC CTGTGCGCAA CAGGTTGAAA TCCTGCGCGG GCCGTTACG
451 CTCTTGTA CA GCTCGGgcaa tgtggccgGG GCTGGtcaat gttgccgatg
501 gAAAAAtccc ccaaaaATg cc..

```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```

g147.pep (partial)
1  ..MRREAKMAQI TLKPIVLSIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHGET GDMADFSPDH AIMVDTALSQ QVEILRGPVT
151 LLYSSGNVAG AGQCCRWKNP PKNA..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

```

m147.seq (partial)
1  ..CCGCATAAAA CTGAGCAATC GGTGGATTG GAAACGGTCA GCGTCGTCGG
51  CAAAAGCCGT CCGCGCGCCA CGTCGGGGCT GTTGCACT TCGACCGCCT
101 CCGACAAAAT CATCTCCGGC GATACCTTGC GCCAAAAGC CGTCAACTTG
151 GCGGACGCTT TAGACGGCGT ACCGGGCATC CACGCTTCG AATACGGCGG
201 CGGCGGCTCT GCTCCGTC TCGCGGTCA AACAGGCAG CGGATTAAG
251 TGTGAACCA TCACGGCGAA ACAGGCGATA TGGCGGATT TTCGCCGAT
301 CACGCCATTA TGGTAGATAC CGCCTTGTG CAACAGGTCG AAATCCTGCG
351 CGGGCCGGTT ACGCTCTTGT ACAGCTCGGG CAATGTGGCG GGGCTGGTCG
401 ATGTTGCCGA TGGCAAAATC CCCGAAAAA TGCCTGAAAA CGGCGTATCG
451 GGCGAACTCG GATTGCGTTT GAGCAGCGGC AATCTGAAAA AACTCACGTC
501 CGGCGGCATC AATATCGGTT TGGGCAAAAA CTTTGTATTG CACACGGAAG
551 GGCTGTACCG CAAATCGGGG GATTACGCCG TACCGGTTA CCGCAATCTG
601 AAACGCCTGC CCGACAGCCA CGCCGATTG CAAACGGGCA GCATCGGGCT
651 GTCTTGGGTT GCGAAAAAG GTTTATCGG CGTAGCGTAC AGCAGCGTC
701 GCGACCAATA TGGTCTGCCT GCCACAGCC ACGAATACGA TGATTGCCAC
751 GCCGACATCA TCTGGCAAAA GAGCTTGATT AACAAACGCT ATTTACAGCT
801 TTATCCGCAC CTGTTGACCG AAGAAGACAT CGATTACGAC AATCCGGGCT
851 TGAGCTGCGG CTTCACGAC GACGATAATG CACACGCACA CACCACAGC
901 GGCAGACCGT GGATAGACCT GCGCAACAAA CGCTACGAAC TCCGTGCCGA
951 ATGAAGCAA CCGTTCCCG GTTTGAAGC CCTGCGCGTA CACCTGAACC
1001 GCAACGACTA CCGCCACGAC GAAAAAGCAG GCGATGCAGT CGAAAACTTT
1051 TTTAACAACC AAACGCAAAA CGCCCGCATC GAGTTGCGCC ACCAACCCAT

```

```

1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACAAACCGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCCGACC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACAGC CACAACACAA ACTCAGCCTG ACCGCCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAATCTG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCCTTCG GTAACCTACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGCGCG CGACTTCTAC GGCGCGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCCGTCT GAAAAACCTG CTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC
1951 GACCGTATCG ATGCCAATTG GGACTACTAC CGCGTGTTCG CCCAAACAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCGG ACACCATATG CTCAACCTCG
2051 GCGCAAACCTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACA GCAGCTTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGCGCGC GTGAACGTGA
2201 AGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1  ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STADKIIISG DTLRQKAVNL
51  GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNFVL HTEGLYRKSG DYAVPRYRNL
201 KRLPDSHADS QTGSIGLSWV GEKGFIVGAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQKSLI NKRYLQLYPH LLTEEDIDYD NFGLSGCFHD DDNAHAHTHS
301 GRPWIDLRNK RYELRAEWKQ PFPGFALRV HLNRRNDYRD EKAGDAVENF
351 FNNQTQNARI ELRHQPIGRL KGSWGVQYLQ QKSSALSAIS EAVKQPMLLD
401 NKVQHYSEFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IDRENYNHP
451 LPDLGAHRQT ARSFALSGNW YFTPQHKLSL TASHQERLPS TQELYAHGKH
501 VATNTFEVGN KHLNKNERSNN IELALGYEGD RWQYNLALYR NRFGNYIYAQ
551 TLNDGRGPKS IEDDSEMCLV RYNQSGADFY GAEGEYFKP TPRYRIGVSG
601 DYVRGRLLNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

m147.pep                                10      20      30
                                         PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
g147      MRREAKMAQITLKPVL SILLINTPLLAQAHETE QSVGLETVSVVGKSR PRATSGLLHTS
                                         10      20      30      40      50      60

m147.pep      40      50      60      70      80      90
TASDKIIISGDTLRQKAVNLGDALDGVPGI HASQYGGGASAPVIRGQTGRRIKVLNHHGET
g147      TASDKIIISGDTLRQKAVNLGDALDGVPGI HASQYGGGASAPVIRGQTGRRIKVLNHHGET
                                         70      80      90      100     110     120

m147.pep      100     110     120     130     140     150
GDMADFSPPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGLVDVADGKIPEKMPENGVS
g147      GDMADFSPPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGAGQCCRWNPPKNA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

```
a147.seq
1  ATGCGACGAG AAGCCAAAAT GGCACAAACT ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCAAGCG CATGGAAGTG
101 AGCAATCAGT GGGCTTGGA ACGGTCAGCG TCGTCGGCAA AAGCCGTCGG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGCGAC AAAAAGCCGT CAACTTGGGT GATGCTTTAG
251 ACGGCGTACC GGGCATTCAT GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAGTGT TGAACCATCA
351 CGGCGAAACG GGCGACATGG CGGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTCGCAA CAGGTCGAAA TCCTGCGCGG TCCGGTTACG
451 CTCTTGTA CA GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGCGGATGG
501 CAAAATCCCC GAAAAAATGC CTGAAACGG CGTATCGGGC GAACTCGGAT
551 TGCGTTGAG CAGCGGCAAT CTGAAAAAC TCACGTCGGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAACCT TGTATTGCAC ACGGAAGGGC TGTACGCCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTGCGAA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATAACGC GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGG
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCGGTTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAACCTTTTT AACAACCAAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCGATGCT GCTTGACAAT AAAGTCAAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTACGCTT
1351 GAAGCGGCG TACGCGTGGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAACCGGCC CGCTATTTCG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAAACT CAGCCTGACC GCCTCCCATC AGGAACGCCT
1551 GCGGTCACG CAAGAGCTGT ACGCACACGG CAAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAAAC TTAAACGACG
1751 GACGCGGCCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACGACA CCGCGCTACC GCATCGGCGT TTCCGCGGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACCGCCAC TCATTGCCCA AGCCGACCAA AACGCCCTC GCGTTCGGG
2001 TGCGCGCTC GCGTCCACC TGAAAGCCTC GCTGACCGAC CGCATCGATG
2051 CCAATTGGA CTACTACCGC GTGTTGCGCC AAAACAAACT CGCCCGCTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGGAATTG GTACGTCAA GCCGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CGGCGCGTG AACGTGAAGT TTAA
```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

```
a147.pep
1  MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRQGTGRR IKVLNHHGET GDMADFSPDH AIMVDSALSQ QVEILRGFVT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVSF ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKSGD YAVPYRNLK RLPDSHADSQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEDIDIDYN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNAIE LRHQPIGRK
401 GSWGVOYLQ KSSALSATSE AVKQPMLLDN KVQHYFFGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENNYHPL PDLGAHRQTA RSFALSGNWI
501 FTPQHKLSLT ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR
```

601 YNQSGADFYG AEGEIYFKPT PRYRIGVSGD YVRGRLKNLP SLPGREDAYG
651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLDYYR VFAQNKLARY
701 ETRTPGHHML NLGANYRRNT RYGEWNWYVK ADNLLNQSVY AHSSFLSDTP
751 QMGRSFTGGV NVKF*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLETVS	VVVGKSRPRATSGLLHTS
a147	MRREAKMAQTT	TLKPIVLSILLINTPLLSQA	HGTEQSVG	LETVS	VVVGKSRPRATSGLLHTS	
	10	20	30	40	50	60
m147.pep		40	50	60	70	80
		TASDKIISGDTLRQKAVNLGDALDGV	PGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET			
a147		TASDKIISGDTLRQKAVNLGDALDGV	PGIHASQYGGGASAPVIRGQTGRRIKVLNHHGET			
		70	80	90	100	110
m147.pep		100	110	120	130	140
		GDMADFS	PDHAIMVDTALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
a147		GDMADFS	PDHAIMVDSALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
		130	140	150	160	170
m147.pep		160	170	180	190	200
		ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRN	LNKRLPDSHAD			
a147		ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRN	LNKRLPDSHAD			
		190	200	210	220	230
m147.pep		220	230	240	250	260
		TGSIGLSWVGEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHL		
a147		TGSIGLSWVGEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADI	IWQKSLINKRYLQLYPHL		
		250	260	270	280	290
m147.pep		280	290	300	310	320
		LTEEDIDYDNPG	SCGFHDDNAHAH	THSGRPWIDL	RNKRYELRAEWKQFPFGFEALRVH	
a147		LTEEDIDYDNPG	SCGFHDDDAHAH	AHNGKWPIDL	RNKRYELRAEWKQFPFGFEALRVH	
		310	320	330	340	350
m147.pep		340	350	360	370	380
		LNRNDYRHDEKAGDAVENFF	NNQTQ	NARIELRHQPIGRLKGSWGVQY	LQKSSALS	SAISE
a147		LNRNDYRHDEKAGDAVENFF	NNQTQ	NARIELRHQPIGRLKGSWGVQY	LQKSSALS	SATSE
		370	380	390	400	410
m147.pep		400	410	420	430	440
		AVKQPM	LLDNKVQHYSFFGVEQANWDNFT	LEGGVRVEKQKASIQYDKALIDRENYYNHPL		
a147		AVKQPM	LLDNKVQHYSFFGVEQANWDNFT	LEGGVRVEKQKASIRYDKALIDRENYYNHPL		
		430	440	450	460	470
m147.pep		460	470	480	490	500
		PDLGAHRQTAR	SFALSGNWYFT	PQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK		
a147		PDLGAHRQTAR	SFALSGNWYFT	PQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK		
		490	500	510	520	530
m147.pep		520	530	540	550	560
		HLNKERSNNIELALGYEGDRWQYNLALYRN	RFRGNYIYAQTLNDGRGPKSIEDDSEM			
a147		HLNKERSNNIELALGYEGDRWQYNLALYRN	RFRGNYIYAQTLNDGRGPKSIEDDSEM			
		570				

	550	560	570	580	590	600
m147.pep	580	590	600	610	620	630
	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPPIAQDDQ					
a147	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQ					
	610	620	630	640	650	660
m147.pep	640	650	660	670	680	690
	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
m147.pep	700	710	720	730		
	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGctgg  ttcaTCCCCG
51  AgctATgagt  gtcggcgCGC  TTGccgAcaa  AATCCGCAAA  AtcgaAAact
101 gCCGCAAAA  AGgcaTCTTA  TTCCACGACA  TCACGCCCGT  CCTGCAAAAGT
151 GCGGAATACT  TCCGCCTTTT  GGTTCGATTG  CTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGCTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAg  CTCaACGtcg  gctTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCCTATCG  CAAAGCTAcg  cgcTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGa  tgccgTCAAA  CCCGGTTCGC
401 GCGTCCTGCT  GGTTCGATGAT  TTGGTTGCCA  CGGGCGGCAC  AATGCTTGCC
451 GGGCTGGAAC  TGATCCGCAA  ACTCGGCGGG  GAAATTGTCT  AAgccgcgcC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGCGCAAGTG
551 GCGCGCCCTT  ATTTACCCCTG  CTTCAAAACG  AAGGCTGCAT  GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK
101 KGKLPFETVS  QSYALEYGEA  AVEIHTDAVK  PGSRVLLVDD  LVATGGTMLA
151 GLELIRKLGG  EIVEAAAILE  FTDLQGGKNI  RASGAPLFTL  LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148.seq
1  ATGGCGTTAA  AAACATCAAA  CTTGGAACAC  GCAATGCTGG  TTCATCCCCG
51  AGCTATGAGT  GTCGGCGCGC  TTGCCGACAA  AATCCGCAAA  ATCGAAAAC
101 GGCCGCAAAA  AGGCATCTTA  TTCCACGACA  TCACGCCCGT  CCTTCAAAGC
151 GCGGAATACT  TCCGCCTTTT  GGTTCGATTG  TTGGTTTACC  GCTATATGGA
201 TCAGAAAATC  GACATCGTTG  CCGGTTTGGA  CGCGCGCGGC  TTCATTATCG
251 GCGCGGCACT  CGCCTACCAg  CTCaACGTCG  GTTTCGTCCC  CATCCGCAAA
301 AAAGGCAAGC  TGCCTTTTGA  AACCCTATCG  CAAAGCTACG  CGCTCGAATA
351 CGGGGAAGCT  GCGGTGGAAA  TCCACACCGA  TGCGGTCAAA  CTCGGTTCGC
401 GCGTGCTGCT  GGTTCGATGAT  TTGATTGCCA  CGGGCGGCAC  GATGCTTGCC
451 GGACTGGAAC  TGATCCGCAA  ACTCGGCGGA  GAAATTGTCT  AAGCCGCCGC
501 CATTTTGGAA  TTTACCGACC  TTCAAGGCGG  CAAGAATATC  CGTGAAGCG
551 GCGCGCCCTT  ATTTACCCCTG  CTTCAAAACG  AAGGCTGTAT  GAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148.pep
1  MALKTSNLEH  AMLVHPEAMS  VGALADKIRK  IENWPQKGIL  FHDITPVLQS
51  AEYFRLLVDL  LVYRYMDQKI  DIVAGLDARG  FIIGAALAYQ  LNVGFVPIRK

```

101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDLATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTCGGTGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAAAC
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCGT	CCTGCAAAGC
151	GCGGAATACT	TCCGACTTTT	GGTTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CGGTTTGGA	CGCGCGCGGC	TTCATTATCG
251	GCGCGGCACT	CGCCTACCAG	CTCAACGTCG	GTTTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGAAA	TCCACACCGA	TGCCGTCAAA	CTCGGTTCCG
401	GCGTGCTGCT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGACTGGAGC	TGATCCGCAA	ACTCGGCGGG	GAAATTGTCT	AAGCCGCCGC
501	CATTTTGGA	TTTACCGACC	TTCAAGGCGG	CAAGAATATC	CGTGCAAGCG
551	GCGCGCCCTT	ATTACCCCTG	CTTCAAAACG	AAGGCTGTAT	GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDQKI	DIVAGLDARG	FIIGAALAYQ	LNVG FVPIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	LGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m148.pep  LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYLEYGEA
          |||
a148      LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYLEYGEA
          70      80      90      100     110     120

          130     140     150     160     170     180
m148.pep  AVEIHTDAVKLGSRVLLVDDLATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
          |||
a148      AVEIHTDAVKLGSRVLLVDDLATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
          130     140     150     160     170     180

          190     200
m148.pep  RASGAPLFTLLQNEGCMKGX
          |||
a148      RASGAPLFTLLQNEGCMKGX
          190     200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

```

g149.seq
1  ATGTTGATTG ACAACAATGT CCGCCATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAACCTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATCCGTAC GACAAAGCAT TGATTGATCG AGAAACTAC
151 TACAACCAGC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCCTC
201 GTTCGCACTT TCGGGCAACT GGTATTTTAC GCCACACCAC AAACCTAGCC
251 TTACCGCCTC CCATCAGGAA cgCCTGCCGT CAACGCaaga actGtACgca
301 cacggcAAGC ACgtcgccac CAACACCTTT GAagtcgga acaaACACCT
351 CAACAAAGaG CgttccaacA atategaACT CGCGCTGGgc tAcaaaggcg
401 accGCTGGCA ATACAATCTG GCAGCCTACC GCAACCGaTt CGGCAACTAC
451 ATTTACGCCC AAACCTTAaa cgacggacgC GGCCCCAAAT CCATCgaaga
501 cgacagcgaa ATGaagcTCG TCGCTACAA CCAATCCGGT GCCGACTTCT
551 ACGgcgcgga aggcgaaatc tACTTcaaaC CGAcACCGCG CTACCGCATC
601 GGTGTTTCCG GCGACTatgt acgaggccgT CTGAAAAACC TGCCGTCCTT
651 ACCCGGCAGG gaagatccCT AcggcAAACG TCcettcaTC GCACAAGCCG
701 ACCAAAACGC CCCCCTGATT ccggctGCGC GCCTCGGCTT CCACCTGAAA
751 ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCCAAAAC AAACCTGCCC GCTACGAAAC GCGTACGCCC GGACACCATA
851 TGCTCAACCT CCGTGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGctc aACcaatCcg tTTACGCCCa
951 cAGCAGCTTC CTCTCTGATA CGCCGCAaAt gGGCCGCAGC TTtgccgGCg
1001 gcgtaAACGT GaAGTTtaa

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

```

g149.pep
1  MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSFAL SGNWYFTPHH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YKGDWQYNL AAYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVS GDYVVRGR LKNLPSLPGR EDPYGRPFPI AQADQNAPRI PAARLGFHLK
251 TSLTDRIDAN LDYYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

```

m149.seq
1  ATGCTGCTTG ACAACAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATGCG GACAACCTCA CGCTTGAAGG AGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATTCACTAC GACAAAGCAT TGATTGATCG GGAAACTAC
151 TACAACCACC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAACCTAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACgtcgccac CAACACCTTT GAAGTCGGCA ACAAACACCT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGTAACCTAC

```

```

451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
501 CGACAGCGAA ATGAAGCTCG TGCGGTACAA CCAATCCGGC GCCGACTTCT
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601 GCGGTTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAAAC TGCCTTCCCT
651 ACCCGGCAGA GAAGATGCCT ACGGCAACCG TCCTTTCATC GCACAGGACG
701 ACCAAATGCG CCCCCTGTT CCGGTGCGC GCCTCGGCTT CCACCTGAAA
751 GCCTCGCTGA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCCCAAAC AAACCTCGCCC GCTACGAAAC GCGCAGCCCC GGACACCATA
851 TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCC
951 CAGCAGCTTT CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACCGGCG
1001 GCGTGAACGT GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 598; ORF 149>:

m149.pep

```

1  MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIYQ DKALIDRENY
51  YNHPLPDLGA HRQTARFAL SGNWYFTPOH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFNGY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVGSDYVRGR LKNLPSLPGR EDAYGNRPFI AQDDQONAPRV PAARLGFHLK
251 ASLTDRIDAN LDYRVFAQN KLARYETRTP GHHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 149 shows 95.9% identity over a 339 aa overlap with a predicted ORF (ORF 149.ng) from *N. gonorrhoeae*:

m149/g149

m149.pep	10	20	30	40	50	60
	MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIYQ DKALIDRENY YNHPLPDLGA					
g149	MLIDNNVRHYSFFGVEQANW DNFTLEGGVR VEKQKASIRYDKALIDRENY NQPLPDLGA					
	10	20	30	40	50	60
m149.pep	70	80	90	100	110	120
	HRQTARFALSGNWYFTPOH KLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
g149	HRQTARFALSGNWYFTPHH KLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	130	140	150	160	170	180
	RSNNIELALGYEGDRWQYNL AAYRNRFNGY IYAQTLNDGRGPKSIEDDSEM KLVRYNQSG					
g149	RSNNIELALGYKDRWQYNL AAYRNRFNGY IYAQTLNDGRGPKSIEDDSEM KLVRYNQSG					
	130	140	150	160	170	180
m149.pep	190	200	210	220	230	240
	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGRE DAYGNRPFI AQDDQONAPRV					
g149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGRE DPYKRPFI AQADQONAPRI					
	190	200	210	220	230	240
m149.pep	250	260	270	280	290	300
	PAARLGFHLKASLTDRIDAN LDYRVFAQNKLARYETRTPGHHMLNLGAN YRRNTRYGEW					
g149	PAARLGFHLKTSLTDRIDAN LDYRVFAQNKLARYETRTPGHHMLNLGAN YRRNTRYGEW					
	250	260	270	280	290	300
m149.pep	310	320	330	340		
	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					

420

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX
310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq
1 ATGCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51 GGCAAACTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAAACTAC
151 TACAACCATC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTCAC GCCACAACAC AAACCTCAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGCAACTAC
451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
501 CGACAGCGAA ATGAAGCTCG TCGCTACAA CCAATCCGGT GCGGACTTCT
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601 GGCGTTTCCG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT
651 ACCCGGCAGG GAAGACGCCT ACGGCAACCG CCCACTCATT GCCCAAGCCG
701 ACCAAAACGC CCCTCGCGTT CCGGCTGCGC GCCTCGGCGT CCACCTGAAA
751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCCAAAAC AAACCTCGCC GCTACGAAAC GCGCACGCCG GGACACCATA
851 TGCTCAACCT CGGCGCAAAC TACCGCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA
951 CAGCAGCTTC CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACCGGCG
1001 GCGTGAACGT GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep
1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51 YNHPLPDLGA HRQTARFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSQDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV PAARLGVHLK
251 ASLTDRIDAN LDYYRVFAQN KLARYETRTP GHMMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

m149/a149 98.8% identity in 339 aa overlap

m149.pep	10	20	30	40	50	60
a149	10	20	30	40	50	60
m149.pep	70	80	90	100	110	120
a149	70	80	90	100	110	120
m149.pep	130	140	150	160	170	180
a149	130	140	150	160	170	180
m149.pep	190	200	210	220	230	240
a149	190	200	210	220	230	240
m149.pep	250	260	270	280	290	300
a149	250	260	270	280	290	300

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 601>:

g149-1.seq

1	ATGGCACAAA	TCACACTCAA	ACCCATTGTT	TTATCAATTC	TTTTAATCAA
51	CACACCCCTC	CTCGCCCAAG	CGCATGAAAC	TGAGCAATCG	GTGGGCTTGG
101	AAACCGGTAG	C6TGCTCGCG	AAAAGCCGTC	CGCGCGCGAC	TCGGGGGCTG
151	CTGCACACTT	CGACCGCCTC	CGCAAAAATC	ATCTCCGGCG	ATACTTTGCG
201	CCAAAAAGCC	GTCACATTGG	GGCAGCGTTT	GGACGGCGTA	CCGGGCATCC
251	ACGCTTCGCA	ATACGGCGCG	GGCGCATCCG	CTCCCGTTAT	TCGCGGTCAA
301	ACGGGCAGAC	GGATTAAAGT	ATTGAACCAT	CACGGCGAAA	CCGGCGATAT
351	GGCGGACTTT	TCTCCCGATG	ACGCCATTAT	GGTAGATACC	GCCTTGTCGC
401	AACAGGTTGA	AATCTCTCGC	GGTCCGGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GGGTGTCGA	TGTTGCCGAT	GGAAAAATCC	CGCAAAAAAT
501	GCCTGAAAAC	GGCGTATCGG	GCGAagccgG	ATTGCGTTTG	AGCAGCGGCA
551	ATTTAGAAAA	ACTGACATCC	CGAGGACATCA	ATATCGGAGT	GGGCAAAAAAC
601	TTCTGCTGTC	ATACCGAAGG	CTTGTACCGC	AAATCGGGCG	ATTACCCGCT
651	ACCGCGTTAC	CGCAATCTGA	AACGCCTGCC	CGACAGCCAT	CCCGATTTCG
701	AAACGGGGAG	CATCGGGCTG	TCTTGGGTGG	GCGAAAAAGG	CTTTTATGGC
751	CGACCATACA	CGCAGCCGTG	CGACCGCTAC	GGCCTGCGCT	CCCCACAGCCA
801	CGAATACGAT	GATTGCCACG	CGACATCAT	CTGGCAAAAG	AGGTTGATCA
851	ACAAACGCTA	TTTGCGACTT	TATCCGCACT	TGTTGACCGA	AGAAGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTCGCGC	TTCCCAGCAG	CGCAGCGTGC
951	ACACGCACAC	ACCCACAACG	CGAAACCGTG	GATAGACCTG	GCGACAACAA
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGC	CATTCCCCGG	TTTTGAAGCC
1051	CTCGCGGTAC	ATCTGAACCG	CAATGACTAC	CACCACGACG	AAAAAGCAGG
1101	CGATGCACTA	GAAAACTTCT	CTAGACAACAA	AACACACAAC	CGCGGTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	CGCGCTTTCG	GCCATTCCCG	AAACCGTCCA
1251	ACAAACGATG	TTGATTGACA	ACAATGCTCG	CAATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAATTGGGAC	AACTTCACGC	TTGAAGCGCG	GTCTACGGCTG
1351	GAaaaaCAAA	AAGCCTCCAT	CCGGTACGAC	AAAGCATTTA	TTGATCGAGA
1401	AAACTACTAC	AACACGCCCC	TGCCCGACCT	CGGCGCGCAC	GCCCAACCCG
1451	CCCGCTCGTT	CGCACTTTCG	GGCAACTGGT	ATTTCAGCCG	ACACCAACAA
1501	CTCAGCCTGA	CCGCTCTCCA	TCAGGAACGC	CTCGCGTTAA	CGCAAGAACT
1551	GTACGCCACG	GGCAAGCAGC	TCGCCACCAC	CACCTTTTGA	GTGGGCAACA
1601	AACACCTCAA	CAAGAGCGGT	TCCAACAATA	TGCAACTTCG	GCTGGGGTAC
1651	GAAGCGGACC	GCTGGCAATA	CAATCTGGCA	GCCTACCGCA	ACCGATTTCG
1701	CAACTACATT	TACGCGCCAA	ACCTTAACGC	CGGACGCGCG	CCCAAAATCCA
1751	TCGAAGACGA	CAGCGAAATG	AAGTCTGTGC	GCTACAACCA	ATCCGCTGCC
1801	GACTTCTACG	GCGCGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCGCGCTA
1851	CCGCATCGGT	GTTTCTCGCG	ACTATGTACG	AGGCCGTCTG	AAAAACCTGC
1901	CGTCCCTATC	CGGCAGGGAA	GATCCCTACG	GCAACCGTCC	CTTCAATCGCA
1951	CAAGCCGACC	AAAACGCCCC	CCGCAATTCC	GCTGGCGCGC	TCGGGTTCCA
2001	CCTGAAAAAC	TCGCTAACCG	ACCGTATCGA	TGCAATTTTG	GACTACTTACC
2051	GCGTGTTCGC	CCAACACAAA	CTCGCCCGCT	ACGAAACCTG	TACGCGCCGGA
2101	CCACCATATG	CCAAACTCGG	TCCAACATAC	CGCCGCAATA	CGCGCTATGG
2151	CGAGTGGAA	TGCTACGTCA	AAGCGACAAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCACACG	CAGTCTTCTC	TCTGATACGC	CGCAATGGG	CCGACGTTTT
2251	ACCGCGCGCG	TAAACGTGAA	GTTTTTAA		

This corresponds to the amino acid sequence <SEQ ID 602; ORF 149-1.ng>:

g149-1.pap

1	MAQITLKP	IV	LSILLINTPL	LAQAHETEQS	VGLETVS	VVG	KSRPRATSG	L
51	LHSTASDKI	ISGDTLRQKA	VNLGDALGV	PGIHASQYGG	GASAPVLLY	SG		
101	TGRIKVLNH	HGETGDMAF	SPDHAIMDVT	ALSQQVEILR	GPVTLLYSSG			
151	NVAGLVDVAD	GKIPKMPEN	GVSGEAGLRL	SSGNLEKITS	AGINTGLGKN			
201	FVLHTEGLYR	KSGDYAVRY	RNLKRLPSKH	ADSQRTSYGL	SWVGKGKGFJ			
251	AAYSDRDRY	GLPAHSHEYD	DCHADIIWQ	SILINKRYLQ	YPHLLTEEDI			
301	DYDNPGLSG	FHDGDGAHAF	THNGKPIIDL	RNKRYELRAE	WKQPFPGFEA			

```

351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRKGSWGVQ
401 YLGQKSSALS AIPETVQQPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDRWQYNLA AYRNRFNGYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSPGPRE DPGKRPFFIA
651 QADQNAPRIP AARLGFHLKT SLTDRIDANL DYRVVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGG
101 AAACGGTCAG CGTCGCGGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GGCGGATTTT TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTGCGCAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAC GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGAAAAA ACTCACGTCC GCGGCGATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTTAC CGCAATCTGA AAGCGCTGCC CGACAGCCAC CCGGATTTCG
701 AAACGGGCGC CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCGTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAACCGCTA TTTACAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCAGACCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GCTACGAACT CCGTGCCGAA TGGAAAGCAAC CGTTCGCCGG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCGATC GAAAACTTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCGCCA CCAACCCATA GGTCGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTAA
1251 ACAACCGATG CTGCTTGACA ACAAAGTGCA ACATTACAGC TTTTCGGTG
1301 TAGAACAGGC AAACCTGGAC AACTTCACGC TTGAAGGAGG CGTACCGGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAACCTACTA AACCACCCCG TGCCCGACCT CGCGCGCACG CGCCAAACCG
1451 CCGGCTCAAT CGCACTTTCG GGCAACTGGT ATTTACGCCC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCCGTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAACACG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGCGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTACATT TACGCCCAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGCGGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTTCGGCGG ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGAGAA GATGCCTACG GCAACCGTCC TTTTCATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAATTTG GACTACTACC
2051 GCGTGTTCGC CAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACCTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCTCT TCTGATACGC CGCAAATGGG CCGCAGCTTT
2251 ACCGCGCGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pep

```

1 MAQTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVVDVAD GKIPKMPEN GVSSELGLRL SSGNLEKLTS GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 VAYSRRRDQY GLPAHSHEYD DCHADIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPGLSG FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQPPFGFEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTQN ARIELRHQPI GRKGSWGVQ
401 YLQKSSALS AISEAVKQPM LLDNKVQHY S FFGVEQANWD NFTLEGGVRV
451 EKQKASIQYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

```

551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSPGRE DAYGNRPFIA
651 QDDQNAPRVP AARLGPHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

m149-1/g149-1 96.2% identity in 758 aa overlap

	10	20	30	40	50	60
m149-1.pep	MAQTTLKPIVLSILLINTPLLAQAHETE	QSV	DLET	SVVVGKSRPRATSGLLHTSTASDKI		
g149-1	MAQITLKPIVLSILLINTPLLAQAHETE	QSV	GLET	SVVVGKSRPRATSGLLHTSTASDKI		
	10	20	30	40	50	60
	70	80	90	100	110	120
m149-1.pep	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
g149-1	ISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m149-1.pep	SPDHAIMVDTALSQQVEILRGPV	TL	LYSSGNVAGLVDVADGKIPEKMPENGVS	GELGLRL		
g149-1	SPDHAIMVDTALSQQVEILRGPV	TL	LYSSGNVAGLVDVADGKIPEKMPENGVS	GEAGLRL		
	130	140	150	160	170	180
	190	200	210	220	230	240
m149-1.pep	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRN	LKRLPDSHADSQTGSIGL			
g149-1	SSGNLEKLTSGGINIGLGKNFV	LHTEGLYRKSGDYAVPRYRN	LKRLPDSHADSQTGSIGL			
	190	200	210	220	230	240
	250	260	270	280	290	300
m149-1.pep	SWVGEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI				
g149-1	SWVGEKGFIVAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI				
	250	260	270	280	290	300
	310	320	330	340	350	360
m149-1.pep	DYDNPGLSCGFHDDNAHAHTHSGRP	WIDLNRNKRYELRAEWKQPPGFEALRVHLNRNDY				
g149-1	DYDNPGLSCGFHDDNAHAHTHSGRP	WIDLNRNKRYELRAEWKQPPGFEALRVHLNRNDY				
	310	320	330	340	350	360
	370	380	390	400	410	420
m149-1.pep	RHDEKAGDAVENFFNNQTNARIEL	RHQPIGRKSGVQVYLQKSSALS	SAISEAVKQPM			
g149-1	HHDEKAGDAVENFFNNKTHNARIEL	RHQPIGRKSGVQVYLQKSSALS	SAIPETVQQPM			
	370	380	390	400	410	420
	430	440	450	460	470	480
m149-1.pep	LLDNKVQHYSFFGVEQANWDN	FTLEGGVRVEKQKASIQYDKALIDRENYYNHPLPDLGAH				
g149-1	LIDNNVRHYSFFGVEQANWDN	FTLEGGVRVEKQKASIRYDKALIDRENYYNQPLPDLGAH				
	430	440	450	460	470	480
	490	500	510	520	530	540
m149-1.pep	RQTARSFALSGNWFYTPQHKLSLT	ASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR				
g149-1	RQTARSFALSGNWFYTPHKKLSLT	ASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR				
	490	500	510	520	530	540
	550	560	570	580	590	600
m149-1.pep	SNNIELALGYEGDRWQYNLALY	RNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
g149-1	SNNIELALGYEGDRWQYNLAAY	RNRFGNYIYAQTLNDGRGPKSIEDDSEM	KLVRYNQSGA			
	550	560	570	580	590	600
	610	620	630	640	650	660
m149-1.pep	DFYGAEGEIIYFKPTPRYRIG	VSGDYVRGRLKNLPSPGRE	DAYGNRPFIAQDDQNAPRVP			
g149-1	DFYGAEGEIIYFKPTPRYRIG	VSGDYVRGRLKNLPSPGRE	DPYGRPFIAQADQNAPRIP			
	610	620	630	640	650	660

	670	680	690	700	710	720
m149-1.pep	AARLGFLHKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
	:	:	:	:	:	:
g149-1	AARLGFLHKTSLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN					
	670	680	690	700	710	720
	730	740	750	759		
m149-1.pep	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
g149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

a149-1.seq

1	ATGGCCACAAA	CTACACTCAA	ACCATTGTGT	TTATCAATTC	TTTTAATCAA
51	CACACCCCTC	CTCTCCCAAG	CGCATGGAAC	TGAGCAATCA	TGCGGCTTGG
101	AAACGGTCAG	CGTCGTCGGC	AAAAGCCGTC	CGCGCGCCAC	TTCGGGGCTG
151	CTGCACACTT	CTACCGCCTC	CGACAAATAC	ATCAGCGCGC	ACACCTTTCG
201	ACAAAAGGCC	GTCAACTTGG	GTGATGCTTT	AGACGGCGTA	CCGGGCATCC
251	ATGCCTCGCA	ATACGGCGGC	GGCGCATCCG	CTCCCGTTAT	TCGCGGTCAA
301	ACAGGCGAGC	GGTTAAAGTT	GTTGAACCAT	CACGGCGAA	CGGGCGACAT
351	GGCGGACTTC	TCTCCAGACC	ATGCAATCAT	GCTGGACAGC	GCCTTGTCGC
401	AACAGGTCGA	AATCCTGCGC	GGTCCGGTTA	CGCTCTTGTA	CAGCTCGGGC
451	AATGTGGCGG	GGCTGGTFCG	TGTTGCCGAT	GGCAAAATTC	CCGAAAAAAT
501	GCCTGAAAA	GGCGTACGTT	GCGAACTCGG	ATTGCGTTTC	AGCAGCGGCA
551	ATCTGAAAA	ACTCAGCTCC	GGCGGCATCA	ATATCGGTTT	GGCAAAAAAC
601	TTTGATTATG	ACACGGAAGG	GCTGTACCGC	AAATCGGGGG	ATTACGCCGT
651	ACCGCGTTAC	CGCAATCTGA	AACGCGCTGC	CGACAGCCAC	CCCGATTTCG
701	AAACGGGCGC	CTACGGGCTG	TCTTGGGTTG	CGCAAAAAAG	CTTTATCGGC
751	CGAGCATACA	GGCAGCGTCG	CGACCAATAT	GGTCTGCCTG	CCCACAGCCA
801	CGAATACGAT	GATTGCCACG	CTGCACATCAT	CTGGCAAAAG	AGATTTGATTA
851	ACAAACGCTA	TTTGCAGCTT	TATCGCGACC	TGTTGACCGA	AGAGGCATC
901	GATTACGACA	ATCCGGGCTT	GAGCTGCGGC	TTTCACGACG	ACGATGATGC
951	ACACGCCCTT	CGCCACAACG	CGAAACCTTG	GATAGACCTG	CGCAACAAC
1001	GCTACGAAC	CGCGGCCGAA	TGGAAGCAAC	CGTTCGCCGC	TTTTGAAGCC
1051	CTGCGCGTAC	ACCTGAACCG	CAACGACTAC	CGCCACGACG	AAAAAGCAGG
1101	CGATGCGAGT	GAAACCTTTT	TTAACAACCA	AACGCAAAAC	CGCCGATATC
1151	AGTTGCGCCA	CAACCCATA	GGCGCTCTGA	AAGGCACTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	TGCTTTATCT	GCCACATCCG	AAGCGGTCAA
1251	ACAACCGATG	CTGCTTGACA	ATAAAGTGCA	ACATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAACTGGGAC	AACTTCACGC	TTGAAGCGCG	CGTACGCGTG
1351	GAAAAACAAA	AAGCCTCCAT	CCGCTACGAC	AAAGCATTGA	TGTATCGGGA
1401	AAACTACTAC	AACCATTTCC	TGCCCGACCT	CGCGCGGCAC	CGCCAAACCG
1451	CCCGCTCAT	CGCACTTTTC	GGCAACTGTG	ATTTCAACGC	ACAAACAAA
1501	CTCAGCCTGA	CCGCTTCCCA	TCAGGAACGC	CTGCCGTCAA	CGCAAGAGCT
1551	GTCAGCAGAC	GGCAAAACAG	TGCCCAACAA	CACCTTTGAA	GTGGGCAACA
1601	AACACTTCAA	CAAGAGCGT	TCACAACATA	TCGAATCTGC	ATCCGGCTAC
1651	GAAGGCGACC	GCTGGCAATA	CAATCTGGCA	CTCTACCGCA	ACCGCTTCGG
1701	CAACTACATT	TACGCCCAAA	CCTTAAACGA	CGGACGCGGC	CCCAAAATCA
1751	TGCAAGACGA	CAGCGAATG	AAGCTCGTGC	GCTACAACCA	ATCCGGTTCG
1801	GACTTCTACG	CGCGGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCGCGCTA
1851	CCGCACTCGC	GTTTCCGGCG	ACTATTGTAC	AGGCCGTCTG	AAAAACCTGC
1901	CTTCCCTACC	CGGACGGGAA	GACGCCCTAC	GCAACCGCCC	ACTCATTTCC
1951	CAAGCGGACC	AAACGCGCCC	TCCGGTTCCG	GCTGCGGCGC	TCGGCGTGCA
2001	CCTGAAAGCG	TCGCTGACCG	ACCGCATCGA	TGCCAATTTG	GACTACTACC
2051	GCGTGTTCGC	CCAAAACAAA	CTGCCCCGCT	ACGAAACCGC	CACGCCCGGA
2101	CACCATATGC	TCAACTCTGG	CGCAAACTAC	CGCCGAATA	CGCGCTATTG
2151	CGAGTGAAT	TGTTACGTCA	ACGCCGACAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCACAG	CAGCTTCTCT	TCTGATACGC	CGCAAATGGG	CCGACGTTTT
2251	ACCGCGCGCG	TGAACGTGAA	GTTTAA		

This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

a149-1.pep

1	MAQTTLKPIV	LSILLINTPL	LSQAHGTEQS	VGLETVSVVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQKA	VNLGDALDGV	PGIHASQYGG	GASAPVIRGQ
101	TGRRIRKVLNH	HGETGDMADF	SPDHAIMDVS	ALSQOVELLR	GPVTLVYSSG
151	NVAGLVQVAD	GKIQEKMPEN	GVSGELGLRL	SSGNLEKLTs	GGINIGLGKN
201	FVLHTEGLRY	KSGDVAVPRY	RNLKRLPDSh	ADsQTGSYL	SWPGLKEFID
251	AYsDRDRDQY	KLPAHSHEYD	RCHADIIWQK	SLINKRYLQL	YVHLLTEGGI
301	DYDNPGLSCG	FHDDDDAHAH	AHNKGPIWDL	RNKRYELRAE	WKQFFPGFEA

351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVO
 401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
 451 EKQKASIRYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPOHK
 501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
 551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
 601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DAYGNRPLIA
 651 QADQNAPRVP AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
 701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
 751 TGGVNVKF*

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
m149-1	MAQTTLKPIVLSILLINTPLLAQAHETEQSVDELTVSVVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a149-1.pep	SPDHAIMVDSALSQQVEILRGVPTLLYSSGNVAGLVVDVADGKIPEKMPENGVSSELGLRL					
m149-1	SPDHAIMVDTALSQQVEILRGVPTLLYSSGNVAGLVVDVADGKIPEKMPENGVSSELGLRL					
	130	140	150	160	170	180
	190	200	210	220	230	240
a149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
m149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
	190	200	210	220	230	240
	250	260	270	280	290	300
a149-1.pep	SWVGEKGFIGAAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
m149-1	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a149-1.pep	DYDNPGLSGCGFHDDDAHAHNGKPWDLRNKRYELRAEWKQPFPGFEALRVHLNRNDY					
m149-1	DYDNPGLSGCGFHDDDAHAHNGKPWDLRNKRYELRAEWKQPFPGFEALRVHLNRNDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
a149-1.pep	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQYLGQKSSALSATSEAVKQPM					
m149-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQYLGQKSSALSATSEAVKQPM					
	370	380	390	400	410	420
	430	440	450	460	470	480
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPLPDLGAH					
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIQYDKALIDRENYNHPLPDLGAH					
	430	440	450	460	470	480
	490	500	510	520	530	540
a149-1.pep	RQTARSFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
m149-1	RQTARSFALSGNWFYTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
	490	500	510	520	530	540
	550	560	570	580	590	600
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMCLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660

a149-1.pep	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPFLIAQADQNAPRVP
m149-1	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPFLIAQDDQNAPRVP
	610 620 630 640 650 660
a149-1.pep	670 680 690 700 710 720
	AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGANYRRNTRYGEWN
m149-1	AARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGANYRRNTRYGEWN
	670 680 690 700 710 720
a149-1.pep	730 740 750 759
	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
m149-1	WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
	730 740 750

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

g150.seq (partial)

```

1  ..TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGTA
101 GCGGTTTCGA TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCCTGCCG GTTGCTCCCG
251 CACTGTATAT CCATTTTCGAA CTCACGCAA ACACCCCGCG CTTTGTCAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCCGGCAAAA CTGACGGCGG AACAAATCGC CGGCCTGTGC
451 CGCCCGCTTG CGCCGCGCCT GTATTGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCGTTTC GAACACGAAG
551 GCGCGCCAG GCGGGCGGCG GCATCGGGT TCTTTGCCGA CCGGCTGGAA
601 GAGGACGGCA CGGTGCGCGT GTTTGCGGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGGCG
701 TCGCACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA
751 GGCAGAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAAATA TGTGCAGGAC
901 AAAATCCGCG AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC
951 GCATATCTAT GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GAAGTGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGCAG GGCATTGCGA CGAAGACGGC
1051 GCAGAAAGAT ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTATTATGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

g150.pep (partial)

```

1  ..YCKADFPFAA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAAGKTLF VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLPED SRKPIVMIGS GTGVAPFRAF VQQRAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDF LHYRDFAWSR DQEEKIYVQD
301 KIREQAELW QWLQEGAHY VCGDAAKMAK EVEAALLDVI IGAGHSDEDEG
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

m150.seq

```

1  ATGCAGAACA CAAATCCGCC ATTACCGCCT CTGCCGCCCG AAATCACGCA
51  GCTCCTGTCG GGGCTGGACG CGGCACAATG GGCGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGGCGGAGAA ACCTTTTTCG GTAACCGTCC TTTCCGCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCCGCCCG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAAAACATG CCGGCGAAGC CCGCCTGCTG CTGGTTACCT CCACCAAGG
351 CGAAGGCGAA CCGCCGAAAG AAGCCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCCGAAATTG GACAACTCC AATTGCGCGT ACTGGGTTTG

```

```

451 GCGGACAGTT CCTATCCGAA TTTCTGTCAG GCAGGTAAAG ATTTGACCG
501 GCGTTTTGAA GAATTGGGCG CAAAACGGCT GCTCGAACGC GTTGATGCGG
551 ATTTGGACTT TACCGCCTCC GCAAACGCCT GGACAGATAA TATCGCCGCA
601 CTCTTAAAG AAGAAGCCGC AAAAAACCGG GCAACGCCCG CGCCGAGAC
651 AACGCCCCCC GCCGGCCTTC AGACGGCACC GGATGGCAGG TACTGCAAGG
701 CAGCCCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT CACCGCCCGC
751 CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGTA GCGGTTTCGGA
801 TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGGTTT GACAACGATC
851 CGGCACTGGT CAGGGAAATC CTAGACCTGC TCGGCATCGA TCCGGCAACG
901 GAAATACAGG CGGGCGGAAA GATGATGCCG GTTGC GCGCG CACTTTCATC
951 TCATTTTCGAA CTCACGCAAA AACTCCGGC TTTCTGCAAA GGCTATGCCG
1001 CGTTCGCCCCA TTATGAAGAA CTCGATAAAA TCATTGCCGA TAACGCCGTT
1051 TTGCAGGATT TCGTGCAAAA CACGCCTATT GTCGATGTGC TGCACCGCTT
1101 CCCGGCAAGC CTGACGGCAG AACAATTCAT CCGTTTACTG CGTCCGCTTG
1151 CACCCCGTTT GTATTTCGATT TCTTCAGCAC AGGCGGAAGT GGGCGATGAA
1201 GTGCATTTAA CTGTCGGCGT GGTTTCGTTT GAACACGAAG GCCGCGCCAG
1251 AACGGGCGGC GCATCGGGTT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
1301 CGGTGCGCGT GTTTGTGGAA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
1351 AGCCGCAAGC CGATTGTGAT GATCGGCTCG GGCACCGCGC TCGCACCGTT
1401 CGCGCCTTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA GGCAAAAAC
1451 GGCTGATTTT CGGCAATCCG CATTTTGCCC GTGATTTTCT CTATCAAACC
1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGGT ACGATTTTCG
1551 CTGGTCCCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
1601 AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
1651 GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT
1701 GGATGTGATT ATCGGGGCAG GACATTTGGA CGAAGAGGGC GCAGAAGAAT
1751 ATTTGGATAT GCTGCGCGAA GAAAACGCT ATCAGCGTGA TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 610; ORF 150>:

m150.pep

```

1  MQNTNPPLPP LPPETIQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
51  TALPAAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
101 KNIAGERLL LVTSTQGEGE PPKEAVVLHK LLNGKKAPKL DKLQFAVLGL
151 GDSSYPNFCQ AGKDFDRRFE ELGAKRLLER VDADLDFTAS ANAWTDNIAA
201 LLKEEAAKNR ATPAPQTTTP AGLQTAPDGR YCKAAPFPAA LLANQKITAR
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDPAT
301 EIQAGGKMP VARALSSHFE LTQNTPAFVK GYAAFAHYEE LDKIADNAV
351 LQDFVQNTPI VDLHRFPAS LTAEQFIRLL RPLAPRLYSI SSAQAEVGDE
401 VHLTVGVVRF EHEGRARTGG ASGFLADRL EEDGTVRVFVE RNDGFRLPED
451 SRKPIVMIGS GTGVAPFRAF VQQRAAENAE GKNWLI FGNP HFARDFLYQT
501 EWQQFAKDF LHRDYFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHY
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

	210	220	230	240	250	260
m150.pep	LLKEEAAKNRATPAPQTTTPAGLQTAPDGRYCKAAPFPAA LLANQKITARQSDKDVRHIE					
g150	YCKADFPFAALLANQKITARQSDKDVRHIE					
				10	20	30
	270	280	290	300	310	320
m150.pep	IDLSGSDLHYLPGDALGVWFDNDPALVREILDLLGIDPAT EIQAGGKMPVARALSSHFE					
g150	:					
	40	50	60	70	80	90
	330	340	350	360	370	380
m150.pep	LTQNTPAFVKGYAAFAHYEELDKIADNAV LQDFVQNTPIVDLHRFPASLTAEQFIRLL					

	: : : :
g150	LTQNTPAFVKGYATFADNDELDRIAADNAVLQGFGVQSTPIAGVLHRFPKLTAEQFAGLL
	100 110 120 130 140 150
	390 400 410 420 430 440
m150.pep	RPLAPRLYSISSAQAEEVGDEVHLTVGVVRFEHEGRARTGGASGFLADRLEEDGTVRVFVE
	: : : :
g150	RPLAPRLYSISSSQAEEAGDEVHLTVGAVRFEHEGRARAGGASGFADLRLEEDGTVRVFAE
	160 170 180 190 200 210
	450 460 470 480 490 500
m150.pep	RNDGFRLPEDSRKPIMIGSGTGVAPFRAFVQQRAAENAEKGKNWLIFGNPHFADFPLYQT
	: : : :
g150	RNDGFRLPEDSRKPIMIGSGTGVAPFRAFVQQRAAENAEGRNWLI FGNPHFAADFLYQT
	220 230 240 250 260 270
	510 520 530 540 550 560
m150.pep	EWQQFAKDGLHRYDFAWSRDQEEDIYVDKIREQAEGLWQWLQEGAHIVYCGDAAKMAK
	: : : :
g150	EWQQFAKDGLHRYDFAWSRDQEEDIYVDKIREQAEGLWQWLQEGAHIVYCGDAAKMAK
	280 290 300 310 320 330
	570 580 590 600
m150.pep	DVEAALLDVIIGAGHLDEEGAEEYLDMRLRECKRYQRDVYX
	: : : :
g150	EVEAALLDVIIGAGHSDEDGAEGYLDMLRECKRYQRDVYX
	340 350 360 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 611>:

a150.seq	1	51	101	151	201	251	301	351	401	451	501	551	601	651	701	751	801	851	901	951	1001	1051	1101	1151	1201	1251	1301	1351	1401	1451	1501	1551	1601	1651	
	ATGCAGAACA	CAAATCCGCC	ATTACCGCCT	ATGCCGCCCC	AAATCACGCA																														
	GCTCTGTGTCG	GGGCTGGACG	CGGCACAATG	GGCGTGGCTG	TCCGGCTACG																														
	CTTCCGCAAA	AGGCGAAGG	GGGCGATCTG	CAGGACTGCC	CGCGCTTACG																														
	ACGGCATTGC	CGACGGCAGA	ACCTTTTTC	GTAACCGTCC	TTTCCGCCTC																														
	GCAAACCGGC	AATGCGAAAT	CCGTTGCCGA	CAAAGCGGCG	GACAGCCTGG																														
	AAGCCGCGCG	CATCCAAGTC	AGTCGCGCCG	AACTGAAAGA	CTATAAAGCG																														
	AAAAACATCG	CCGCGCAACG	CCGCTGTCTG	CTGGTTACCT	CCACCCAAGG																														
	CGAAGGCGAA	CCGCGCGAAG	AAGCCGTCGT	CTGTGCACAA	CTGCTGAACG																														
	GCAAAAAAGC	CCCGAAATTG	GACAAACTCC	AATTTGCCGT	ACTGGGTTTG																														
	GGCGACAGCT	CCTATCCGAA	TTTCTGCCGG	GCGGGCAAG	ATTTTCGACAA																														
	ACGTTTTGAA	GAATTTGGCG	CAAAACGCCT	GCTCGAACGC	GTTGATGCGG																														
	ATTTGGACTT	TGCGCGCCGC	GCAGACGGAT	GGACAGATAA	TATCGCCGCA																														
	CTCTTAAAG	AAGAAGCCGC	AAAAAACCGG	GCAACGCCCC	CGCCGCAGAC																														
	AACGCCCCCC	GCCGGCCTTC	ACGCGCACC	GGATGGCAGG	TACTGCAAGG																														
	CAGACCCCTT	TCCCGCCCGC	CTGCTGGCCA	ATCAGAAAT	CACCGCCCCG																														
	CAATCCGATA	AAGACGTGCG	CCACATCGAA	ATCGATTGA	GCGGTTGGGA																														
	TTTGCCTAC	CTCCCGGGCG	ACGCGCTCGG	CGTTTGGTTT	GACAACGATC																														
	CGGCACTGGT	CAGGGAATC	CTAGACCTGC	TCGGCATCGA	TCAGGCAACG</																														

1701 GGATGTGATT ATCGGGGCAG GACATTGGA CGAAGAGGGC GCAGAAGAAT
1751 ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA TGTTTATTGA

This corresponds to the amino acid sequence <SEQ ID 612; ORF 150.a>:

a150.pep
1 MQNTNPPLPP MPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
51 TALPTAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
101 KNIAGERRLL LVTSTQGEGE PPEEAVVLHK LLNGKKAPKL DKLQFAVLGL
151 GDSSYPNFCR AGKDFDKRFE ELGAKRLLER VDADLDFAAA ADGWTDNIAA
201 LLKEEAAKNR ATPAPQTPP AGLQTAPDGR YCKADFPFAA LLANQKITAR
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDQAT
301 EIQAGGKTL P VASALLSHFE LTQNTPAFVK GYAPFADDDE LDRIAADNAV
351 LQGFVQSTPI ADVLHRFPK LTAEQFAGLL RPLAPRLYSI SSSQAEVGDE
401 VHLTVGAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
451 SRKPIVMIGS GTGVAFPPRA VQQRAAENAE GKNWLFFGNP HFARDFLYQT
501 EWQQFAKDG F LHRYPFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHY
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

m150/a150 94.8% identity in 599 aa overlap

	10	20	30	40	50	60
m150.pep	MQNTNPPLPPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQ	TALPTAEPFS				
a150	MQNTNPPLPPPEITQLLSGLDAAQWAWLSGYAWAKAGNGASAGLPALQ	TALPTAEPFS				
	70	80	90	100	110	120
m150.pep	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL				
a150	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL	VTVLSASQTGNAKSVADKAAADSLEAAGIQVSRAELKDYKAKNIAGERRLL				
	130	140	150	160	170	180
m150.pep	PPKEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDRREEL	PPKEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCQAGKDFDRREEL				
a150	PPEEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCRAGKDFDKRFEEL	PPEEAVVLHKLLNGKKAPKLDKLQFAVLGLGDSSYPNFCRAGKDFDKRFEEL				
	190	200	210	220	230	240
m150.pep	VDADLDFASANAWTDNIAALLKEEAAKNRATPAPQTPPAGLQTAPDGRYCKA	VDADLDFASANAWTDNIAALLKEEAAKNRATPAPQTPPAGLQTAPDGRYCKA				
a150	VDADLDFASANAWTDNIAALLKEEAAKNRATPAPQTPPAGLQTAPDGRYCKA	VDADLDFASANAWTDNIAALLKEEAAKNRATPAPQTPPAGLQTAPDGRYCKA				
	250	260	270	280	290	300
m150.pep	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI				
a150	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI	LLANQKITARQSDKDVRHIEIDLSGSDLHYLPGDALGVWFDNDPALVREI				
	310	320	330	340	350	360
m150.pep	EIQAGGKMPVARALSSHFELTQNTPAFVKGYAAFAHYEELDKIADNAVLD	EIQAGGKMPVARALSSHFELTQNTPAFVKGYAAFAHYEELDKIADNAVLD				
a150	EIQAGGKTLPPVASALLSHFELTQNTPAFVKGYAPFADDDELDRIAADNAV	EIQAGGKTLPPVASALLSHFELTQNTPAFVKGYAPFADDDELDRIAADNAV				
	370	380	390	400	410	420
m150.pep	VDVLRFPASLTAEQFIRLLRPLAPRLYISSAQAEVGVHVLTVGVVRFEEH	VDVLRFPASLTAEQFIRLLRPLAPRLYISSAQAEVGVHVLTVGVVRFEEH				
a150	ADVLRFPKLTAEQFAGLLRPLAPRLYISSAQAEVGVHVLTVGAVRFEHGR	ADVLRFPKLTAEQFAGLLRPLAPRLYISSAQAEVGVHVLTVGAVRFEHGR				
	430	440	450	460	470	480
m150.pep	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAVQ	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAVQ				
a150	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAVQ	ASGFLADRLEEDGTVRVFVERNDGFRLPEDSRKPIVMIGSGTGVPFRAVQ				
	490	500	510	520	530	540
m150.pep	GKNWLIFGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQD	GKNWLIFGNPHFARDFLYQTEWQQFAKDGFLHRYDFAWSRDQEEKIYVQD				

```

a150      GKNWLF FGNPHF ARDFLY QT EWQQ FAKD GFLHRY DFAWSR DQEEKI YVQDKI REQA EGLW
           490      500      510      520      530      540

           550      560      570      580      590      600
m150.pep  QWLQEGAH IYVCGD AAKMAK DVEA ALLDV IIGAGH LDEEGA EYLDML REEKRY QRDVYX
           |||||
a150      QWLQEGAH IYVCGD AAKMAK DVEA ALLDV IIGAGH LDEEGA EYLDML REEKRY QRDVYX
           550      560      570      580      590      600

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 613>:

g151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCACACGTCG ACCACGGCAA
51  AACCATTTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGA AAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTG
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGGCGAAG
251 TGGAGCGCGT TTGGGGGATG GTGGATTGCG TCGTCTTGTT GGTGGACGCA
301 CAGGAAGGTC CGATGCCGCA AACCGGTTTC GTGACCAAAA AAGCCTTGCG
351 TTGGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAACCGTCCG
401 CCCGTCCGAG CTGGGTTATC GACCAGACTT TCGAGTTGTT CGACAACTTG
451 GGTGCGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTACG CTTCAGGTTT
501 GAGCGGCTTT GCCAAGCTGG AAGAAAccga CGAGAGCAGC GATATGCGCC
551 CGCtggttcgA CACCATCCTA AAATACAcgc ctgCACCGAG CGGCAGCGCG
601 GACGAGCCGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTGATGAAC CACGAGCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGCTTGGA CCGTGCCGC TTGAAGAAGC
801 CGAAGCCGCG GACATTGTGA TTATTTCCGG TATCGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCA AAGGCCTGCC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTAAACA CCAGCCCGCT
951 CGCAGGTACA GAAGGC AAAT TCGTGACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTTGCCC TGCGCGTGGA AGACACCGCC
1051 GatgCCGACG TGTTCCGCGT ATCcgGGCGC GGCGAACTGC ACCTGACGAT
1101 TTTGCTGGAA AATATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAGC
1151 CGCGCGTCGT GTACCGAGAC ATCGACGGTC AAAATGCGA ACCTTATGAA
1201 AACCTGACTG TGGACGTACc cgacgacAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACCAA TATGGAAAGC GACGGCAACG
1301 GacgCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TCATGACCCT GACGCGCGGC GTCGGGCTGA TGAgccacGT
1401 GTTcgacgac tacgcgcccg tcaAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTactggt GtcccaAGAG CAGGGCGAGG CGGTTGCTTA CGCCTTGTTG
1501 AATCTTGAAG ACCGCGGCCG TATGTTGCTA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGCCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTCACCAATA TCCGTGCCAG CGGTACCGAC
1651 GAAGCGGTGC GCCTGACCAC GCCGATCAAA CTGAcgcTGG AAGGCGCGGT
1701 CGAGTTTATC GACGATGACG AGCTGGTGGA AATCAGCCG CAAtccatcc
1751 gcctgcgcat gcgttacctG AGCGaattgg aacgccgcg tcaTTTTAA
1801 AagctgGATT AA

```

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

g151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGCHIN IVDTPGHADF GGEVERVLGM VDCVLLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESS DMRPLFDTL KYTPAPSGSA
201 DEPLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HEQQIAQGRI
251 NQLLGFKGLE RVPLEEAEAG DIVISGIED IIGIVTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPVE
401 NLTVDPDDN QGAVMEELGR RRGELTNMES DGNRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVDD YAPVKPMPG RHNGVLVSQE QGEAVAYALW

```

501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMYL SELERRRHFK
 601 KLD*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCG ACCACGGCAA
 51 AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
 251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
 301 CAGGAAGGCC CGATGCCGCA AACCCTTTC GTGACCAAAA AAGCCTTGGC
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAGCCGTCCG
 401 CTCGTCCGAG CTGGGTATC GACCAAACCT TCGAGCTGTT CGACAACTTG
 451 GGCGCGACCG ACGAGCAGTT GGATTTCCTG ATTGTTTACG CTTCAGGGTT
 501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
 551 CGCTGTTCGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
 601 GACGAAACGC TGCAACTGCA AATTTCCTCA CTCGACTACG ACAACTACAC
 651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
 701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC
 751 AACCAGCTTT TGGGTTTCAA AGGTTTGGA CGCGTGCCGC TTGAAGAAGC
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATCGAAGAC ATCGGTATCG
 851 GCGTAACCAT CACCGACAAA GACAAATCCA AAGGCCTACC GATGTTGAGC
 901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGCT
 951 GGCGGGTACG GAAGGCAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
 1001 TGCAAAAAGA ATTGCTGACC AACGTGCGCC TGCGCGTGGA AGATACCGCC
 1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GCGGAGCTGC ACCTGACCAT
 1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAC
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAAATGCGA ACCGTATGAA
 1201 AACCTGACCG TGGATGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
 1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG
 1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
 1351 CAAGGCGAAT TTATGACCTT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
 1401 GTTCCAGCAT TACGCGCCCG TCAAACCCGA TATGCCCGGC CGCCACAACG
 1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTGTGG
 1501 AATCTGGAAG ACCGCGGCCG TATGTTGTA TCGCCCAACG ACAAATCTA
 1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
 1651 GAAGCCGTTT GCCTGACCAC GCCAATCAAG CTGACGCTGG AAGGTGCGGT
 1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCAGCCCG CAATCCATCC
 1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCGCCCG CCACTTTAAA
 1801 AAGCTGGATT GA

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLLVDA
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDLIL KYTPAPSGSA
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HDQQIAQGRI
 251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPKGLPMLS
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
 351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
 401 NLTVDPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
 451 QGEFMTLTRG VGLMSHVDDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
 501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
 601 KLD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

m151.pep	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
g151	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
	10	20	30	40	50	60
m151.pep	70	80	90	100	110	120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
	70	80	90	100	110	120
m151.pep	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFLFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN					
g151	KPIVVINKIDKPSARPSWVIDQTFLFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
	130	140	150	160	170	180
m151.pep	190	200	210	220	230	240
	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
g151	DMRPLFDITILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
	190	200	210	220	230	240
m151.pep	250	260	270	280	290	300
	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
g151	HEQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
	250	260	270	280	290	300
m151.pep	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR					
g151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLOKELLTNVALRVEDTADADVFRVSGR					
	310	320	330	340	350	360
m151.pep	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDVDDNQAVMEELGR					
g151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDVDDNQAVMEELGR					
	370	380	390	400	410	420
m151.pep	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
g151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVDDYAPVKPDMPG					
	430	440	450	460	470	480
m151.pep	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
g151	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
	490	500	510	520	530	540
m151.pep	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					
	550	560	570	580	590	600

m151.pep KLDX
 ||||
 g151 KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

```
a151.seq
1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGA AAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG
251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGGC
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAAATCGAC AAACCGTCCG
401 CCCGTCGAG CTGGGTCATC GACCAAACTT TCGAGCTGTT CGACAACTTG
451 GGCGCGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTATG CTTCCGGTCT
501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
551 CGCTGTTCGA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCTCA CTGACTACG ACAACTACAC
651 CGGCCGCCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC
701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGGC GACATCGTGA TATTTCCGG TATTGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCGTT
951 GGCAGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGGA AGATACCGCC
1051 GATGCCGACG TGTTCGCGT ATCCGGGCGC GGCGAGCTGC ACCTGACCAT
1101 TTTGCTGGAA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATGCGA ACCGTATGAA
1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCCG CGCCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG
1301 GACGCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGCTTC
1351 CAAGGCGAAT TTATGACCTT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCTGGC CGCCACAACG
1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTGG
1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGTA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCCGTTC GCCTGACCAC GCCGATTAAG CTGACGCTGG AAGGTGCGGT
1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCATTTCAAA
1801 AAGCTAGATT GA
```

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

```
a151.pep
1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDLIL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQIAQGRI
251 NQLLGFKGLE RVPLEAEAG DIVIISGIED IGIGVTITDK DNPKGPLMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVFD D YAPVKPDMPG RHNGVLVSQE QGEAVAYALW
501 NLEDRGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD
551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK
601 KLD*
```

m151/a151 99.8% identity in 603 aa overlap

10 20 30 40 50 60

m151.pep	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
a151	MKQIRNIAIIAHVDHGKTTLVDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
	10 20 30 40 50 60
m151.pep	70 80 90 100 110 120
a151	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
	70 80 90 100 110 120
m151.pep	130 140 150 160 170 180
a151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDES
	130 140 150 160 170 180
m151.pep	190 200 210 220 230 240
a151	DMRPLFDITILKYTPAPSGSADETQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
	190 200 210 220 230 240
m151.pep	250 260 270 280 290 300
a151	HDQQIAQGRINQLLGFKGLERVPLEEAEAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
	250 260 270 280 290 300
m151.pep	310 320 330 340 350 360
a151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLQKELLTNVALRVEDTADADVFRVSGR
	310 320 330 340 350 360
m151.pep	370 380 390 400 410 420
a151	GELHLTILLENMRREGYELAVGKPRVVYRDIIDGQKCEPYENLTVDPDDNOGAVMEELGR
	370 380 390 400 410 420
m151.pep	430 440 450 460 470 480
a151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
	430 440 450 460 470 480
m151.pep	490 500 510 520 530 540
a151	RHNGVLVSQEQGEAVAYALWNLEDGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK
	490 500 510 520 530 540
m151.pep	550 560 570 580 590 600
a151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK
	550 560 570 580 590 600
m151.pep	KLDX
a151	KLDX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAaaca aACCaaagt ctgGGacttc cCacccgcc ttTCCactG
51  GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGGTCG GGCTGCTCGT CCTTTTCCTG

```

```

151 CTCGTATTCC GCCTCTGCTG GGGCATTGG GGCAGcgATA CCGCCCGTTT
201 CTCccgTtTC GTCCGAGGTT GGGCAGGTAT ACGCGGCTAT CTGAAAAAcg
251 gCATTCCCGA ACAtatcCAG CCCGGACACA ACCCCTTGGG CGCACTgatg
301 gtcGTTGCGC TTTTGgccgc cgtcTCATTT CAagtcggcA CGGGGCTTTT
351 Tgccgccaat gaaaacacct tcagcaCCAA cggctacctc aaccatttgg
401 tttccgaaca tacgGGCAGC CTTATACGGA AAATCCACCT CAACTTTTTC
451 AAGTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCATATTC AAAAAGAAAA ACCTCGTCCG CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CGCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 620; ORF 152.ng>:

g152.pep

```

1 MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KAGGDMQWH TRVGLLVFLF
51 LVFRLCWGIW GSDTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAN ENTFTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVFSVAH IAAVAAYRIF KKKNLVRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

m152.seq

```

1 ATGAAAAACA AAACCAAGT CTGGGACCTC CCCACCCGCC TTTTCCAATG
51 GCTGCTTGCC GCGTCCCTGC CCTTTATGTG GTATAGCGCG AAAGCCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTCGT CCTTTTCTCG
151 CTCGTATTTC GCCTCTGCTG GGGCATTGG GGCAGCGATA CCGCCCGTTT
201 TTCCCGTTTC GTCCAAGGCT GGGCAGGCAT ACGCGGCTAT CTGAAAAACG
251 GTATTCCCGA ACACATCCAG CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGCCCGC CGTGTCTTTC CAAGTCGGCA CCGGGCTTTT
351 TGCCGCCGAT GAAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGCG
401 TTTCCGAACA TACGGGCAGC CTTATGCGGA AAATCCACCT CAACTTTTTC
451 AAGTGCTCG CCGTTTTTTC TGCAATCCAC ATCGCCGCCG TCGCCGCATA
501 CCGGTATTC AAAAAGAAAA ACCTCATCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCAGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGGTTGC CTCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 622; ORF 152>:

m152.pep

```

1 MKNKTKVWDL PTRLFHWLLA ASLPFMWYSA KAGGDMQWH TRVGLFVLFL
51 LVFRLCWGIW GSDTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD ENTFTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAIH IAAVAAYRVF KKKNLILPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVASLA AAAILLLS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/g152

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMQWHTRVGLFVLFLLVFRLCWGIW					
	: : : : :					
g152	MKNKTKVWDFPTRLFHWLLAASLPFMWYSAKAGGDMQWHTRVGLLVFLFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	: : : : :					
g152	GSDTARFSRFVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN					
	70	80	90	100	110	120

436

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS	SAIHIAA	VAAYRVFKK	NNLILPMI		
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFS	SAVHIAA	VAAYRIFKKN	LVLRPMI		
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALS	SVASL	AAAAI	LLLSX		
g152	TGFKYIEGKTSIRFAGKAALAAALS	VAAAL	AAAAI	LLLSX		
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

a152.seq

1	ATGAAAAACA	AAACCAAGT	CTGGGACTTC	CCACCCGCC	TTTCCACTG
51	GCTGCTTGCC	GCATCCCTAC	CCTTTATGTG	GTATAGCGCG	AAAACCGCG
101	GCGATATGCT	GCAATGGCAC	ACGCGCGTCG	GGCTGTTTAT	CCTTTTCCTG
151	CTCGTATTCC	GCCTCTGCTG	GGGCATTTGG	GGCAGCGATA	CCGCCCGTTT
201	CTCCCGTTTC	GTCCGCGGAT	GGTCGGGTAT	CAGAGAGTAT	ATGAAAAACG
251	GTATTCCCGA	ACACGTCCAA	CCCGGACACA	ACCCCTTGGG	CGCACTGATG
301	GTCGTTGCGC	TTTTGGCCGC	CGTGTGCTTC	CAAGTCGGCA	CAGGGCTTTT
351	TGCCGCCGAT	GTAACACCT	TCAGCACCAA	CGGCTACCTC	AACCATTGCG
401	TTTCCGAACA	TACGGGCAGC	CTTATGCGGA	AAATCCATCT	CAACTTTTTC
451	AAACTGCTCG	CCGTTTTTTC	CGCAGTCCAC	ATCGCCGNCG	TCGCCGCATA
501	CCGCGTGTTT	AAAAAGAAAA	ACCTCGTCCT	CCCGATGATA	ACCGGCTTCA
551	AATACATCGA	AGGCAAAACC	TCAATCCGCT	TTGCCGGCAA	AGCCGCGCTT
601	GCCGCCGCAT	TATCGGTTGC	CGCGCTTGCC	GCAGCCGCCA	TCCTGCTCCT
651	GTCCTGA				

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

a152.pep

1	MKNKTKVWDF	PTRLFWLLA	ASLPFMWYSA	KTGGDMLQWH	TRVGLFILFL
51	LVFRLCWGIW	GSDTARFSRF	VRGWSGIREY	MKNGIPEHVQ	PGHNPLGALM
101	VVALLAAVSF	QVGTGLFAAD	VNTFSTNGYL	NHLVSEHTGS	LMRKIHLNFF
151	KLLAVFSAVH	IAXVAAYRVF	KKKNLVLPMI	TGFKYIEGKT	SIRFAGKAAL
201	AAALSVAALA	AAAILLS*			

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDL	PTRLFWLLA	ASLPFMWYSA	KAGGDMQWH	TRVGLFVFL	LVFRLCWGIW
a152	MKNKTKVWDF	PTRLFWLLA	ASLPFMWYSA	KAGGDMQWH	TRVGLFVFL	LVFRLCWGIW
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRF	VQGWAGIR	GYLKNGIPE	HIQPGHNPL	GALMVVALL	AAVSFQVGTGLFAAD
a152	GSDTARFSRF	VRGWSGIRE	YMKNNGIPE	HVQPGHNPL	GALMVVALL	AAVSFQVGTGLFAAD
	70	80	90	100	110	120
	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS	SAIHIAA	VAAYRVFKK	NNLILPMI		
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFS	SAVHIAA	VAAYRVFKK	NNLVLRPMI		
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALS	SVASL	AAAAI	LLLSX		
a152	TGFKYIEGKTSIRFAGKAALAAALS	VAAAL	AAAAI	LLLSX		
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```
g153.seq
1  atgggggtttg cttacAgtat gacgtatatc gaggtCGGga taccggaggc
51  ggcataccgtc ctttCgctGC CCGAGATgat ggcctgatG GTGTTtCagg
101 attATGGTTT TttggcCGAA GTGATGTTTG TGtgaCTTT cGGCGcgcCG
151 GTTCTGTtTc TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTGCG TTCGGGCCGG CGTTTTATCT
351 GATGTTTCGG CTGTCTGGTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTCCTA ATCGGGCGGC TGACGGGGAA TAATGCGGTT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTTCcg
501 cgacAGTgcc gaatccCCCT GCGGGGTGTg cgGCGcgga CTgtacggcg
551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCtgac ggcggcggtT
601 GTTTTGTAAT TCCctgCcaa TATCctgccc attatGAttt cgtccAATCc
651 tgccgccacg GAGGcCAACA CCATCTTTAG CGGCATCGCT TATATGTGGG
701 ACGagggcgA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGGCGGCACG
801 GTTCGCTTTG CCGGCGGGCG CAAAGAAATT GTCGCACCTC tacCGCATCA
851 CCGAAGCGGT CCGCGCTGCG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCcaca TTATGCCGCG CGCGTCATTG CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTTT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```
g153.pep
1  MGFAYSMTYI EVGIPEAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR FGPAYFLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGNNAV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYGGRPKSL S ISSAFLTA AV
201 VLYFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIAAARFAL PAGAKLSHL YRTEAVGRV SMIDIFVII
301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL L WDKRASDGIA
351 FNETEKYD*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```
m153.seq
1  ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTCGGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CCGCGCGCCG
151 GTTCTGTtTc TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTGCG TTCGGGCCGG CGTTTTATCT
351 GATGTTTCGG CTGTCTAGTTA TGCTGATTCT GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCGG
501 CGACAGTGCC GAATCCCCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTCTGTCG CGTTTCTGAC GCGGCGGTT
601 ATTTTGTAAT TCCCTGCCAA TATCTGCCG ATTATGATT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG
701 ACGAGGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGGTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCCCG
801 CTTTCGCTTT CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
851 CCGAAGCGGT CCGCCGCTGG TCGATGATTG ATATTTTGTG GATTATTATT
901 TTGATGTGTT CGTTCACAC TTATGCCGCG CGCGTCATTG CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA
```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```
m153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY
```

```

101 IKLSSVAEVR FGPAFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNAV
151 QTASEGKTC SRCLYFRDSD ESVPCVCGAE LYRRDPKSL ISSAFLTA
201 ILYPANPAA IMISSNPAT BPNCTVGNIE YMRDGBRDL AAVIFSALV
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIT
301 LMCSFTHYAA RVIPGSAAY FCLVVILTML SAYYFDPRL LWDRASDGLA
351 FNTEKTHD*

```

m153 / g153 96.1% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFDYGF	LAEVMFVLTFGAPVLFLLCLYV				
	: : :					
g153	MGFAYSMTYIEVGIPGAASVLSLPEMMRLMVFDYGF	LAEVMFVLTFGAPVLFLLCLYV				
	10	20	30	40	50	60
m153.pep	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTL	VAYIKLSSVAEVRFGPAFYLMFA				
g153	YAALIRKQAYPALRLATRVMLRQAMMVDVFFVSTL	VAYIKLSSVAKVRFGPAFYLMFA				
	70	80	90	100	110	120
m153.pep	LSVMLIRTSVSVPQHVVYFQIGRLTGDNAVQTASEGK	TCCSRCLYFRD	SAESPCGVCGAE			
g153	LSVMLIRTSVSVPQHVVYFQIGRLTGNNNAVQTASEGK	TCCSRCLYFRD	SAESPCGVCGAE			
	130	140	150	160	170	180
m153.pep	LYRRRPKSLSSISSAFLTAAVILYFPANILPIMISSN	PAATEVNTILNGIAYMWDEGDRLI				
g153	LYGGRPKSLSSISSAFLTAAVVLYFPANILPIMISSN	PAATEANTIFSGIAYMWDEGDRLI				
	190	200	210	220	230	240
m153.pep	AAVIFSASILVPVLKIAAMSVLIAARFALPAGAKKL	SHLYRITEAVGRWSMIDIFVII				
g153	AAVIFSASILVPVLKIAAMSVLIAARFALPAGAKKL	SHLYRITEAVGRWSMIDIFVII				
	250	260	270	280	290	300
m153.pep	LMCSFH	TYAARVIPGSA	AAVYFCLVVIL	TMLSAYYFDPRL	LWDK	KRASDGI
g153	LMCSFH	TYAARVIPGSA	AAVYFCLVVIL	TMLSAYYFDPRL	LWDK	KRASDGI
	310	320	330	340	350	359
m153.pep	IAFN	ETEKHD	X			
g153	IAFN	ETEKDY	X			
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 629>:

```

a153.seq
1  ATGGCGTTTG  CTTACGGTAT  GACGTATATC  GAGGTCGGGA  TACCGGGTGC
51  GGCATCCGTC  CTTTCGCTGC  CCGAGATGAT  GCGCCTGATG  GTGTTTCAGG
101 ATTATGGTTT  TTTTGCCGAA  CGTGATGTTT  TGCTGACCTT  CGGCGCGCGG
151 GTTCTGTTTC  TGCTGCTGTG  CCTGTATATC  TATGCGCGCG  GTATACGGAA
201 ACAGGCGTAT  CCTGCGCTGC  GTTTGGCAAC  GCGTGTGATG  GTGCGCTTGA
251 GACAGCGCAT  GATGCTGGAT  GTGTTTTTTT  TTTCCACTTT  GGTGGCGTAT
301 ATCAAGCTCT  CGTCTGTGGC  AGAGGTTCCG  TTCGGATCGG  CGTTTTATCT
351 GATGTTCCGG  CTGTCCGGTA  TGCTGATTCC  GACTTCGGTA  TCGTTTCCCC
401 AGCATTGGGT  GTATTTTCAA  ATCGGGCGGC  TGACGGGGGA  TAATGCGGTT
451 CAGACGGCAT  CGGAAGGTAA  AACCTGTTGC  AGCGCTGCC  TGTATTTCCG
501 CGACAGTGCC  GAATCCCCCT  CGGCGGTGTG  CGGTGCGGAA  CTGTACCGCC
551 GACGGCCGAA  AAGTCTGAGT  ATTTGCTCGG  CGTTTCTGAC  GCGGCGGGT
601 ATTTTGTATT  TCCCTGCCAA  TATCTGCCG  ATTATGATT  GCGCCAATCC
651 TGCCGCCACG  GAGGTCAATA  CCATCCTTAA  CGGCATCGCT  TATATGTGGG
701 ACGAGGGCGA  CAGGCTGATT  GCGGCGGTTA  TTTTCAGCGC  GAGTATTTTG
751 GTGCCGGTAC  TGAAGATTGC  GGCATATCTG  GTTTTGATTG  CGTCCGCCCC
801 CTTCGCTTTG  CCAACGGGTG  CAAAGAAATT  GTCGCACTCT  TACCGCATC

```

```

851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCC GCGCCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMMRLM VFQDYGFLAE VMFVLTFGAP
51  VLELLLCLYV YAALIRKQAY PALRLATRV M VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAEVR FGSAFYLMFA LSVMLIRTSV SVPQHWVYFQ IGRLTGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL S ISSAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDR LI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGIA
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMV FQDYGFLAEVMFVLTFGAPVLFLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMV FQDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRV M VRLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRV M VRLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSV SVPQHWVYFQIGRLTGDNVQTASEGKTCCSRCLYFRD SAESPCGVCGAE					
a153	LSVMLIRTSV SVPQHWVYFQIGRLTGDNVQTASEGKTCCSRCLYFRD SAESPCGVCGAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSL S ISSAFLTA AVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDR LI					
a153	LYRRRPKSL S ISSAFLTA AVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDR LI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHTYAA RVIPGSAAVYFCLVVILTMLSAYYFDPRL WDKRASDGIAFNETEKHDX					
a153	LMCSFHTYAA RVIPGSAAVYFCLVVILTMLSAYYFDPRL WDKRASDGIAFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCTCAAG CACGCGTCCG
51  CAAAAACAAC accttctctCT CCGCCGCTCTG GCTGTCCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCAATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CAAAAAGGC GTGGAAGTTA CTGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtaa CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

```

```

401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGcg GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAATCG AAAGCGCGCA TTTCGAcccG
601 TCCGACCAAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCAAGCG CGATTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCCT GTcgaATACA AAGGGctgaA
951 TGTcggCATG GTTTCCGATG TCCCTTATTT TGACCGCAAt gacagCCTGC
1001 ACCTgtTTGA aaacggctgg aTTcccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAAACAACA
1101 ATTCCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCGGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGTTTTGG ATGACTTGCA GGTCAAATTG GCGGATTTGC
1301 TGGACaaatT CAACAATCTG CCATTggata aAACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaaTCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACTCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGagacgta caAAATAcgc tgCaAAGTTT
1551 GGACAAAACC TTAAAgacg TtcaACCCGT CATTAACTT TTGaaAGAAA
1601 aacCCaaCgc actGATTtTc aacaACAGCA GCAAAGAccc tATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

g154.pep

```

1  MTDNSPPFNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGLTL SGSYIAFTPG KSGEAKDVFQ
151 VQDIPPVTAI QSGGLRLNLI GKNDRIILNVN SPVLYENFMV GQIESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSAPLPLAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVIRIIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGKK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATRG GGLDDLQVKL ADLLDKFNNL PLDKTVAELN
451 GSLAELKSAL KSANAALSSI DKLVGNPQTQ NIPNELNQT LKELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

m154.seq

```

1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCG GCTGGTTCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAG AAATCCGCA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTATCAAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCCACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGAGC AGGCAAAAGA CGTGTTCCTA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTGCGGCG CGATTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTGCGCC GTCGAGTACA AAGGGCTGAA
951 TGTGCGGCTG GTTTCCGACG TTCCTTATTT CGACGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGGAAA TCAATGCCGA CGAACAAGC AAAGAACATT GGAAACAACA
1101 ATTTTCAGAC GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

```

```

1201 TCACCTAAGC TGCGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATG GCGGATTTCG
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTCGCTTG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCTG AAAGAGTTGC GCACAACCT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAATACGC TGCAAAGTTT
1551 GGACAAACT TTAAAGACG TTCAACCGT GATTAATACT TTGAAAGAAA
1601 AACCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

```

m154.pep
1  MTDNSPPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTL LSGSYIAFTPG KSDEAKDVPQ
151 VQDIPPVTAI GQSGRLNLNI GKNDRIILNV SPVLYENFMV QQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFPFQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFPQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVABL N
451 GSLAELEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQL KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

	10	20	30	40	50	60
m154.pep	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
g154	MTDNSPPPNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
	10	20	30	40	50	60
m154.pep	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	SGVTGLGTL LSGSYIAFTPG KSDEAKDVPQ VQDIPPVTAI GQSGRLNLNI GKNDRIILNV					
g154	SGVTGLGTL LSGSYIAFTPG KSDEAKDVPQ VQDIPPVTAI GQSGRLNLNI GKNDRIILNV					
	130	140	150	160	170	180
m154.pep	SGVTGLGTL LSGSYIAFTPG KSDEAKDVPQ VQDIPPVTAI GQSGRLNLNI GKNDRIILNV					
g154	SGVTGLGTL LSGSYIAFTPG KSDEAKDVPQ VQDIPPVTAI GQSGRLNLNI GKNDRIILNV					
	130	140	150	160	170	180
m154.pep	SPVLYENFMV GQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
g154	SPVLYENFMV GQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
	190	200	210	220	230	240
m154.pep	SPVLYENFMV GQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
g154	SPVLYENFMV GQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
	190	200	210	220	230	240
m154.pep	KLSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFPFQ					
g154	KLSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFPFQ					
	250	260	270	280	290	300
m154.pep	KLSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFPFQ					
g154	KLSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFPFQ					
	250	260	270	280	290	300
m154.pep	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
g154	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
	310	320	330	340	350	360
m154.pep	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
g154	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
	310	320	330	340	350	360
m154.pep	KEHWKQFPQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQFPQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATRG					
	370	380	390	400	410	420
m154.pep	KEHWKQFPQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQFPQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA SPKLRPHTVY AGDTVIATRG					
	370	380	390	400	410	420

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154.pep	GGLDDLQVKLADLLDKFDKLPDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
	: : : : :					
g154	GGLDDLQVKLADLLDKFNNPLDKTVAELNGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154.pep	NIPNELNQTLELRITTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	: : : : :					
g154	NIPNELNQTLELRITTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154.pep	NSSSKDPIPKGSRX					
	:					
g154	NNSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCATCAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TCGCGGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTTCG
401 ACATCGCCTT TACACCCGCG AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCCT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTGACCCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTGAT TCCGCCAGCC GTTCTGGGCT GGAAGCGGCG ATCAATATCG
701 AAACCACAGG CAGCGGCATC AACTCAATT CCGCCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTGATT TGATTCGCCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTAAT ACACGCGGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTGCGCT GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTCCGATG TTCTTATTTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGAAG TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTGAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGACCGGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGGG ACGATTGCA GGTCAAATTG GCGGATTGCG
1301 TGGACAAGTT CGACAAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCGTTG CCGAGCTCAA ATCCCACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAAACTGG TCGGCAAAAC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAAATACGC TGCAAAGTTT
1551 GGACAAAACC TTTAAAGACG TTCAACCCGT CATTAACACT TTGAAAGAAA
1601 AACCCAACGC GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154.pep
1  MTDNSPPFNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVFG

```

151 VQDIPPVTAI QSGSLRLNLI GKNDRIILNVN SPVLYENFMV QOVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAEKSTL KSANAALSSI DKLVGKPTQ NIPNELNQT LKELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDEIPK
551 GSR*

m154/a154 100.0% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNHQAQARVRKNNTFLSAVWLVLPLIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
a154	MTDNSPPPNHQAQARVRKNNTFLSAVWLVLPLIALIAGGWLWVKEIRNRGPVVTLLMDSAE					
	10	20	30	40	50	60
m154.pep	70	80	90	100	110	120
	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
a154	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
	70	80	90	100	110	120
m154.pep	130	140	150	160	170	180
	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVQVQDIPPVTAIGQSGSLRLNLIGKNDRIILNVN					
a154	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVQVQDIPPVTAIGQSGSLRLNLIGKNDRIILNVN					
	130	140	150	160	170	180
m154.pep	190	200	210	220	230	240
	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
a154	SPVLYENFMVGQVESAHFDPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTSGSI					
	190	200	210	220	230	240
m154.pep	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYYTAFFKQ					
a154	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYYTAFFKQ					
	250	260	270	280	290	300
m154.pep	310	320	330	340	350	360
	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
a154	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
	310	320	330	340	350	360
m154.pep	370	380	390	400	410	420
	KEHWKQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
a154	KEHWKQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
	370	380	390	400	410	420
m154.pep	430	440	450	460	470	480
	GGLDDLQVKLADLLDKFDKLPLDKTVAELNGSLAEKSTLKSANAALSSIDKLVGKPTQ					
a154	GGLDDLQVKLADLLDKFDKLPLDKTVAELNGSLAEKSTLKSANAALSSIDKLVGKPTQ					
	430	440	450	460	470	480
m154.pep	490	500	510	520	530	540
	NIPNELNQT LKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
a154	NIPNELNQT LKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
	490	500	510	520	530	540

```

                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1  atGAAaatcg GtaccCCACG CGAGTCAtta tcCGGCGAAA cccgcgtagc
51  ctgcAcgccc gCCACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAGgt TTGGCGGCAA GTTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CTTGCGCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCTCCG ATTTCCCGCG CTCAGGCCTT GGACGCTTGT TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAAGTGC CGCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GCGGCGACG GAGACGgtA CGCCAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTGT CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACGCG CGCCATTCCG GGCAAACCCG CTCCCAAGCT
801 GATTACCAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAACCG GCAACGGCGT GAAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcgaAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTTCCCGCCT CGcgcgaTTc aggtTTCgc cggccgCAG CAAAcgcgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagccc AgccGaaacc tgttCCctg
1201 tgggAAAaac tcgCGCCGCG CGCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcaccgcag CATTTCTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGCTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGAgttcggt aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAAATCG GTCAGGGcaa cggcttcgtT TCgctGCTGT
1451 CGTTTGTGTC CATCCTGATT GCCGGCATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTTAAG AAAGGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDVPR ISRAQALDAL SSANISGYR AVIEAANAFG
151 RFFTGTITAA GKVPQAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKLDFLQES GGSGDGYAKV MSDEFIAAEM KLFQAEQAEV
251 DIIITTAaip GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTGNVVKII GYTDMANRLA GQSSQLYATN LVNLTLLSP NKDGEITLDF
351 EDVIRNMTV TRDGEITFPF PPIQVSARPO QTPSEKAAPA AKPEPKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAAFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIGQNGFV SLLSFVAILI AGINIFGGFA
501 VTRRLNMFK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1  ATGAAAATCG GTATCCACG CGAGTCATTA TCCGCGGAAA CCCGCGTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGTGCAGGT TTGGCGGCAA GTTTGACGCA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAACG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```

```

301 TTGGTCGAAG CCTTGC GCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTCGCGCG CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTGTGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GCGGCGAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCT
801 GATTACCAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTCACCCG CCGGGCGGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAG ACGGCGAAAT CACGTTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGGAAAA AACTCGCGCC CGCGTCAATC GCCGCCGTCT TGGTACTGTG
1251 GGTCGGCGCG GTCGCACCCG CAGCATTCCT GAACCACTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGTGATGTC GGTAAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGCGA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1  MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMVPR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTQGITA AAGKVPAPQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGKK FLKLDLPQES GSGDGYAKV MSDEFIAAEM KLFQAEQAEV
251 DIIITTAAP GKPAKPLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVSKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QPTPSEKAVP AAKPEPKPVP
401 LWKKLAPAVI AAVLVVLWGA VAPAAFLNHF IVFVLACVIG YVWVNVSHS
451 LHTPLMSVTN AISGIIVVGA LLQIQGNGF VLLSFLVAIL IAGINIFGGF
501 AVTRRLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
          10      20      30      40      50      60
m155.pep  MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
          |||
g155      MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
          10      20      30      40      50      60

          70      80      90      100     110     120
m155.pep  AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMVPR
          |||:|||||
g155      AAVWACPLIYKVNAPSEGEPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMVPR
          70      80      90      100     110     120

          130     140     150     160     170     180
m155.pep  ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPAPQVLVIGAGVAGLAA
          |||
g155      ISRAQALDALSSMANISGYRAVIEAANAFGRFFTQITAAGKVPAPQVLVIGAGVAGLAA

```

446

	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155						
	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155						
	250	260	270	280	290	
	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155						
	310	320	330	340	350	
	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
m155.pep	370	380	390	400	410	420
	VTHDGEITFPFPIQVSAQPQQTPEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLVWVGA					
g155	: : : : :					
	360	370	380	390	400	410
	VTRDGEITFPFPIQVSARPQQTPEKAAPAKPEPKPVPLWKKLAPAAIAAVLVLVWVGA					
m155.pep	430	440	450	460	470	480
	VAPAAFLNHFIVFVLACVIGYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
g155						
	420	430	440	450	460	470
	VAPAAFLNHFIVFVLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIGQGNGF					
m155.pep	490	500	510			
	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
g155						
	480	490	500	510		
	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

a155.seq

1	ATGAAAATCG	GTATCCCACG	TGAGTCATTA	TCCGGCGAAA	CCCGCGTCGC
51	CTGTACGCC	GCCACCGTCG	CCCTGCTGGG	CAAACGCGC	TTTGAAACCG
101	TTGTCGAAAG	CGGCGCAGGT	TTGGCGGCAA	GTTTGGACGA	TGCCCGTTAC
151	CAAGCAGCAG	CGGCAACCGT	TGCCGACAAA	GCAGCGGTTT	GGGCATACCC
201	TTTAATTAT	AAGGTTAACG	CGCCGTCCGA	AGACGAGCTG	CCGCTGCTCA
251	AAGAAGGACA	GACCATCGTC	AGCTTCCTGT	GGCCGCGCCA	AAACGAGGCT
301	TTGGTCGAAG	CCTTGCGCGC	CAAGAAAGTG	AACGCGCTGG	CAATGGACAT
351	GGTGCCCGC	ATTTCGCGCG	CGCAGGCTTT	GGACGNTTTG	TCTTNGATGG
401	CAAACATCAG	CGGCTACCGC	GCCGTGATTG	AAGCCGCCAA	CGCCTTCGGC
451	CGTTTNTTCA	CCGGCCAAAT	TACTGCCGCA	GGCAAAGTGC	CGCCCGCGCA
501	GGTTTGTGTG	ATTGGTGCAG	GTGTGGCAGG	TTTGGCGGCG	ATCGGTACGG
551	CAAACCTCGT	CGGCGCAGTG	GTACGCGTGT	TCGATACCCG	CCTG.AAGTG
601	GCGGAACAAT	TAGAATCGAT	GGCGGGCAAG	TTCTTGAAAC	TCGACTTCCC
651	GCAAGAATCG	GGCGGCAGCG	GCGACGGCTA	CGCCAAAGTG	ATGAGCGACG
701	AATTTATCGC	CGCCGAGATG	AAGCTTTTTG	CCGAGCAGGC	GAAAGAAGTG
751	GACATCATCA	TCACCACCGC	CGCCATTCCG	GGCAAACCCG	CGCCCAAGCN
801	NNTNANCAAA	GAAATGGTCG	AAAGCATGAA	ACCCGGCTCC	GTCATCGTCG
851	ATTTGGCGGC	GGCGACGGGC	GGCAACTGCG	AACTACCAA	ACAGGGCGAA
901	TTGTTTCGTAA	CCGGCAACGG	CGTGAAAATC	ATCGGCTACA	CCGACATGGC
951	AAACCGCCTT	GCCGGACAGT	CTTCGCAGCT	TTACGCCACC	AACTTGGTCA
1001	ACCTGACCAA	GCTGTTAAGC	CCGAACAAAG	ACGGCGAAAT	CACGCTGGAC
1051	TTGCAAGACG	TGATTATCCG	CAACATGACC	GTTACCCGCG	ACGGCGAAAT
1101	CACCTTCCCG	CCTCCGCCGA	TTCAAGTTTC	CGCCCAACCG	CAGCAAACGC
1151	CGTCTGAAAA	AGCCGCGCCT	GCCGCCAAGC	CCGAACCGAA	ACCCGTTCCC

```

1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTCCGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTGGAAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCT GCATCATCGT
1401 CGTCGCGCGC CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
 51 QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDMPVR ISRAQALDXL SXMANISGYR AVIEAANAFG
151 RXFTGQITAA GKVPAPQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDLPQES GSGGDYAKV MSDEFIAAEM KLFQAEQAKEV
251 DIIITTAAP GKPAKXXXK EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LFVTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLVVGA VAPAAFLNHF IVFVLACVIG YVVVWNVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQNGF VSLLSFVAIL IASINIFGGF
501 FVTRRLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

	10	20	30	40	50	60
m155.pep	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m155.pep	AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQTIVSFLWPRQNEALVEALRAKKVNALAMDMPVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m155.pep	ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGTGQITAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFGRXFTGTGQITAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m155.pep	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGSGGDYAKVMSDEFIAAEM					
a155	IGTANSLGAVVRFDTLXVAEQLESMGGKFLKLDLPQESGSGGDYAKVMSDEFIAAEM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m155.pep	KLFQAEQAKEVDIIITTAAPGKPAKPLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLFQAEQAKEVDIIITTAAPGKPAKXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m155.pep	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m155.pep	VTHDGEITFPFPPPIQVSAQPQQTPEKAVPAAPKPEPKVPLWKKLAPAVIAAVLVLVVGA					
a155	VTRDGEITFPFPPPIQVSAQPQQTPEKAAPAAKPEPKVPLWKKLAPAXIAAVLVLVVGA					
	370	380	390	400	410	420

448

	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFLACVIGYYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
a155	VAPAAFLNHFIVFLACVIGYYVWVNVSHSLHTPLMSVTNAISGIIVVGALLQIGQGNGF					
	430	440	450	460	470	480
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRRMLNMFKKGX					
a155	VSLLSFVAILIASINIFGGFFVTRRMLNMFRRGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTTCTG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCAACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG ATTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTTCG
351 CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
1  MTFAYWCILI ACLKPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRLAFIWCY
101 IADKAALRSL MWAGGFACTV GLFVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGGTTTTCTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCAC AGCAAAACGG TTTTGAAGCC TTGCAACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC GCGCAATCG ACCATCAACA
251 CGCTTGCCGT CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTTCG
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
1  MTFAYWCILI ACLKPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQQNGFEA FAPFAAAVLT AHATGNAAQS TINTLACLFI LFRLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

	10	20	30	40	50	60
m156.pep	MTFAYWCILIACLKPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA					
g156	MTFAYWCILIACLKPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQQNGFEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m156.pep	FAPFAAAVLTAAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFACTV					

449

```

g156      FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWAGGFAC TV
              70          80          90          100          110          120

m156.pep  GLFVAAAX
           |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
  1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
 51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101  ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151  CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTTGCACCGT TTGCAGCCGC
201  CGTTTGTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251  CGCTTGCCGG CCTGTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301  ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351  CTGCACCGTC GGGCTGTTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
  1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAARA
 51  HAAQONGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LFRFAFIWCY
101  IADKAALRSL MWVGGFVCTV GLFVVAAX*

```

m156/a156 90.6% identity in 127 aa overlap

```

              10          20          30          40          50          60
m156.pep      MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
              |||||
a156          MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAAQONGFEA
              10          20          30          40          50          60

              70          80          90          100          110          120
m156.pep      FAPFAAAVLTAHATGNAAQSTINTLACLFILFRLAFIWCYIADKAAMRSLMWAGGFAC TV
              |||||
a156          FAPFAAAVLTAHATGNAGQATVNTLAGLFILFRLAFIWCYIADKAALRSLMWVGGFVCTV
              70          80          90          100          110          120

m156.pep      GLFVAAAX
              |||||
a156          GLFVVAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
  1  atgaggaacg aggAAAAACg cgcctgcgc cgcgaattgC gCgGgcggcg
 51  ttcgcAAATg GGgcgagacg tGCGggCGGC GGCGgCgata Aaaatcaacc
101  gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151  cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201  ACGCgGCGCA AAactctatc tgccttATAT CGAACCGCAC ACGCGCGGA
251  TGTGTTTAC GCCGTATCCT GAACGCGGAA TGGAAACGGA ACGCAAGCGC
301  GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351  GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGCGAAG
401  GCTACCGTTT GGGGCAGGCA GCGGCTATT ACGATGCGAC GCTTTCGGCG
451  ATGAAATACC GTTTGCAGGC GAAAACCGTG GGCGTGGGCT TTGCCTGCCA
501  GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551  TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLKRYI KRGRKIGVYW
51  PMGKELRLGG FVRAAQKRGK KLYLPYIEPH TRRMWFTYP ERGMERERKR
101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGACQLVD RLPREAHDLP LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
1  ATGAGGAACG AGGAAAACG CGCCCTGCGC CGCGAATTGC GCGGGCGGCG
51  TTCGCAAATG GGGCGGGACG TGCGGGCGGC GGCAACGGTA AAAATCAACC
101 ACCTGCTCAA ACGTTATATT AAAAAAGGCG GAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACC CGT TCGCGCGGGA
251 TGTGTTTAC GCCGTATCCT GCCGATGGAG TAAACAAGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
351 GCATGATTTC AACCTCCTGC TTGTGCCAGT GGTCCGTATG GACAGGCTGG
401 GCTACCGCTT GGGACAGGCA GCGGCTATT ACGATGCGAC GCTTTCAGCG
451 ATGAAATACC GTTTCAGGC AAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTGCCG TCGAGGCGCA CGACCGGTCT TTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
1  MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLLKRYI KKGRKIGVYW
51  PMGKELRLDG FVRAAQKRGK ELYLPYIEPR SRRMWFTYP ADGVKQERKR
101 GRAKLHVPQF AGRKRVHDL NLLVPVVG M DRLGYRLGQA GGYDATLSA
151 MKYRLQAKTV GVGACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALR	RELGRRSQM	GRDVRAAATV	KINHLLKRYI	KKGRKIGVYW	PMGKELRLDG
g157	MRNEEKRALR	RELGRRSQM	GRDVRAAAAI	KINRLKRYI	KRGRKIGVYW	PMGKELRLGG
	10	20	30	40	50	60
m157.pep	FVRAAQKRG	AELYLPYIE	PRSRMWFT	PYPADGVKQ	ERKRGRAKL	HVPQFAGR
g157	FVRAAQKRG	AKLYLPYIE	PHTRRMWFT	PYPERGMER	ERKRGRAKL	HVPQFAGR
	70	80	90	100	110	120
m157.pep	NLLLV	VPVGM	DRLGYRL	GQAGGYD	ATLSAMKYR	LQAKTVG
g157	SVLLV	PLVGI	DREGYRL	GQAGGYD	ATLSAMKYR	LQAKTVG
	130	140	150	160	170	180
m157.pep	LDGFVSEAGI	LCFX				
g157	LDGFVSEAGI	LCFX				
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
1  ATGAGGAACG AGGAAAACA CGCCTTGCGC CGAGAGTTGC GCCGCGCCCG
51  CGCGCAGATG GGCATCAAG GCGGTTGGC GCGGGGCAA ACGATTAACC
```

451

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTTATC TGCCTTATAT CGAACC GCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGAACGCGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCCGCATA GACCGGAGG
401 GCTACCGCTT AGGACAGGCA GGCGGCTATT ACGATGCGAC GCTTGGCGCG
451 ATGAAATACC GTTTGCAGGC AAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

a157.pep

```

1 MRNEEKHALR RELRRARAQM GHQGRLAAGQ TINRLLKRYI KRGRKIGVYW
51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWTFYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQ	MGRDVR	AAATVKINHL	LKRYIKKGR	KIGVYWP	MGKELRLDG
	:	: :		: :		
a157	MRNEEKHALRRELRRARAQ	MGHQGR	LAAGQTINR	LLKRYIKRGR	KIGVYWP	MGKELRLDG
	10	20	30	40	50	60
	70	80	90	100	110	120
m157.pep	FVRAAQKRGAE	LYLPYIEPR	SRRMWTFYP	PADGVKQER	KRGRAKLH	VPQFAGRKRVHDL
	:		: :	:		
a157	FVRAAQKRGAK	LYLPYIEPR	SRRMWTFYP	PESGME	REIRIRGRA	KLNVPQFAGRKIRVHGL
	70	80	90	100	110	120
	130	140	150	160	170	180
m157.pep	NLLLVFVVGMDRLGYRL	GQAGGY	DATLSAM	KYRLQAKTV	GVGFACQ	LVDRLPVEAHDRS
	: : : :					
a157	SVLLVPLVGIDREGYRL	GQAGGY	DATLAAM	KYRLQAKTV	GVGFACQ	FVDRLPREPHDLL
	130	140	150	160	170	180
	190					
m157.pep	LDGFVSEAGILCFX					
a157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

g158.seq

```

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
51 CCGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAAcCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTCGCGCT GGATTCGCGG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTCGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCGCG AGAATTGGAC
451 GATTCCGGGC TGCGTGACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG
 851 TATTTTGGGA TTTTATTAGTG AAGGAACTGG GAAAAAATAT GAATAGAACG
 901 AATACCAAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep

1 MKTNSEELTV FVQVVEGSGF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLNLT EEGAQYFERR QRILQEMAAA ETEMLAVHEV PQGVLRVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNLL RLRVFLDFLV KELGKNMNRN
 301 NTK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq

1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAAG
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCGATGGCA AATTCTGCCG
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC
 151 AACC GCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATTT
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTGAGCGT GGATTCCGCG
 301 ATGCCGATGG TGCTGCATCT GCTGGCGCGG CTGGCAGCAA AATTCAACGA
 351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTTCGAA GGCTATATCA
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC
 451 GATTCCGGGC TCGCTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT
 501 CGCCAGTCCT GAATACCTGG CAAACACGG CACGCCGCAA TCTACAGAAG
 551 AGCTTGCCCG CCACCAATGT TTAGGCTTCA CCGAACCCGG TTCTCTAAAT
 601 ACATGGGCGG TTTTAGATGC GCAGGGAAAT CCCTATAAGA TTTCACCGCA
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGTT
 701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGCTGAA
 751 GGAAAGTTAA TTCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC
 801 CTTTAATGCT GTTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG
 851 TATTTTGGGA TTTTATTAGTG GAGGAACTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep

1 MKTNSEELTV FVQVVEGSGF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL
 51 NRTTRQLSLT EEGAQYFERR QRILQEMAAA ETEMLAVHEI PQGVLSVDSA
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSE GYINLIERKV DIALRAGELD
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE
 251 GKLIPLLAEQ TSKTHPFNA VYYSKAVNLL RLRVFLDFLV EELGNNLCG*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSGFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
g158	MKTNSEELTVFVQVVEGSGFSRAAEQLEMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m158.pep	EEGAQYFERRAQRILQEMAAEETEMLAHVHEIPQGVLSVDSAMPVHLHLLAPLAAKFNERYP					
g158	EEGAQYFERRAQRILQEMAAEETEMLAHVHEVPQGVLRVDSAMPVHLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

	130	140	150	160	170	180
m158.pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLAEQTSKTHPNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
g158	DFLVDNDITEGKLIPLFAEQTSNKTHPNAVYYSDKAVNLRRLRVFLDFLVKELGKNMNR					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158.seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTTGTTC AAG	TGGTGGA AAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGCAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCCG	CTGGCAGCAA	AATCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGACAG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TTAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTTAGATGC	GCAGGGAAT	CCCTATAAGA	TTTACCCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTCAGGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTTGGA	TTTTTTAGTG	GAGGAACCTG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158.pep

1	MKTNSEELTV	FVQVVEGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRRR	QRILQEMAAA	ETEMLAVHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFNERYP	HIRLSLVSS	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQC	LGFTTEPGSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYYSKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
a158	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRRQRILQEMAAAEETEMLAVHEIPQGVLSVDSAMPVHLHLLAPLAAKFNERYP					
a158	EEGAQYFRRRQRILQEMAAAEETEMLAVHEIPQGVLRVDSAMPVHLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

454

	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSDKAVNLRRLRVFLDFLVEELGNNLCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

g160.seq

1	ATGGAcattc	tgGACAAact	ggtcgatCTC	GCccaATTGA	CGGGCAGTGC
51	GGATGTGCAG	TgcctTTTGG	GCGGACAATG	gcATGaaacc	TTGCAACGCG
101	AAGGGCTGGT	ACACATTGTT	ACGGCGGGCA	GCGGTTATCT	CTGCATCGAC
151	GGCGAAACTT	CCCCGCGTCC	GGTCGGCACG	GGCGATATTG	TATTTTCC
201	GCGCGGCTTG	GGTCATGTGT	TGAGCCACGA	CGGAAAATAC	GGAGAAAGTT
251	TACAACCGGA	CATACGACAA	AACGGCACAT	TTATGGTCAA	ACAGTGC
301	AACGGGCTGG	ATATGAGCCT	GTTTTCGCC	CGTTTCCGCT	ACGACACCCA
351	CGCCGATTG	ATGAACGGGC	TGCCGGAAC	CGTTTTCTG	AACATTGCC
401	ATCCAAGTTT	GCAATATGTG	GTTTCAATGC	TGCAACTGGA	AAGCGAAAAA
451	CCTTTGACGG	GGACGGTTTC	CGTGGTCAAC	GCATTACCGT	CCGTCTGCT
501	GGTGCTTATC	CTGCGCGCCT	ATCTCGAACA	GGATAAGGAT	GTCGAACTCT
551	CGGGCGTATT	GAAAGTTTGG	CAGGACAAAC	GTTTGGGACA	TTTGATCCAA
601	AAGGTGATAG	ACAAACCGGA	AGACGAATGG	AATATTGACA	AAATGGTTGC
651	CGCCGCCAAT	ATGTCGCGCG	CGCAACTGAT	GCGCCGCTTC	AAAAGCCAAG
701	TCGGACTCAG	CCCGCACGCC	TTTGTGAACC	ATATCCGCTT	GCAAAAAGGC
751	GCATTGCTGC	TGAAGAAAAC	CCCGGATTTC	GTTTGGAGG	TCGCGCTGTC
801	GGTGGGCTTT	CAGTCGGAAA	CGCATTTCGG	CAAGGCGTTC	AAACGGCAAT
851	ATCACGTTTC	GCCGGGGCAA	TACCGGAAAG	AAGCGGGGCA	AAAATAA

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

g160.pep

1	MDILDKLVDL	AQLTGSADVQ	CLLGGQWHEH	LQREGLVHIV	TAGSGYLCID
51	GETSPRPVGT	GDIVFFPRGL	GHVLSHDGKY	GESLQPDIRQ	NGTFMVKQCG
101	NGLDMSLFCA	RFRYDTHADL	MNGLPETVFL	NIAHPSLQYV	VSMLQLESEK
151	PLTGTVSVDN	ALPSVLLVLI	LRLAYLEQDKD	VELSGVLKGW	QDKRLGHLIQ
201	KVIDKPEDEW	NIDKMVAAN	MSRAQLMRRF	KSQVGLSPHA	FVNHIRLQKG
251	ALLLKKTPDS	VLEVALSVGF	QSETHFGKAF	KRQYHVSPGQ	YRKEGGQK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

m160.seq

1	ATGGACATTC	TGGACAAACT	GGTCGATTTC	GCCCAATTGA	CGGGCAGTGT
51	GGATGTGCAG	TGCCTTTTGG	GCGGACAATG	GTCGGTACGG	CATGAAACCT
101	TGCAACGCGA	AGGATTGGTA	CACATTGTTA	CATCGGGCAG	CGGCTATCTC
151	TGCATCGACG	GCGAACTTTC	CCCGCGTCCG	GTCAGTACAG	GGGATATTGT
201	ATTTTCCCG	CGCGGCTTGG	GTCATGTGTT	GAGCCACGAC	GGAAAATGCG
251	GAGAAAGTTT	ACAACCGGAT	ATGCGGCAGC	ACGGTGCGTT	TACGGTCAAG
301	CAGTGCGGCA	ACGGACAGGA	TATGAGCCTG	TTTTGCGCCC	GTTTCCGCTA
351	CGACACCCAC	GCCGATTGTA	TGAACGGGCT	GCCTGAAACC	GTTTTCTCTA
401	ACATTGCCCA	TCCGAGTTTA	CAGTATGTGG	TTTCAATGCT	GCAACTGGAA
451	AGCAAAAAAC	CTTTGACGGG	GACGGTTTCC	ATGGTCAACG	CATTGTCGTC

455

```

501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGCGG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCTT TTGTGAACCA TATCCGCTTG
751 CAAAAGGCGG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTTGTGCGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCCTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
  51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
 101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
 151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
 201 LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
 251 QKGALLLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
 301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

m160.pep	10	20	30	40	50	60
	MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP					
g160	MDILDKLVDLAQLTGSADVQCLLGGQW---HETLQREGLV HIVTAGSGYL CIDGETSPRP					
	10	20	30	40	50	
m160.pep	70	80	90	100	110	120
	VSTGDIVFFPRGLGHVLSHDGKCGESLQPD MRQHGAFTVK QCGNGQDMSLFCARFRYDTH					
g160	VGTGDIVFFPRGLGHVLSHDGKYGESLQPD IRQNGTFMVKQCGNGLDMSLFCARFRYDTH					
	60	70	80	90	100	110
m160.pep	130	140	150	160	170	180
	ADLMNGLPETVFLNIAHPSLQYVVSMLQLESKKPLTGTVSMVNALSSVLLVLILRAYLEQ					
g160	ADLMNGLPETVFLNIAHPSLQYVVSMLQLESEKPLTGTVS VNALPSVLLVLILRAYLEQ					
	120	130	140	150	160	170
m160.pep	190	200	210	220	230	240
	DKDVELSGVLKGWQDKRLGH LIQKVIDKPE DEWNVDMVA AANMSRAQLM RRFKSRVGLS					
g160	DKDVELSGVLKGWQDKRLGH LIQKVIDKPE DEWNI DKMVA AANMSRAQLM RRFKSQVGLS					
	180	190	200	210	220	230
m160.pep	250	260	270	280	290	300
	PHAFVNHIRLQKGALLLKKNPDSVLSVALSVGFQSETHFGKAFKRQYHVSPGQYRKEGGQ					
g160	PHAFVNHIRLQKGALLLKKTPDSVLEVALSVGFQSETHFGKAFKRQYHVSPGQYRKEGGQ					
	240	250	260	270	280	290
m160.pep	KX					
g160	KX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
  1 ATGGACATTC TGGACAAACT GGTGATTTC GCCCAATTGA CGGGCAGTGT
 51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```

```
101 TGCAACGCGA AGGATTGGTA CACATTGTTA CATCGGGCAG CGGCTATCTC
151 TGCATCGACG GCGAAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTCCCG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCGGCA ACGGACAGGA TATGAGCCTG TTTTGCGCCG GTTCCGCTA
351 CGACACCCAC GCCGATTTGA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCTGCTG GTGCTTATCC TGCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTGCG TTTTGTGCGT
801 CGCACTGTG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGTCAAT ACCGGAAGA AGGCGGGCAA
901 AAATAA
```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```
a160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFVTK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*
```

m160/a160 100.0% identity in 301 aa overlap

```
          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||||
a160      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          10      20      30      40      50      60

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFVTK QCGNGQDMSL FCARFRYDTH
          |||||
a160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFVTK QCGNGQDMSL FCARFRYDTH
          70      80      90      100     110     120

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLESKKPLTGT VSMVNALSSVLLVLILRAYLEQ
          |||||
a160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLESKKPLTGT VSMVNALSSVLLVLILRAYLEQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||||
a160      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          190     200     210     220     230     240

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLLKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||||
a160      PHAFVNHIRL QKGALLLKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          250     260     270     280     290     300

m160.pep KX
          ||
a160      KX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGGACA CCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGGTGCTG CTCCTTGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTCAGGAA
451 CCGCGGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GCGGTGGCGA TGTCGTCggt ttgggagacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGGCGA CAAATTCACG GTTGCCCTCGC tttcctaTAt gaccgtcGTC
751 TTTCCGCCCC TGTCTGCCGC ATTTTCTCTg ggcaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCCGCCCCAT TGCCTTCAA CAGCGGCTGC AAGCCCTCTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVTLGAAAVL RRDTERTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPFSRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSEF SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GCGGGCCTGC TTTACCATTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTGCCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTCA
151 ACCGTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCAC TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCCG TTTACACGCA GCGGTGCTG CTCCTTGTT
401 TTGCCGGCGT GGTATTGCTG CTTAATCCCT CGTTCCGCAG CGGTCAGGAA
451 ACGGCGGCAC TCGCCGGGCT GCGGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCGTCGGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTG
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGGCGA CAAATTCACG GTTGCCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTCTCTG GGCGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCCGCCCCAC TGCCTTCAA CAGCGGCTGC AATCCCTGTT CCGCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLFS
51  TVALGAAAVL RDXFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPFSRSGQE

```

151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
 201 LTGWHTLSEF SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
 251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
 301 *

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	: : : : :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLSTVTLGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSIFLAVESFLILKE					
	: : : : :					
g161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLTTGVTLSYTSIFLAVESFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFAGVVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	: : : : :					
g161	RISVYTQAVLLLGFAGVVLLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTRAYKVGDKFT					
	: : : : :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSFPSAVYLSIGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	: : : : :					
g161	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	X					
g161	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

a161.seq

1	ATGGATACCG	CAAAAAAGA	CATTTTAGGA	TCGGGCTGGA	TGCTGGTGCC
51	GGCGGCCTGC	TTTACCATTA	TGAACGTATT	GATTAAAGAG	GCATCGGCAA
101	AATTTGCCCT	CGGCAGCGGC	GAATTGGTCT	TTTGGCGCAT	GCTGTTTTCA
151	ACCGTTGCGC	TCGGGGCTGC	CGCCGTATTG	CGTCGGGACA	CCTTCCGCAC
201	GCCCCATTGG	AAAAACCACT	TAAACCGCAG	TATGGTCGGG	ACGGGGGCGA
251	TGCTGCTGCT	GTTTACGCG	GTAACGCATC	TGCCTTTGGC	CACCGGCGTT
301	ACCCTGAGTT	ACACCTCGTC	GATTTTTTTG	GCGGTATTTT	CCTTCTGAT
351	TTTGAAAGAA	CGGATTTCCT	TTTACACGCA	GGCGGTGCTG	CTCCTTGTTT
401	TTGCCGGCGT	GGTATTGCTG	CTTAATCCCT	CGTCCGCAG	CGGTACAGAA
451	ACGGCGGCAC	TCGCCGGGCT	GGCGGGCGGC	GCGATGTCCG	GCTGGGCGTA
501	TTTGAAAGTG	CGCGAACTGT	CTTTGGCGGG	CGAACCCGGC	TGGCGCGTCG
551	TGTTTTACCT	TTCCGTGACA	GGTGTGGCGA	TGTCATCGGT	TTGGGCGACG
601	CTGACCGGCT	GGCACACCCT	GTCCTTTCCA	TCGGCAGTTT	ATCTGTCGTG
651	CATCGGCGTG	TCCGCGCTGA	TTGCCCAACT	GTCGATGACG	CGCGCCTACA
701	AAGTCGGCGA	CAAATTCACG	GTTGCCTCGC	TTTCTATAT	GACCGTCGTT
751	TTTTCCGCTC	TGTCTGCCGC	ATTTTTCTG	GCCGAAGAGC	TTTTCTGGCA
801	GGAAATACTC	GGTATGTGCA	TCATCATCCT	CAGCGGTATT	TTGAGCAGCA

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMIFS
51 TVALGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT
201 LTGWHITLSEF SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR
301 *

m161/a161 99.3% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMIFSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMIFSTVALGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGAFAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGAFAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHITLSEFSVAVYLSICIGVSALIAQLSMT RAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHITLSEFSVAVYLSICIGVSALIAQLSMT RAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq
1 ATGGTTATTT TGACGACTTT GTTTTTTGTG TGTGTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG
101 TCATTTTTTAC CGAGTTCAGC TGGTTTATG TTTTAACGTT TTCCATTTTT
151 ctgGGTTTtc tgctGATACT CTCGGTCAGC GGTTTGGGAA ACATcagGCT
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCCTGGGCC TGATGTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGTCGGCG CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCACG
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG ACCCCTACTGT
801 TTACCTGTGG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAATC
851 TGGTGCCTCT CAGTTTGAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTGAAT CTTGGACGGT GCTTTATTGG GCGTGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTGTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCGGGGTT TTGCTCATCC CCGGCTGTGT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGCGGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CCCTGTTTTT TGTAATTCT GCCGACTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGTTGGC
1301 AGGCGGTTAT GTGGGCGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCTGA TTGTTTCCCT
1401 GCGGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCATGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CCGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTGCGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAAGTC
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1  MVILTTLEFFV CVLVVLVLT PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51 LGFLLLLSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFASQ
201 LGAGLQEMGW IAENSGVQV LIIAVMSLA VVSAISGVKG GVKVLSELNL
251 GLAFLLEFFV LAADPTVYLL SAFGDNIGNY LGNLVRSLK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLEFFVTS ADSGIYVLNN ITSRDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FTWGGKWKER LVRIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVQDEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1  ATGTTATTT TGACGACTTT GTTTTTTGTC TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGTC TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACAGGTT GTTCATTGG GCGTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTT
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

```

```

651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGCCTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTGTGTT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGGAAATC
851 TGGTGCGCCT CAGTTTAAAT ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTGTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGAAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCAGAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTATTAT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGCTG CCGTGGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAAGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCC
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGCT
1651 CCGGTCGATA AAATGTTTCA TCGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGCTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAAC TG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

```

m163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELOR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFFYVLTFSIFLGFLILSVS
          |||
g163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFFYVLTFSIFLGFLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
          :|||
g163      GLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ
          70      80      90     100     110     120

          130     140     150     160     170     180

```

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIENSFSVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSELNLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVMSAVAVLLMRSGGLGNLQSMTLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKQTASPMHELQR
g163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEQDILKFLKHTASPMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGGTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

```

```

201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACAG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTTT
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCGG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGACAGTT TTGATTATCG CCGCCGTCAT GTCCTTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGTCTTGCCT TTTTGTGCT GTTTTTTGT TTTGGCGGCG GTCCCACTGT
801 TTACCTGTTG TCGGCATTGC GCGACAACAT AGGGAACCTAC CTCGGAATC
851 TGGTGCGCCT CAGTTTTTAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGCG
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTAT GTGGGCGGTG CTGATGTCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGGC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGAT
1451 TGAGTGCAGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCCG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCAGC AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLEFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIOW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLEFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSEK TYAYERHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVEGV LLIPGLFGVL
351 WFTVFGNTAI WLNDGVAGGV LEKMTSSPET LLEKFFNYLP LPELTSIVSL
401 LVISLFEVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMVG LMSAVAVLLM
451 RSGGLNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

          10      20      30      40      50      60
m163.pep  MVILTTLEFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISIF LGFLLILSVS
          |||||
a163      MVILTTLEFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFISIF LGFLLILSVS
          10      20      30      40      50      60

          70      80      90     100     110     120
m163.pep  SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA EPLMHYFSDI TAGTPEHRQQ

```

```
|||||
a163      SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ
              70      80      90      100     110     120

              130      140      150      160      170      180
m163.pep  QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
              |||||
a163      QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
              130      140      150      160      170      180

              190      200      210      220      230      240
m163.pep  MALLATFFGIITTLGFGASQLGAGLQEMGWIENSFSVQVLIIAAVMSLAVVSAISGVGK
              |||||:|||||
a163      MALLATFFGIITTLGFGASQLGAGLQEIOWIENSFSVQVLIIAAVMSLAVVSAISGVGK
              190      200      210      220      230      240

              250      260      270      280      290      300
m163.pep  GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              |||||
a163      GVKVLSSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
              250      260      270      280      290      300

              310      320      330      340      350      360
m163.pep  WFESWTVLYAWWCWAPFVGLFIARISKGRITREFVFGVLLIPGLFGLVWFTVFGNTAI
              |||||
a163      WFESWTVLYAWWCWAPFVGLFIARISKGRITREFVFGVLLIPGLFGLVWFTVFGNTAI
              310      320      330      340      350      360

              370      380      390      400      410      420
m163.pep  WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              |||||:|||||
a163      WLNDGVAGGVLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
              370      380      390      400      410      420

              430      440      450      460      470      480
m163.pep  ITS RDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
              |||||
a163      ITS RDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSM TLIVSLP FALLMLIMCFSL
              430      440      450      460      470      480

              490      500      510      520      530      540
m163.pep  WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKQTASPAMHELQR
              |||||
a163      WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQTQEODILKFLKHTASPAMHELQR
              490      500      510      520      530      540

              550      560      570      580      590      600
m163.pep  ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              |||||:|||||
a163      ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
              550      560      570      580      590      600

              610      620      630      640      650      660
m163.pep  HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
              |||||
a163      HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
              610      620      630      640      650      660

m163.pep  X
          |
a163      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGCGC TTCCTGTTTC CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCC GTCGAAAAAA TCATTTGGAC GGACAAAAGC
151 CGGCCGGCCG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCGG CCAACCCCGG ATAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTcctg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAATc cgttttCCcC ttttccaacg TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTCAGATG GTTCAACCGC
601 ATCCGCTGTG TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCCGCGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCCTC GTCGCCGTCA ATACGCCCGA ACGGCAAAAA
751 GCCCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGCGCA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTC GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAAACG GGCgATTTCG TTACCATAGA
951 CGAGGACGCG TTTATCTTTA TCGTCGACCG CAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GGCGTGAAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTTGG
1151 GCGAGGACGA aatccgccgc caccTGCgTA CCGTGCTGGC AAATTTCAAA
1201 ATCCCCAAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDLGRQPR INDLAHIYT SGTGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MULLPIYMAC
151 SILLVKSVFP FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWFYRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKDD LIISKGQNVY PREIEEEIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCTGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATCCAC
201 AGAATTTATT ACCGCTATT TCGCCATCTC CGCCATCGGC GCGGTGCGCG
251 TACCGATGAA CACATTTTGG AAAAAACAGC AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGCGCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGGCGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGGATAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTG
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCGT TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATTCC CCGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGAAGGCTA

```

```

951 CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGCCAAAGCC
1051 GTCGATGAAG AATTGGTCGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTGAT
1251 TATTTCCAA GGTCAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301 ACAAACCTCGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTSGTTG HPKGALISYA NLFANLNGIE
201 RIFKISKRD R FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNV L
251 KQTLKRA TV FLGVPAIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFP R AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVP R GEVGELIVRG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDEGFIF V DRKKDLIISK GQNVYPREIE EEIYKLDAVE AAAVIGVKDR
451 YADEEIVAF V QLKEGMDLGE NEIRRLRLTV LANFKIPKQI HFKDGLPRNA
501 TGKVLKRV LK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

	60	70	80	90	100	110
m164.pep	GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK					
g164						
				10	20	30
	120	130	140	150	160	170
m164.pep	ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT					
g164						
	40	50	60	70	80	90
	180	190	200	210	220	230
m164.pep	SGTTGHPKGALISYANL FANLNGIERIFKISKRD R FIVFLPMFHSFTLTAMVLLPIYMAC					
g164						
	100	110	120	130	140	150
	240	250	260	270	280	290
m164.pep	SIILVKSVFPFSNV LKQTLKRA TV FLGVPAIYTAMSKAKI PWYFRWFNRIRLFISGGAP					
g164						
	160	170	180	190	200	210
	300	310	320	330	340	350
m164.pep	LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNT PERQKARSVG IPLPGLEAKAVDEEL					
g164						
	220	230	240	250	260	270
	360	370	380	390	400	410

467

```

m164.pep  VEVP RGEV GELIV RGG SVM RGYL NM PAAT DE TIV NGWL KTGF VTI DE DGF IFIV DRKKD
           |||||
g164       VEVP RGEV GELIV RGG SVM RGYL NM PAAT DE TIV NGWL KTGF VTI DE DGF IFIV DRKKD
           280      290      300      310      320      330

           420      430      440      450      460      470
m164.pep  LIISK GQNV YPRE IE EEE IYK L DAVE AAA VIG VKDR YADE EIV AFV QLKE GMD LGE NE IRR
           |||||
g164       LIISK GQNV YPRE IE EEE IHK L DAVE AAA VIG VKDR YADE EIV AFV QLKE GMD LGE DE IRR
           340      350      360      370      380      390

           480      490      500      510
m164.pep  HLRTV LANFK IPKQ IHFK DGL PRNAT GKVL KRVL KEQ FDN KX
           |||||
g164       HLRTV LANFK IPKQ IHFK DGL PRNAT GKVL KRVL KEQ FEG NXX
           400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCTTATT TCGCCGTATC CGCCATCGGC GCGGTTGCCG
251 TACCGATGAA CACATTTTGT AAAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGCGCTGT CAAAAGAATT
351 GCGGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCGGCT TCCCGCAAAA ACCCGACTTG GGCGGCAAC CCGGATAAAA
501 TGATTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TCCCCTTTTC CAACGTTTGT
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACGCGC ATGAGCAAGA CGAAATCCC TTGGTATTTC AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATGCG TGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCTGCG CCGGTTTGGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTG AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGTGA TCGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCG TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPDL GRQPRINDLA HIIYTSCTTG HPGKALISYA NLFANLNGIE
201 RIFKISKRRD FIVFLPMFHS FTLTAMVLLP IYMACSIIIV KSVFPFSNVL
251 KQALLKRATV FLGVPPIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEV GELIVRG GSVMRGYLM PAATDETIVN GWLKTGDFVT
401 IDEDFIFIV DRKKDLISK GQNVYPREIE EEIYKLDAVE AAAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRTV LANFKIPKQI HFKDGLPRNA

```

501 TGKVLKRVLK EQFDGNK*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQAEAAVAYLQNIQVKGFDIVA					
a164	MNRTYANFYEMLAACRKNNGTAVFDGKEKTAYRALKQAEAAVAYLQNIQVKGFDIVA					
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETTG					
a164	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDGRQPRINDLAHIIYTSGETTG					
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
a164	HPKGALISYANLFANLNGIERIFKISKDRFIVFLPMFHSFTLTAMVLLPIYMACSIILV					
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
	KSVFFFSNVLKQTLKRVATVFLGVPPIYATAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	KSVFFFSNVLKQTLKRVATVFLGVPPIYATAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEELVEVPR					
a164	ILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVGIPLPGLEAKAVDEELVEVPR					
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLIISK					
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLIISK					
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHRLTV					
a164	GQNVYPREIEEEIYKLDAAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHRLTV					
	430	440	450	460	470	480
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq

1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GGCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC GTTTTGTCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGAAGat gTGGCGTTGG AATCGTCAAA cGCGTGAAC
151 AACGcCGgca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccggac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGC GGAAGGCAAG
301 TTGGAagaCA ATTCCCTTCAT CAATGCcgtg ccgcatatGT Ctttgggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgcGTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCCGCCG Aaggcacgga tgtcgATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCCTCTT CCTCGGCGCG GGC GGCGCGG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCGGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGC GCGCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CcTGCTGGgC gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

g165.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFKTQKLFEN MEFSTDNRKI
151 SDWAPLIMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GLPVSGLFRR NSNPETAEOH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSFM DLPLSIHMDN LYPLMRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

m165.seq (partial)

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGTCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGAAGAT gTGGCGTTGG AATCGTCAAA cGCGTGAAC
151 AACGCGGCA CGGGGCATTC CGCGCTGTGc GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCG TGTCGGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GGC GCGCGCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

m165.pep (partial)

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD AFKTQKLFEN MEFSTDNRKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGVKTEF

```

201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
 251 SGIPEGKGYG GFPVSGLFFR NSNPETAQEH NAKVYQASV GAPPMSVPHL
 301 DTRNVDGKRH LMFGPYAGFR SNFLKQGLM DLPLSIHMDN LYPMLCAGWA
 351 NMPLTK...

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m165 / g165 97.2% identity in 356 aa overlap

	10	20	30	40	50	60
m165.pep	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
g165	MAEATDVVLVGGGIMSATLGVLLKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165.pep	ELNYAPLGANGIIDPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165	ELNYAPLGADGVINPARALNIAEQFHVSQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165.pep	HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
g165	HCRYLQKRYDVFKTQKLFENMEFSTDNRKISDWAPLMRGRDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165.pep	GRLTRQMVKYLGKGVKTEFNHVEDIKRESGAWVLKTADTRNPDGQLTLRTRFLFLGA					
g165	GRLTRQMVKYLGKGVKTEFNHVEDIKRESGAWVLKTADTRNPDWQLTLRTRFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165.pep	GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL					
g165	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	
m165.pep	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK					
g165	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSFMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
g165	ELRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

a165.seq

1	ATGGCTGAAG	CGACAGACGT	TGTCTTGGTG	GGCGGCGGCA	TTATGAGCGC
51	GACTTTGGGC	GTTTGTCTCA	AAGAACTCGA	ACCGTCTTGG	GAAATCACCC
101	TGATTGAACG	CTTGAAGAT	GTGGCGTTGG	AATCGTCAAA	CGCGTGGAAC
151	AACGCCGGCA	CGGGGCATTC	CGCGCTGTGC	GAATTGAACT	ATGCGCCGTT
201	GGGTGCAAAT	GGGATTATCG	ATCCGGCGCG	CGCCCTCAAT	ATTGCCGAAC
251	AGTTTCATGT	CAGCCGCCAG	TTTTGGGCGA	CGTTGGTCGC	GGAAGGCAAG
301	TTGGAAGACA	ATTCTTCAT	CAATGCCGTG	CGCATATGT	CTTTGGTGAT
351	GAATGAAGAC	CATTGTTCTT	ATCTTCAAAA	ACGTTATGAC	GCGTTTAAAA
401	CCCAAAACT	TTTTGAAAAT	ATGGAATTTT	CCACCGATCG	GAACAAAATT
451	TCCGATTGGG	CTCCGCTGAT	GATGCGCGGC	CGGGACGAAA	ACCAACCCGT
501	CGCCGCCAAC	TACTCCGCCG	AAGGCACGGA	TGTCGATTTC	GGACGGCTGA
551	CGCGCCAAAT	GGTGAAATAT	TTGCAGGGCA	AGGGCGTAAA	AACCGATTTC

```
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGTGACCCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACGCG CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCACTTATG GATTGCGCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATAA CCTGCTGGGC GAATGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGAT TGCTGGGCGC GTCGCCGGC GCATGCACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGC TATACCGCGA
1451 AAGTGTGGA TATTAA
```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

```
a165.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGKVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAQHN NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLEYYPEA NPDDWELITA QQRVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*
```

m165/a165 99.7% identity in 356 aa overlap

```
10 20 30 40 50 60
m165.pep MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC
|||||
a165 MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNNAGTGHSALC
10 20 30 40 50 60

70 80 90 100 110 120
m165.pep ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED
|||||
a165 ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED
70 80 90 100 110 120

130 140 150 160 170 180
m165.pep HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF
|||||
a165 HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAAANYSAEGTDVDF
130 140 150 160 170 180

190 200 210 220 230 240
m165.pep GRLTRQMVKYLQKGKVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
|||||
a165 GRLTRQMVKYLQKGKVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
190 200 210 220 230 240

250 260 270 280 290 300
m165.pep GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSPVPHL
|||||
a165 GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSPVPHL
250 260 270 280 290 300
```

	310	320	330	340	350
m165.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK				
a165	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG				
	310	320	330	340	350
	360				
a165	ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS				
	370	380	390	400	410
	420				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGGCGGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAagat  gTGGCGTTGG  AATCGTCAAA  cGCGTGGAAC
151 AACGcCGGca  CGGGGCATTC  CGcGCTGTGc  GAATTGAACT  AtgcgccGCT
201 GGGtgccgac  ggcgtcatca  ATCCGGCGCg  cgCCCTGAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGcga  cgctggtCGC  GGAAGGCAAG
301 TTGGAAGACA  ATTCCTTCAT  CAATGCCGTG  CCGCATATGT  CTTTGGTGAT
351 GAACGAAGAC  CACTGCCGTT  ACCTGCAAAA  ACGCTATGAT  GTGTTTAAAA
401 CGCAGAAACT  TTTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CtccgCTGAT  TATGCGCGGC  CGGGACGAAA  ACCAACCCGT
501 CGCCGCCAAC  TATTCGCCCG  AAGGCACGGA  TGTCGATTTC  GGACGGCTGA
551 CGCGCCAGAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCGAGTTC
601 AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAACCCGCC  GATACCCGCA  ACCCAGACTG  GCAGCTCACC  CTCGCCACCC
701 GCTTCCTCTT  CCTCGGCGCG  GCGGCGGCGC  CACTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTACCCG  TGTCCGGCCT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAAAC  AACGCCAAAG
851 TGTACGGGCA  GGCTTCCGTC  GCGCGCGCCG  CGATGTCCGT  CCCGCACCTC
901 GACACACGCA  ACGTAGACGG  CAAACGACAC  CTTATGTTTC  GTCCTTACGC
951 AGGTTTCCGT  TCCAACCTCC  TCAAGCAAGG  CTCGTTTATG  GATTGCGCGC
1001 TGTCATCCCA  TATGGACAAC  CTCTATCCCTA  TGCTGCGCGC  CGGCTGGGCG
1051 AATATGCCGC  TGACCAATAA  CCTGCTGGGC  GAATTGCGTA  AAACCAAGA
1101 AGAACGCTtt  gCCTCCCTGC  TGgaatacta  cccGaggcag  acccGACGAc
1151 tggtaactcat  caccgagcnc  acGCGTcata  tcattanata  tgactCGaaa
1201 ctgcgcgtgc  tgcagttgta  cgagattgtg  ccaCGCGacg  ctgcgtcgcg
1251 cattctggag  cgtcgcgcg  catcacgctn  tgcgctgata  tccgctgatg
1301 acactgtctc  gaGCGcgccc  gtcttggaag  gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV  GGGIMSATLG  VLLKELEPSW  EITLIERLED  VALESSNAWN
51  NAGTGHSAIC  ELNYAPLGAD  GVINPARALN  IAEQFHVSRQ  FWATLVAEGK
101 LEDNSFINAV  PHMSLVMNED  HCRYLQKRYD  VFKTQKLFEN  MEFSTDRNKI
151 SDWAPLMIRG  RDENPVAAN  YSAEGTDVDF  GRLTRQMVKY  LQSGKVKTEF
201 NRHVEDIKRE  SDGAWVLKTA  DTRNPDWQLT  LRTRFLFLGA  GGGALTLLQK
251 SRIPEGKYGG  GLPVSGLFFR  NSNPETAEOH  NAKVYGQASV  GAPPMSPVPHL
301 DTRNVDGKRH  LMFGPYAGFR  SNFLKQGSFM  DLPLSIHMDN  LYPMLRAGWA
351 NMPLTKYLLG  ELRKTKEERF  ASLLEYYPQR  TRRLVLITQX  TRHIIYDSK
401 LRVLQLYEIV  PRDARSRIE  RRGASRXALI  SADDTAPSAP  VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG  CGACAGACGT  TGTCTTGGTG  GCGGCGGGCA  TTATGAGCGC
51  GACTTTGGGC  GTTTTGCTCA  AAGAACTCGA  ACCGTCTTGG  GAAATCACCC
101 TGATTGAACG  CTTGGAAGAT  GTGGCGTTGG  AATCGTCAAA  CGCGTGGAAC
151 AACGCCGGCA  CGGGGCATTC  CGCGCTGTGC  GAATTGAACT  ATGCGCCGTT
201 GGGTGCAAAAT  GGGATTATCG  ATCCGGCGCG  CGCCCTCAAT  ATTGCCGAAC
251 AGTTTCATGT  CAGCCGCCAG  TTTTGGGCGA  CGCTGGTTCG  GGAAGGCAAG
301 TTGGAAGACA  ATTCCTTCAT  CAATGCCGTG  CCGCATATGT  CTTTGGTGAT
351 GAATGAAGAC  CATGTGTTCT  ATCTTCAAAA  ACGTTATGAC  GCGTTTAAAA
401 CCCAAAAACT  TTTTGAAAAT  ATGGAATTTT  CCACCGATCG  GAACAAAATT
451 TCCGATTGGG  CTCGCTGAT  GATGCGCGGC  GGGACGAAA  ACCAACCCGT
501 CGCCGCCAAC  TACTCCGCCG  AAGGTACGGA  TGTCGATTTC  GGACGGCTGA
551 CGCGCCAAAT  GGTGAAATAT  TTGCAGGGCA  AGGGCGTAAA  AACCGAGTTC
601 AACCGCCACG  TCGAAGACAT  CAAACGCGAA  TCCGACGGCG  CGTGGGTGCT
651 CAAAACCGCC  GATACCCGCA  ACCCCGACGG  GCAGCTCACC  CTCGTACCC
701 GCTTCCTCTT  CCTCGGCGCG  GCGGCGGCGC  CGCTGACCCT  GCTGCAAAAA
751 TCCGGCATCC  CCGAAGGCAA  AGGCTACGGC  GGCTTCCCG  TGTCCGGCCT
801 GTTCTTCCGC  AACAGCAACC  CCGAAACCGC  CGAACAAAC  AACGCCAAAG

```

```
851 TGTACGGGCA GGCCTCCGTC GGCAGCGCCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACTA CCCCAGGCA AACCCGACG
1151 ACTGGGAAT CATACCGCA GGGCAACGCG TCCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCGCAT TGCTGGGCGC GTCGCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GGGCGGATGA AATTATCGCC TATACCGCA
1451 AAGTATTGGA TATTTAA
```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

m165-1.pep

```
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDNRKI
151 SDWAPLMMRG RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQGGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFFVSGLFRR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSMD LPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIHKD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAQVLDI*
```

m165-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSW	EITLIERLED	VALESSNAWN	NAGTGHSALC	
g165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSW	EITLIERLED	VALESSNAWN	NAGTGHSALC	
	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGI	IDPARALNIAEQFHVS	RQFWATLVAEGK	LEDNSFINAV	PHMSLVMNED	
g165-1	ELNYAPLGADGV	INPARALNIAEQFHVS	RQFWATLVAEGK	LEDNSFINAV	PHMSLVMNED	
	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDA	FKTQKLFENMEF	STDNRKISDW	APLMRGRDEN	QPVAA	NSAEGTDVDF
g165-1	HCRYLQKRYDV	FKTQKLFENMEF	STDNRKISDW	APLMRGRDEN	QPVAA	NSAEGTDVDF
	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKY	LQGGKGVKTEF	NRHVEDIKRE	SDGAWVLKTA	DTRNPDGQLT	LRTRFLFLGA
g165-1	GRLTRQMVKY	LQGGKGVKTEF	NRHVEDIKRE	SDGAWVLKTA	DTRNPDGQLT	LRTRFLFLGA
	250	260	270	280	290	300
m165-1.pep	GGGALTLLQK	SGIPEGKGYG	GFFVSGLFRR	NSNPETAQH	NAKVYQASV	GAPPMSVPHL
g165-1	GGGALTLLQK	SGIPEGKGYG	GFFVSGLFRR	NSNPETAQH	NAKVYQASV	GAPPMSVPHL
	310	320	330	340	350	360
m165-1.pep	DTRNVDGKRH	LMFGPYAGFR	SNFLKQGSMD	LPLSIHMDN	LYPMLCAGW	ANMPLTKYLLG
g165-1	DTRNVDGKRH	LMFGPYAGFR	SNFLKQGSMD	LPLSIHMDN	LYPMLCAGW	ANMPLTKYLLG
	370	380	390	400	410	420
m165-1.pep	ELRKTKEERF	ASLLEYYPEA	NPDDWELITA	GQRVQIHKD	SEKGGVLQFG	TEIVAHADGS
g165-1	ELRKTKEERF	ASLLEYYPEA	NPDDWELITA	GQRVQIHKD	SEKGGVLQFG	TEIVAHADGS
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNNPERADEIIA
:
111
g165-1 ILERRGASRXALISADDTAPSAPVLESVX
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

a165-1.seq
1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGCGCA TTATGAGCGC
51 GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCCTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATGCGCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAACT TTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCTG
501 CGCGCCCAAC TACTCCGCCG AAGGCACGGA TGTGATTTC GGACGGCTGA
551 CGCGCCCAAT GGTGAAATAT TTGCAAGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGCAGCG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGCGCGCGC CGCTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCGCG AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCACCTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACT CCCCAGGGCA AACCCGACG
1151 ACTGGGAAGT CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCGGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTTAA

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

a165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQGGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIPPEGKYG GFPVSGLFRR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GQRVQIIKKD
401 SEKGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLNE NPERADEIIA YTAKVLDI*

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWNNAGTGH	SALC		
m165-1	MAEATDVVLVGGGIMSATLG	VLLKELEPSWEITLIERLED	VALESSNAWNNAGTGH	SALC		
	10	20	30	40	50	60
	70	80	90	100	110	120
a165-1.pep	ELNYAPLGANGIIDPARALN	IAEQFHVSQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
m165-1	ELNYAPLGANGIIDPARALN	IAEQFHVSQFWATLVAEGK	LEDNSFINAVPHMSLVMNED			
	70	80	90	100	110	120
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMR	GRDENQPVAAANYSAEGTDVDF			
m165-1	HCSYLQKRYDAFKTQKLFEN	MEFSTDRNKISDWAPLMMR	GRDENQPVAAANYSAEGTDVDF			
	130	140	150	160	170	180
	190	200	210	220	230	240

```

a165-1.pep  GRLTRQMVKYLGKGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
m165-1      GRLTRQMVKYLGKGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
m165-1      DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVPLMIRLMHQCFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
m165-1      LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
m165-1      YTAKVLDIX

```

a165-1/p33940

sp|P33940|YOJH_ECOLI_HYPOTHETICAL_60.2_KD_PROTEIN_IN_ECO-ALKB_INTERGENIC_REGION
>gi|1736851|gnl|PID|d1016718 (D90850) ORF_ID:o372#5; similar to [SwissProt Accession Number
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical
to 490 residues of YOJH_ECOLI SW: P33940 (492 aa) but contains 56 additional N-term aa; 100 pct
identical to GB: ECOHU49_33
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548
Score = 458 bits (1167), Expect = e-128
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```

Query: 3  EATDVVLVGGGIMSATLGVLKLEPSWEITLIERLEDVALESSNAWNNAGTGHSA LCEL 62
          + TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSA L EL
Sbjct: 30 QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSA LMEL 89

Query: 63 NYAPL GANGIIDPARALNIAEQFHVS RQFWATLVAEGKLED-NSFINAVPHMSLV MNEDH 121
          NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90 NYTPQNADGSISIEKAVAINAEAFQISRQFWAHQVERGVLRTPRSFINTVPHMSFVWGEDN 149

Query: 122 CSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAANYSAEGTDVDFG 181
          ++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150 VNFLRARYAALQQSSLFRGMRYSEDHAQIKEWAPLVMEGRDPQQKVAATRTEIGTDVNYG 209

Query: 182 RLTRQMVKYLGKGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
          +TRQ++ LQ K + + V +KR D W + AD +N Q
Sbjct: 210 EITRQLIASLQKKS N FSLQLSSEVRALKRNDNTWTVTVADLNKGT AQ-NIRAKFVFIGA 268

Query: 241 XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL 300
          Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269 GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVNVNHLAKVYGKASVGAPPMSVPHI 328

Query: 301 DTRNVDGKRHLMFPGPYAGFRSNFLKQGSMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
          DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329 DTRVLDGKRVLFGPFATFSTKFLKNGSLWDLMSSTTTSNVMPMMHVGLDNFDLVKYLVS 388

Query: 361 ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
          ++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+v
Sbjct: 389 QVMLSEEDRFEALKEYYPQAKKEDWRLWQAGQRVQIIKRDAEKGGLRLGT EVVSDQQGT 448

Query: 421 XXXXXXXXXXXXXXXVPLMIRLMHQCFPER--TPSWEGRLKELVPGYGIKLNENPERADEI 478

```

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +
 Sbjct: 449 IAALLGASPGASTAAPIMLNLLLEKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508
 Query: 479 IAYTAKVLDI 488
 + YT++VL +
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq
 1 atggcggcgg cggaaataaa acgccccctc gctgtcgatt tccagcacat
 51 agcgtccggt ctgcacggcg gcatagccgc ttttgccctgc ctgataggggt
 101 tgcagggcgg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc
 151 ggcgatattg cccaccagtt tggcaaaaca ggatggcac acgccgtttt
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg
 251 acgacggctt ccaagtcggt gggatgcttt ccggtcagcc ggacggcggt
 301 ttgttccggc aagcctttaa tcggataact gatttgtttt ttgccgtcgt
 351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta
 401 ttgtcgatgt atttgacttt gaaaaccggg ttcggcgcg cttgtgccgc
 451 attttgcggc tgttcgccc gattttcgga tttgccgcag gcggcaagca
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc
 551 tgatggtttc aaaatgccgt ctgaaatgcc gtctgaaacg tggcaggcgg
 601 aggttcggac ggcattgggt ttatttcaac gggcggtatg cgaccgcac
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgct ttttgcgcgc
 701 ctgcctgcaa aatctcttcg atttgcaag gattagaggt caatgcgttg
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF
 51 GDIAHQFGKQ GMAHAVFRPA RRRVLSVGFH TFADDGFQVV GMLSGQPDGV
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDFD ENRFRRALCR
 151 ILRLFRRIFG FAAGGKQQA AOHGKRYFQH SALLMVSKCR LKRLKRGRR
 201 RFGRHWVYFN GRMPTASRTL SNNSRASLRA FCAPACKISS ICEGLEVNAL
 251 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCATT TCCAGCACAT
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCCTGC CTGATAGGGT
 101 TGCAGGGCGG CATCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC
 151 GGCATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT
 201 CTGCCCAACC TGCCGACTG TCCTTATCAT CGGTTTCCAT ACATTGCGG
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT
 351 TGGTTTTGCC TTCGCTGCTT TGTCCCAAT CCAAACCGGC AATCGCCGTA
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC
 451 GTTTTGCGGC TGTACCGCCG TATTWCGGA TTTGCCGCaC GGCaArGCAG
 501 CAGGCAGCCG CCAATACGG CAAAaAwGT wTTCAGCATT CCACaYTCCT
 551 GATGGTTTCA AAATGCCGTC TGAACGCGG CAGGCGGAGG TTCGGACGGC
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA
 651 ATAATTCGCG TGCTTCTTTA CGCGCTTTCG CCGCGCCTGC CTGCAAAATC
 701 TCTTCGATT GCGAAGGGTC GCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN *VIRQFAAVF
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRALYR
 151 VLRLYRRIXG FAATAXQQA AQYKXXXQH STXLMVSKCR LKRGRRRFRGR
 201 HRVHFNGRMP TASGTLNNNS RASLRAFAAP ACKISSICEG SAVSSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 204 shows 82.0% identity over a 250 aa overlap with a predicted ORF (ORF 204.ng) from *N. gonorrhoeae*:

m204/g204

		10	20	30	40	50	60
m204 . pep		MAAAEIKRPFAVDFQHIASVLHGGIAAFACLIGLQGGMRNXVIRQFAAVFGDIAHQFGKQ :					
g204		MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIGLQGGMRNQVISQFAAVFGDIAHQFGKQ 10 20 30 40 50 60					
		70	80	90	100	110	120
m204 . pep		GMAHAVFCPTCRTVLIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA : : : : ::					
g204		GMAHAVFRPARRRVLSVGFHTFADDGFQVVGMLSGQPDGVLFQRQAFNRITDLFFAVVGFA 70 80 90 100 110 120					
		130	140	150	160	170	180
m204 . pep		FAALSQIQTGNRRIVDIYDFENRFRRALYRVRLRYRRIXGFAATAQQAAAQYGKXXXQH : : : : : :					
g204		FATLSQSQTGNRRIVDVFDENRFRRALCRILRLFRRIFGFAAGGKQAAAQHGKRYFQH 130 140 150 160 170 180					
		190	200	210	220	230	
m204 . pep		STXLMVSKCRLK----RGRRRFGHRHVHFNGRMPTASGTLSNNSRASLRFAAPACKISS : :					
g204		SALLMVSKCRLKCRLKRGRRRFGRHVVYFN GRMPTASRTLSNNSRASLRFCAPACKISS 190 200 210 220 230 240					
		240					
m204 . pep		ICEGS AVSSLX :					
g204		ICEGLEVNAL 250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

a204.seq	1	ATGGCGGCGG	CGGAAATAAA	ACGCCCCCTC	GCTGTCGATT	TCCAGCACAT
51	AGCGTCCGTT	CTGCACGGCG	GCATAGCCGC	TTTTGCCTGC	CTGATAGGGT	
101	TGCAGGCGCG	AATGCGAAAT	CAGGTAATCC	GTCAGTTTGC	CGCCGTCTTC	
151	GGCGATATTG	CCCACCAGTT	TGGCAAAACA	GGTATGGCAC	ACGCCGTTTG	
201	CCGCCAGCC	CGAAGGCGCG	CCCTTCCGT	CGGTTTCCAT	ACATTGCGG	
251	ACGACGGCTT	CCAAGTCGTT	GGGATGCTTG	CCGGTCAGCC	GGACGACGTT	
301	TTGTTCCGGC	AAGCCTTT..	
351	
401	
451	
501	
551AAGAG	GTTCCGGACGG	
601	CATTGGGTTT	ATTTCAACGG	GCGGATACCG	ACCGCATCAC	GTACTTTGCC	
651	CAATAATTCC	CGTGCTTCTT	TCCGCGCTTT	TTCGCGCGCT	GCCTGCAAAA	
701	TCPTCTCGAT	TGCGGAAGGG	TGCGCGGTCA	GCTCGTTGTA	G	

This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:

a204.pep

1	MAAAEIKRPL	AVDFQHIASV	LHGIIAFAFC	LIGLQGGMRN	QVIRQFAAVF
51	GDIAHQFGKQ	GMHAVCRPA	RRRLSVGFH	TFADDGFQVV	GMLAGQDDV
101	LFRQAF....
151KRFRGR
201	HWVYFNGRIP	TASRTLPNNS	RASLRAFCAP	ACKISSICEG	SAVSSL*

m204/a204 54.5% identity in 246 aa overlap

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGAFAACLIQLQGGMNRXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGAFAACLIQLQGGMNRQVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTVLIIGFHTFAADGFGVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRFARRRALSFGHTFADDGFGVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQGNRRIVDIYDFENRFRRLYRVLRLYRRXGFAATAXQQAAYGKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKGRRRRFGHRVHFNGRMPTASGTLNNRSLRAFAAPACKISSICEG					
a204	-----KRFGRHWVYFNGRIPTASRTLPNNRSLRAFAAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

g205.seq

```

1  atgctgaaaa taccttttgc cgtgttgggc ggctgcctgc tgcttgccgc
51  ctgcggcaaa tccgaaaata cggcggaaca gccgcaaat gcggcacaaa
101 ggcgcggcaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgcgcgtc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgctcg cggcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctgggagg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaaactgac tgattacctg atttcgcatt ccgccttgca accctatcag
451 gcaggcaaaa gcggctatgc cgcctgacag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

g205.pep

```

1  MLKIPFAVLG GCLLLAACGK SENTAEQPN AAQSAPKPVF KVKYIDNTAI
51  AGLALQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNTA EDGGLTDYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

m205.seq

```

1  ATGCTGAAwA CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51  tGCGGCAAAT CCGwAAATAC GGCGGTACAG CCGCAAACG CGGTACAAAG
101 CGCGCCGAAA CCGGTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGGA TTTGGGACAA AGCAGCGAAG GCAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGGA AGCCGTCAGC GGCAAATGTA
301 TGGAAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTCGCATGC CGCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

```
m205.pep
1  MLXTXFAVLG  GCLLXCRCGK  SXNTAVQPQN  AVQSAPKPVF  KVIYIDNTAI
51  AGLDLGQSSE  GKTNDGKKQI  SYPIKGLPEQ  NVIRLIGKHP  GDLEAVSGKC
101 METDDKDSPA  GWAENGVCHT  LFAKLVGNIA  EDGGKLTDDL  VSHAALQPYQ
151 AGKSGYAAVQ  NGRYVLEIDS  EGAFYFRRRH  Y*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

```
m205/g205

      10      20      30      40      50      60
m205.pep  MLXTXFAVLGGCLLXCRCGKSXNTAVQPQNNAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE
          |||||
g205       MLKIPFAVLGGCLLLAACGKSENTAEQPQNAAQSAPKPVFKVIYIDNTAIAGLALGQSSE
          |||||

      10      20      30      40      50      60
m205.pep  GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPAGWAENGVCHT
          |||||
g205       GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT
          |||||

      130     140     150     160     170     180
m205.pep  LFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          |||||
g205       LFAKLVGNIAEDGGKLTDLISHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          |||||

m205.pep  YX
          |
g205      Y
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

```
a205.seq (partial)
1  TCCGAACCTC  TTAAGGCTT  GCCGGAACAA  AACGTCGTCC  GGCTGACCGG
51  CAAGCATCCC  AACGACTTGG  AAGCCGTCGT  CGGCAATGT  ATGGAACCGG
101 ACGGAAAGGG  CGCGCCTTCG  GGCTGGGCGG  CAAACGGCGT  GTGCCATACC
151 TTGTTGCCA  AACTGGTGGG  CAATATCGCC  GAAGACGGCG  GCAAACCTGAC
201 GGATTACCTG  ATTTCCGATT  CCGCCCTGCA  ACCCTATCAG  GCAGGCAAAA
251 GCGGCTATGC  CGCCGTGCAG  AACGGACGCT  ATGTGCTGGA  AATCGACAGC
301 GAGGGGGCGT  TTTATTCCG  CCGCCGCCAT  TATTGA
```

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

```
a205.pep (partial)
1  SEPLKGLPEQ  NVVRLTGKHP  NDLEAVVGKC  METDGKGAPS  GWAANGVCHT
51  LFAKLVGNIA  EDGGKLTDDL  ISHSALQPYQ  AGKSGYAAVQ  NGRYVLEIDS
101 EGAFYFRRRH  Y*
```

m205/a205 88.3% identity in 111 aa overlap

```
      50      60      70      80      90     100
m205.pep  KVIYIDNTAIAGLDLGQSSEGKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC
          | : ||||| : || : ||||| : ||
a205       SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC
          10      20      30

      110     120     130     140     150     160
m205.pep  METDDKDSPAGWAENGVCHTLFAKLVGNIAEDGGKLTDLVSHAALQPYQAGKSGYAAVQ
```

480

```

||||| :||| |||||||||||||||||||:||| |||||||
a205      METDGGKGA40PSGWAANGVCHT50LFAKLVGNI60AEDGGKLT70DYLIHSHSALQPYQA80GKS90SGYA90AVQ

                170       180
m205.pep     NGRYVLEIDSEGAFFRRRHYX
              |||||||
a205         NGRYVLEIDSEGAFFRRRHYX
               100        110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 709>:

g205-1.seq (partial)

1	ATGCTGAAAA	TAcCTTTTGC	CGTGTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAAAT	CGGCGGAAAC	GCCGCAAAAT	GCGGCACAAA
101	GCGCGCGGAA	ACCGGTTTTC	AAAGTCAAAT	ACATCGACAA	TACGGCGATT
151	GCGGTTTGGC	CTTTGGGACA	AAGTAGCGAA	GCGAAAACCA	ACGACGGCAA
201	AAAACAAATC	AGTTATCCGA	TTAAGGCTT	GCCGGAACAA	AACGCCGTCC
251	GGCTGACCGG	AAAGCATCCC	ACGACTTTGC	AAGCGCTCGT	CGGCAAAATG
301	ATGGAACCCG	ACGAAAGGA	CAGCCTTTCG	GGCTGGGCGG	AAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAAGACGGC
401	GCAAACTGAC	TGATTACCTG	ATTTCGCATT	CCGCCCTGCA	ACCCTATCAG
451	GACGGGCAAA	GCGGCTATGC	CGCCGTGCAG	AACGGACGCT	ATGTGCTGGA
501	CAATGCACAGC	GAGGGGCGCT	TTTA		

This corresponds to the amino acid sequence <SEQ ID 710; ORF 205-1.ng>:

g205-1.pep (partial).

```

1  MLKIPFAVLG GCLLLAACGK SENTAEQPQN AAQSAPKPVF KVKYIDNTAI
51 AGLALGQSSE GKTNDGKKQI SYPTKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGDKAPS GAEWGVCHT LFAKLVGNIA EDGGKLT DYL ISHSALQPYQ
151 ASGSGYAAVO NGRVYLETDS EFAK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 711>:

m205-1.seq..

1	ATGCTGAAAA	CATCTTTTGC	CGTATTGGGC	GGCTGCCTGC	TGCTTGCCGC
51	CTGCGGCAAA	TCCGAAAAAT	CGGCGGAACA	GCCGCAAAAC	GCGGTACAAA
101	GCGCGCCGAA	ACCGGTTTTC	AAAGTCAAA	ATATCGACAA	TACGGCGATT
151	GCGCGTTTGG	ATTTGGGACA	AAGACGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAAT	AGTTATCCGA	TTAAGGCTT	GCCGGAAACA	AATGTTATCC
251	GACTGATCGG	CAAGCATCCC	GGCAGTCTGG	AAGCTGTCAG	GCGCAAAATG
301	ATGAAACCG	ATGATAAGGA	CAGTCCGCGA	GGTTGGGACG	AAAACGGGCT
351	GTGCCATACC	TTGTTTGCCA	AACTGGTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTGAC	GGATTACCTA	GTCTTCGATC	CCGCGCTCGA	ACCCTATCAG
451	GCAAGCAAAA	GCGGCTATGC	GCGCCGTCAG	ACAGGACGCT	ATGTGCTGGA
501	AATCGACAGC	GAAGGGGCGT	TTTATTCCCG	CCGCGCCAT	TATTGA

This corresponds to the amino acid sequence <SEQ ID 712; ORF 205-1>:

m205-1.pgp

```

1  MLKTSFAVLG GCLLLAACGK SENTAEQPQN AVQSAPKPVF KVKYIDNTAI
51 AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC
101 METDDKDSPA GAEWGVCHT FLAKLVGNIA EDGGKLT DYL VSHAALQPYQ
151 AGSKGYAAPO NGRVYLEIDS EGAFYFRRRH Y*

```

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
g205-1.pep	MLKIPFAVLGGCLLLAAGCKSENTAEQQPNAQAQSAKPKPVFKVKYIDNTAIAGLALGQSSE					
m205-1	MLKTSFAVLGGCLLLAAGCKSENTAEQQPNAVQSAKPKPVFKVKYIDNTAIAGLDLGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
g205-1.pep	GKTNDGKKQTSYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
m205-1	GKTNDGKKQTSYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSPGAWAENGVCHT					

481

```

              70      80      90      100     110     120
          130      140      150      160      170
g205-1.pep  LFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNGRYVLEIDSEGAF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m205-1      LFAKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFYFRRRH
          130      140      150      160      170      180

m205-1      YX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 713>:

```

a205-1.seq (partial)
1  CCTCTTAAAG GCTTGCCGGA ACAAACGTC GTCCGGCTGA CCGGCAAGCA
51  TCCCAACGAC TTGGAAGCCG TCGTCGGCAA ATGTATGGAA ACCGACGGAA
101 AGGGCGCGCC TTCGGGCTGG GCGGCAACG GCGTGTGCCA TACCTGTGTT
151 GCCAAACTGG TGGGCAATAT CGCCGAAGAC GCGGCAAAAC TGACGGATTA
201 CCTGATTTCG CATTCGCCCC TGCAACCCCTA TCAGGCAGGC AAAAGCGGCT
251 ATGCCGCCGT GCAGAACGGA CGCTATGTGC TGGAAATCGA CAGCGAGGGG
301 GCGTTTATT TCCGCCGCCG CCATTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 714; ORF 205-1.a>:

```

a205-1.pep (partial)
1  PLKGLPEQNV VRLTGKHPND LEAVVGKME TDGKGAPSGW AANGVCHTLF
51  AKLVGNIAED GKLTDYLIS HSALQPYQAG KSGYAAVQNG RYVLEIDSEG
101 AFYFRRRHY*

```

m205-1/a205-1 89.0% identity in 109 aa overlap

```

          50      60      70      80      90      100
m205-1.pep KYIDNTAIAGLDLGQSSEKGTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKME
          |||:|||||:|||||:|||||:|||||:|||||
a205-1      PLKGLPEQNVVRLTGKHPNDLEAVVGKME
          10      20      30

          110      120      130      140      150      160
m205-1.pep TDDKDSPAGWAENGVCHTLFAKLVGNI AEDGGKLT DYLV SHAALQPYQAGKSGYAAVQNG
          |||:|||||:|||||:|||||:|||||:|||||
a205-1      TDGKGAPSGWAANGVCHTLFAKLVGNI AEDGGKLT DYLI SHSALQPYQAGKSGYAAVQNG
          40      50      60      70      80      90

          170      180
m205-1.pep RYVLEIDSEGAFYFRRRHYX
          |||:|||||:|||||:|||||
a205-1      RYVLEIDSEGAFYFRRRHYX
          100      110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 715>:

```

g206.seq
1  atgttttccc ccgacaaaac ccttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaca ccgccaaccg aaacccaaac
101 agacagtccg gcaaatccaa gccgtccgca tcagccacat cggccgcaca
151 caaggctcgc aggaactcat gctccacagc ctcggactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggtttacaaa aacgcctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgcctcaa
351 ggccggcgac atcgatttct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcatccatgc ccccggcagc
451 ggcaaaaacca tcaaaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttggg gcgcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 716; ORF 206.ng>:

```

g206.pep
1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT

```

51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD IVFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

```
m206.beq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCGCGA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAATCTAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGCGGACGA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAR AACGCCCTCA ACGTCAAGCT GCCCGGCACC
301 GCCCGCAGCA TGGCGGCGGC AAGCCGAAA ATCCCCGACA GCCGCTCAA
351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTAC
401 ACGTCGGACT CTACATCGCG AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GCGAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

```
m206.pep..
  1  MFPPDKTLFL  CLSALLLASC  GTTSGKHRQP  KPKQTVRQIQ  AVRISHIDRT
51  QGSQELMLHS  LGLIGTPYKW  GGSSTATGFD  CSGMIQFVYK  NALNVKLPRT
101 ARDMAAASRK  IPDSRXKAGD  LVFFNTGGAH  RYSHVGLYIG  NGEFIHAPSS
151 GKTIKTEKLS  TPFYAKNYLG  AHTFTE*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng)

from *N. gonorrhoeae*:

```

m206/g206

                10         20         30         40         50         60
m206.pep      MFPPDKTLFLCLSLALLASCGTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS
                :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
g206          MFSPDKTLFLCLGALLLASCGTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS
                10         20         30         40         50         60

                70         80         90        100        110        120
m206.pep      LGLIGTPYKWGGSSTATGFDCSGMIQFVYKNALNVKLPRTARDMAAASRKIPDSRXKAGD
                :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
g206          LGLIGTPYKWGGSSTATGFDCSGMIQLVYKNALNVKLPRTARDMAAASRKIPDSRLKAGD
                70         80         90        100        110        120

                130        140        150        160        170
m206.pep      LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPPYAKNYLGAHTFFTEX
                :| | | | | | | | | | | | | | | | | | | | | | | | | | | |
g206          IVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPPYAKNYLGAHTFFTE
                130        140        150        160        170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 719>:

a206.seq

```
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGCTCTAGCG CACTGCTCCT
51  CGCCTCATGC GGCAGGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCGCGA TCAGCCACAT CGACCCGACA
151 CAAGGCTCGC AGGAACTCAT GTCTCCAGC CTCCGACTCA TCGGCACGCC
201 CTACAAATGG GCGCGCAGCA GCAACCGAAC CGGCTTCGAT GATCGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGGT GCCGCGCACC
301 GCCGCGGACA TGGCGGCGGC AAGCCGAAA ATCCCGACA GCCGCCTTAA
351 GGCCGCGCAG CTCGTATTCT TCAACACCGG CGGCGCACAC CGTACTACAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCGAGCAGC
451 GGCAAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
  1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
 51 QGSQEMLLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD LVFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

```

      10      20      30      40      50      60
m206.pep MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQEMLLHS
      |||||
a206      MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQEMLLHS
      10      20      30      40      50      60

      70      80      90     100     110     120
m206.pep LGLIGTPYKWGGSSTATGFDCSGMIQFVYKNALNVKLPRTARDMAAASRKIPDSRXKAGD
      |||||
a206      LGLIGTPYKWGGSSTATGFDCSGMIQFVYKNALNVKLPRTARDMAAASRKIPDSRLKAGD
      70      80      90     100     110     120

      130     140     150     160     170
m206.pep LVFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX
      |||||
a206      LVFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX
      130     140     150     160     170
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
  1 atgctgcggc atttaggaaa cgacttcgcc ttgggcgcggt tgtttttcga
 51 tgctgcggtt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggtttgg gcgaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgcccag tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt ctgcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 gtcgtcgccg tatttttcct tgatggtctg cagttcgggt gcggcggcac
501 gcattttcgc catcgaacgg taggagcggt tggtaaatgg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgccgat
601 aatgttggtc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgtcggc gatgtttcgg
701 ataacggatg tggtttcggg accggcatac aggttgaccg ccattttcgg
751 ttttgcccc cggttgga tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
  1 MLRHLGNDFA LGALFFDAAV DVPLLGDGQE VVDHPVENQT GREEEHDGE
 51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGDVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQRQTAA QRVDLVFEK LHHRLRLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEPE ERRCEPVYFT VFQCQLQVVG DVCDNGCGLR TGIQVDRHFR
251 FWPPGWDSG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
  1 ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
 51 GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTGAGGAGG TTGTTGACTA
101 CCCAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTTCGCC TGCATCGGGT CGGTCCGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGTTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGGCGGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCATGGA TACGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTGTGCA GTTGTTTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTGCGCG ATGTTTGCAG
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTCGT TCGGCGGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT CTGCCTTTAG GTTGAGAAT CCAGGTGGAC ATGAAGTGCT
901 GTTCAATCAT GCCGAGCCAG CCGGTCGGGG TTTTGGCGAT GTATTGCGCC
951 TCGGATTTGC CGGATTTGGC ATCGTCGTCC AAGTCGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDFALGALFFDAADV DVPPLGQGQEVVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFRLHRVGRRRVQISLGEHRCRHNDDGQDVVGVAEEVGNPTQPR
101 RCLAQFYGGECQPIQSDDEGDLQQRQAAAQRVDFLVCVKLHHRLLLRHT
151 VVAVFLFDGLQFGCGGTHFRHRAVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQEP EERGEPVYFAVVFQQLQVVG DVCDGCGCLR AGVEVDGGFG
251 FAPFWMAAKGTLTLVLYSLSLRRLMSMLHSPAAQTLCLPLGWRIQVDMKW
301 CSIMPSQPVGLRMYASDL PDLASSSKSE KLTFWKLPSP V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng) from *N. gonorrhoeae*:

m209/g209

m209.pep	10	20	30	40	50	60
	MLRHLGNDFALGALFFDAADV DVPPLGQGQEVVDYPVQYQT GREEEEHDGENQRHDFHHFR					
g209	MLRHLGNDFALGALFFDAADV DVPPLGQGQEVVDHPVENQT GREEEEHDGENQRHDFHHFR					
	10	20	30	40	50	60
m209.pep	70	80	90	100	110	120
	LHRVGRRRVQISLGEHRCRHNDDGQDVVGVAEEVGNPTQPRCLAQFYGGECQPIQSDDEG					
g209	LHRVGRRRVQISLGEHRCRHNDDGQDVVGVAEEVGNPAQPRCLAQFYGGECQPVQADEG					
	70	80	90	100	110	120
m209.pep	130	140	150	160	170	180
	DLQQRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW					
g209	DLQQRQTAQRVDFLVFEKLLHHRLLLRHTVVAVFFDGLQFGCGGTHFRHRTVGGVGQW					
	130	140	150	160	170	180
m209.pep	190	200	210	220	230	240
	IQYGFDDDGXNDNRPAVADDVVQLVQEP EERGEPVYFAVVFQQLQVVG DVCDGCGCLR					
g209	IQYGFDDDGQNDPCAPVADNVVQLVQEP EERRCEPVYFTVVFCQLQVVG DVCDGCGCLR					
	190	200	210	220	230	240
m209.pep	250	260	270	280	290	299
	AGVEVDGGGFGF-APFWMAAKGTLTLVLYSLSLRRLMSMLHSPAAQTLCLPLGWRIQVDMK					
g209	TGIQVDRHFRFWPPGWDGSG					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTTAGGAAA CCACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

```
51 TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201 GCGGGTTTCA ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCCAGCCA
301 AGGTGCCTGG CGCAATTCTA CCGAGGCGAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAG CTGCATCATG GCTTGTGCT GCGCCATACG
451 GTCGTCGCGG TATTCTCTT TGATGGCTTG CAGTTTGGGC GCGGCGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCCAAAA GAGGGGGGAG GCGAACCAGT
651 GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTGCGGC GATGTTGCG
701 ATAACGGATG TGGTCTGTGG GCCGGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGGTGACGC TGGTGCTGTA
801 CAGCTTGTGC TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851 AAACGCTTTG TCCGCCTTTG GGTGGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCATCA TGCCGAGCCA GCCGGTCGGG GTTTGCGGA TGTATTGCGC
951 CTCGGATTG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA
```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```
a209.pep
1 MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51 NQRHDFHHER LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQQRQAAA QRVDFLVCVK LHHGLLRHT
151 VVAVFLFDGL QFGRGGTHER HRTVRGVGQW IQYGFDDG* NDNREAPVAD
201 DVVQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCNDGCGLW AGVEVDGGFG
251 FAPFWIAAKG TLTVLVLSL LRRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*
```

m209/a209 95.6% identity in 341 aa overlap

```
10 20 30 40 50 60
m209.pep MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a209 MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR
10 20 30 40 50 60

70 80 90 100 110 120
m209.pep LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a209 LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG
70 80 90 100 110 120

130 140 150 160 170 180
m209.pep DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a209 DLQQRQAAAQRVDFLVCVKLHHRLLRHTVVAVFLFDGLQFGCGGTHFRHRTVRGVGQW
130 140 150 160 170 180

190 200 210 220 230 240
m209.pep IQYGFDDGXDNRNRPAPVADDVVQLVQEPPEERGGEPPVYFAVVGQLQVVGDVCDGCGLR
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a209 IQYGFDDGXDNRNRPAPVADDVVQLVQKPKEGGGEPPVYFAVVGQLQVVGDVCDGCGLR
190 200 210 220 230 240

250 260 270 280 290 300
m209.pep AGVEVDGGFGFAPFWMAAKGTLTLVLVLSLRLRLMSMLHSPAAQTLCLPLGWRIQVDMKW
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a209 AGVEVDGGFGFAPFWIAAKGTLTLVLVLSLRLRLMSIRQSPAAQTLCPPLGWRIQVDMKW
250 260 270 280 290 300

310 320 330 340
m209.pep CSIMPSQPVGVLRMYSASDLPDLASSSKSEKLTFWKLPSGVX
```

```

|||||
a209      CSIMPSQPVGVLRMYSASDLPLASSKSEKLTFWKLP SGVX
           310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atggtgcggc
51  ggtgggaaac ggggtcgata agtttgggcg tgggtctgat aatcaggttg
101 agtttttgga aggaaacctg attgtagtcg gcgcgtccgg gcgtgccgct
151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgtcgccgcc gtttttgtcc
251 tgttcgcgca ggaacaggtt tttcatgatg ccggattcgg tgtcaaaggt
301 ttcgacgaaa taaacctgcg cgttgcgctt gcccagttta ttgaactcgc
351 cggcttccac caaagacaat tcctgcttct gttcctaaat ttcggcatat
401 tcgcggtcgc gcagctctgc ccacgggtat acccaaagct gcatgacggc
451 aatcaggatg gcaaacggca cggcaaaact catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatag

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
1  MLRIAAANQL GGRNGAAVGN GVDFKFRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGVKG
101 FDEINPAVAL AQVIELAGFH QRQFLLLQLN FGIFAAAQLC PRYHPKLHDD
151 NQDGKRHGKL HDGAYPLFQR QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGTACGGC
51  GGTGGGAAAC GGGGTCTGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTGGA AGGAAACCTG ATTGTAGTCG GCGCGTCCGG GCGTGCCGCT
151 GTAACGGTAG CCGTGCGCGA ATTTCGAGCGT GCGTTTGTG TCCTTCAGCG
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTGCGCGCC GTTTTGTGCC
251 TGTTGCGCGA GGAACAGGTT TTTTCATGATG CCGGATTTCG TATCGAAGGT
301 TTCGACAAAA TAAACCTGCG CGTTGCGCTT GCCCAAAGT TTGAACGCG
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGGTAT ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAAACGCA CCGCAAAGT CATCACGGG CGTATCCATT
501 GTTCAATGC CAATCCGCag GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
1  MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGIEG
101 FDKINPAVAL AQTVELACLH QRQFLLLQLD FSVFAAAXLC PRYHPKLHDD
151 NQNGKRHGKL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

m211/g211

```

           10      20      30      40      50      60
m211.pep  MLRVAAANQLGGRNGTAVGNQVEFLEGNLIVVGASGRAAVTVAVAQFER
           ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g211       MLRIAAANQLGGRNGAAVGNQVEFLEGNLIVVGASGRAAVTVAVAQFER
           10      20      30      40      50      60

           70      80      90     100     110     120
m211.pep  AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH

```

	: : : : :
g211	A F V V L Q R E V T F F G E D D V V A A V F V L F A Q E Q V F H D A G F G V K G F D E I N P A V A L A Q V I E L A G F H
	70 80 90 100 110 120
	130 140 150 160 170
m211.pep	Q R Q F L L L L Q D F S V F A A X L C P R Y H P K L H D G N Q N G K R H G K L H H R A Y P L F Q C Q S A G X
	: :
g211	Q R Q F L L L L Q N F G I F A A A Q L C P R Y H P K L H D G N Q D G K R H G K L H D G A Y P L F Q R Q S A G
	130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 731>:

```
a211.seq
  1  ATGTTGCGGG  TTGCTGCTGC  CAATCAGTTG  GGCGGTCGGA  ATGGTACGGC
51  GGTGGGAAAC  GGGGTCGATG  AGTTTGGGCG  TGGTGCTGAT  AATCAGGTTG
101 AGTTTTGGGA  AGGAAACCTG  ATTGTAGTCG  GCGCGTCGGG  GCGTGCCGCT
151 GTAACGGTAG  CCGTGGCGCA  ATTCAGCGTG  CGGTTTGTTG  TCGTTCACGC
201 AGAAGTTACT  TTCTTTGGCG  AAGATGATGT  TGTCGCCGCC  GTTTTGTGCC
251 TGTTCCGCGA  GGAACAGGTT  TTTCATGATG  CCGGATTCGG  TATCGAAGGT
301 TTCGACAAAA  TAAACCCTGC  CGTTGCGCTT  GCCCAAAC TG  TTGAACCCGC
351 CTGCCTCCAC  CAAAGACAA  T  TCCTGCTTCT  GCTTCAGGAT  TTCAGCGTAT
401 TCGCGGCTGC  GTAGCTCTGC  CCACGGTATC  ACCCAAAGCT  GCATGACGGC
451 AACCAAAACG  GCAAAACGG  CA  CGCAAAAC TG  CATCACC GGG  CGTATCCATT
501 GTTTC AATGC  CAATCCG CAG  GATAG
```

This corresponds to the amino acid sequence <SEQ ID 732; ORF 211.a>:

a211.pep

1	MLRVAAANQL	GGRNGTAVGN	GVDEFGRGAD	NQVEFLEGNL	IVVGASGRAA
51	VTVAQAQER	AFVVQREV	FFGEDDVVAA	VFVFAQEQQV	FHDAGFGIEG
101	FDKINPAVAL	AQTVEPACLH	QRQFLLLLQD	FSVFAAA*LC	PRYHPKLHDG
151	NQNGKRKHGKL	HHRAYPLFQC	QSAG*		

m211/a211 99.4% identity in 174 aa overlap

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNQVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
a211	MLRVAAANQLGGRNGTAVGNQVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVQREVTFFGEDDVVAAVFVLFQAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH					
a211	AFVVVQREVTFFGEDDVVAAVFVLFQAQEQVFHDAGFGIEGFDKINPAVALAQTVEPACLH					
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLCPRYHCLKLHDGNQNGKRHGKLLHRRAYPLFQCQSAGX					
a211	QRQFLLLLQDFSVFAAAXLCPRYHCLKLHDGNQNGKRHGKLLHRRAYPLFQCQSAGX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 733>:

```
g212.seq (partial)
  1  atggacaatc  tcgtatggga  cggcattccc  gacatccgca  cactcgacca
 51  aaccatccgc  aaacacgcac  acccgctcaa  cctgattgtc  tgctccccg
101  ataatcagat  tcccgatttt  caaaccgcac  aagatgcttc  ggactcggaa
151  tgccgtctga  agcaccggtt  ggatcaggca  acccagtgcc  tccagttcga
201  cagcatcaac  ctcatcgaac  acatcctgcc  cgatgtccgc  ttctggcttg
251  ttcccccttc  acgcaccgcg  cgctcgcacg  aacattcca  ccacatttcc
301  tggcagaccg  aagccatccc  gcaaacggaa  agcaagtcgc  acaaaccctg
351  gtttgcaact  ccacaaacat  ccgaacggaa  aaaaccggaa  cacgtcctcg
```

```

401 tcatcgggtgc aggcattgcc ggcgcatcga ccgcccacgc cttagcatca
451 cacggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaatctcgc ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctccgacaca tcctgcccga ctccgacact tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaaca ccataaccac ctctaccgca gcatcacgtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccc aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcacctctct cagccatccg ctgatcgaac tatatgaaaa cacaacgtta
901 accggcattt ccacgacgag agaaaagtgg attgcaagca cgccaaacgg
951 cacatttacc gccacacaca tcactactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaacggccc tcacaccgtc caccctgtt tccgaacaac tgcgttgccg
1101 cgtttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgcactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggatg gaacgaagcc
1201 gaagaagcct caaacgcga agcattggca caccttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRDLQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
251 EKIAGIPLNT PYAEPLCGLY WQHGVLNPP AFVRTLLSHP LIELYENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCGCTCAA CCTGATTATC TGCCTCCCGG
101 ATAATCAGAT TCCCGATTT CAAACCGCAC AAGATGCTTC GGACGGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTTCCA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGGCATATCC GGCGCGGCAA CCGCCACGCG CTTAGCATCA
451 CACGGCATT TCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAGAC CGAACTTTTG CTTGCCGGCT ACGGCTACAC CAAACGCCTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACACG GCGTATGGCT CAATCCACCC GCATTTCGTCC
851 GCACCTCCTT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATTT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCCT
1001 ACCTACCCGA AACCAACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTCCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACGCCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCCGACCACC TTCCCTAGT CGGCGCACTC
1351 GGCGACATTG CCGCCATGCG GCAGACCTAC ACCAACTCG CGCTGGACAA
1401 AAATACCGC ATCGACACCC CATGCCATA CCTGCCAAT GCCTACGTCA
1451 ACACCGCGCA CGGCAACCGC GACTCGCCA CCGCCCCCAT CTGCGCCGCG

```

1501 GmCAwTGcAG CCCAAATCtT AGGCyTGCCC CATCCCTTTT yAcAAcGCCT
 1551 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA
 1601 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep
 1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
 51 CRLKHLRDQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
 101 WQTEAIPQTE SKPDKPWFAL PQTSEKQKPE HILVIGAGIS GAATAHALAS
 151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
 201 LGHILPESET WGGNGIIHLN YSRTEQQRNH ELGLQKHNNH LYRSITSAEA
 251 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
 301 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
 351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSHTGWNEA
 401 EEASNRQALA HLNPALES SL FAANPNQKH QGHAAIRCD S PDHLPVGLA
 451 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
 501 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng)

from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLIIICLPDNQIPDFQTAQDASDAECRLKHLRDQA					
	: : : : :					
g212	MDNLVWDGIPDIRTLDQIRKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRLKHLRDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPKPWFAL					
	: : : : :					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRLHEHFHHISWQTEAIPQTESKSDKPWFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	PQTSEKQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	: : : : :					
g212	PQTSEKQKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIIHLNYSRTEQQRNHELGLQKHNNH					
	: : : : :					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGIIHLNYSRTEQQRNHELGLQKHNNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
	: : : : :					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
	: : : : :					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEASNRQALAHLPALSES					



490

g212
370 380 390 400 410 420
430 440 450 460 470 480
m212.pep
q212

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 737>:

```

a212.seq
1 ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AAACATCCGC AAACACGCAC ACCCGCTCAA CCGTGATTGT TGCCTCCCCG
101 AATATCAGAT TCCCAATTTT CAAACCGCAG AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACC GTTT GGATCAGGCA ACCCAGTGCC TCCAGTTTCA
201 CAGCATCAAC CTGATTGAAC ACATCTGTCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCGC CGCCTGCACG AACCATTTCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAAACGAA AGTAAGCCCG ACAACCCCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCTCTG
401 TTATCGGAGC GGGCATATCC GCGCGGGCAA CCGCCCACGC CTTAGCATCA
451 TACGGCATTT CCGTTACCGT ATTGGAAGCC CGAAAGCCGC CCCAAGCCGC
501 CAGCGGCAAT CGCCAAGGGC TGCTCTACGC CAAATCTCTG CCGCACGACA
551 CCGAACAAC CGAACTGCTG CTTGCCGGCT ACGGCTACAC CAACCGCCTG
601 CTCGGACATA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTTGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCAGCCA GGCAGAAGCC
751 GAAAAAATCG CCGGCATCCC TCTGAACACG CCTCAGCCGC AACCATTATG
801 CGGACTGTTT TGGCAGTACG GCGTATGGCT CAATCCTCCC ACATTCTGTC
851 GCGCCCTCCT CAGGCATCCG CTCATTGGAG TACACGAAGA CACACGGTTA
901 ACCGACATTT CCCACGACGG GGAAGAAGTG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACAGA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCAACCTC GCCACCTGCG CCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TGCCTTGGCG
1101 CGTTTCAGCG GAAAGCTACA TCAGCCCGTC GTGGCAGCGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTTCC AACAGCAGCC ATACCCGATG GAACGAAAGC
1201 GAGGAAGCCT CAAACCGCCA AGCATTTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCCA ACCCAAACCC CCAAAAACAC CAAGGGCACG
1301 CGGCCATACG CTGCGACAGC CCCGACACC ATTCCTTAGT CGGCGCACTC
1351 GGGCAGATTG CCGCTATGCA ACAAACTTAC CGCAAATCTG CGCTGGACAA
1401 AAACATATCG ATCGATGCCC CCTGCCCGTA CCTGCCAAT GCGCTAGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCCAT CTGCGCGGCC
1501 GCCGTTGCAG CCGAAATCCT AGGCTTGCCC CATCCCTCT CAAAACGCCT
1551 CGGCCACGCC CTCACCCCA ACCGCGCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT AACCCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 738: ORF 212.a>:

a212.pep

1	MDNLAWNGIP	DIRTLDTQIR	KHAHPLNLIV	CLPDNQIPNF	QTAQDASDAE
51	CRLKHRLDQA	TQCLQFDSIN	LIEHILPDVR	FWLVPPSRTR	RLHEHFHHIS
101	WQTEAIPQTE	SKPKPWFWAL	PQTSEKQKPE	HILVIGAGIS	GAATAHALAS
151	YGISVTVLEA	RKAAQAAASN	RQGLLYAKIS	PHDTEQTELL	LAGYGYTKRL
201	LGHILPSET	WGGNGIIHLN	YSRTEQQNRH	ELGLQKHHNH	LYRSITQAEA
251	EKIAGIPLNT	PYAEPLCGLF	WQYGVWLNPP	TFVRALLSHP	LIGLHEDTPL
301	TDISHDGEKW	IASTPNGTFT	ATHIIYCTGA	NSPYLPETNL	ATLPLRQIRG
351	QTGLTPSTPF	SEQLRCAVSG	ESYISPSWHG	LHCYGASFIP	NSSHTGWNEA
401	EEASNQRLA	HLNPALESYL	FAANPNPQKH	QGHAAIRCDR	PDHLPLVGAL
451	GDIAAMQQTY	AKALADKNYR	IDAPCFYLPN	AYANTAHGTS	<u>GLATAPICAA</u>
501	AVAAEILGLF	HPLSKRLRHA	LHPNRAITRA	IVRRKDLTP*	

m212/a212 93.7% identity in 539 aa overlap

m212.pep MDNLVWGIPDIRTLDQAIRKHAPPLNLIICLPDNIQIPDFQTAQDASDAECRLKHLRDLQA
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
a212 MDNLAWNGIPDIRTLDQIRKHAPPLNLIIVCLPDNIQIPNFQTAQDASDAECRLKHLRDLQA

	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPSPSRTHHLHEHFHHISWQTEAIPQTESKPKDPWFAL					
a212	TQCLQFDSINLIEHILPDVRFWLVPSPSRTRRLHEHFHHISWQTEAIPQTESKPKDPWFAL					
	130	140	150	160	170	180
m212.pep	PQTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
a212	PQTSERQKPEHILVIGAGISGAATAHALASYGISVTVLEARKAAQAASGNRQGLLYAKIS					
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIHLNYSRTEQQRNHELGLQKHHNH					
a212	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGIHLNYSRTEQQRNHELGLQKHHNH					
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVWLNPPAFVRTLLNHPLIGLHEDTPL					
a212	LYRSITQAEAEKIAGIPLNTPYAEPLCGLFWQYGVWLNPPFTFVRALLSHPLIGLHEDTPL					
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIYCTGANSPLYLPETNLAALPLRQIRGQTGLTPSTPF					
a212	TDISHDGEKWIASTPNGTFTATHIYCTGANSPLYLPETNLATLPLRQIRGQTGLTPSTPF					
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEASNQALAHLPALSESIL					
a212	SEQLRCAVSGESYISPSWHGLHCYGASFIPNSSHTGWNEAEASNQALAHLPALSESIL					
	430	440	450	460	470	480
m212.pep	FAANPNPQKHQGHAAIRCDSPDHPLVGLGDIAMQTYTKLALDKNYRIDTPCPYLPN					
a212	FAANPNPQKHQGHAAIRCDSPDHPLVGLGDIAMQTYAKLALDKNYRIDAPCPYLPN					
	490	500	510	520	530	540
m212.pep	AYVNTAHGTRGLATAPICAAAXXAAQIXGLPHFPXQRLRHALHPNRTIIRAIVRRKDLTPX					
a212	AYANTAHGTRGLATAPICAAVAAEILGLPHPLSKRLRHALHPNRAIIRAIVRRKDLTPX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

```

g214.seq
1  atgatacaaa agatatgtaa gctatttggt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagcgtc aacatttcgc cctcgtgtgt
201 caacgtcaca cgcggcaggc aaaggcggcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaa ggcgggtgag
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccggcaa tgccaaagtg cagcgcggcg ggcaggttgc cgaagggtgcg
401 gtcattacct acaacaccaa aaccgaagtc tataccatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aaccccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

```

1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS LQDANQRTTFS
51 GNVIIIRGTL NISASCVNVT RGRQRRRIE GGRFARPLQP NVGRGQRDGA
101 RSGKQRYLFL RRKHCRSDRQ QCSAARRRC RRCGHYLQHQ NRSLYHQRQH
151 EIGCEIRFQN RQGQRHPAF KHTKNRITPM PSETETQFRR HLPTMPRRD
201 Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 741>:

```
m214.seq (partial)
1 ATGATACAAA AGATATGTAA GCTATTGTGT TTAATAGCAT TTTTTCGGC
51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGCCCGACCA AGTTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTTCAGC
151 GGAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCGCGCT
201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATT...
```

This corresponds to the amino acid sequence <SEQ ID 742; ORF 214>:

```
m214.pep (partial)
  1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGSL DQANQSTTFS
101  GNVVIRQGTI NISAARVNVV RGRQRRRIRE GGRFASPLQP DIGRRQRHGA
151  RTGKQRCLFI CRQHRSLNR* CQSTARRRCR RRCGDYIQHQ NRSLYHQRQH
151  KI...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 214 shows 80.3% identity over a 152 aa overlap with a predicted ORF (ORF 214.ng) from *N. gonorrhoeae*:

m214/g214

	10	20	30	40	50	60
m214.pep	MIQKICKLVLI	AFSASP	AFALQSDSR	QPIQIEADQ	GSILDQANQ	STTFSGNVVIRQ
g214	MIQKICKLV	LIVIFAT	SPAFALQSD	SRRPQIEAD	QGSILDQAN	QRTTTFSGNVIIRQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m214.pep	NISAARVN	VTGRQRR	RIREGGR	FASPLQPD	IGRRQRH	GARTGKQRC
g214	NISASCVN	VTGRQRR	RIREGGR	FARPLQPN	VGRGQRD	GARSGKQRYL
	70	80	90	100	110	120
	130	140	150			
m214.pep	CQSTARRR	CRRCGDI	QHQNRS	SLYHQ	RQH	KI
g214	CQSAARRR	CRRCG	HYLQHQN	RS	SLYHQ	RQHEIGCEIR
	130	140	150	160	170	180
	190	200				
g214	PSETETQ	FRRLP	TEMP	PRDY		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 743>:

```
a214.seq
1  ATGATACAA  AGATATGTAA  GCTATTGTGT  TTAATAGCAT  TTTTTTCGGC
51  GTCCCCCGCT  TTTGCGCTTC  AAAGCGACAG  CAGGCAGCCT  ATTCAGATTG
101 AGGCCGACCA  AGGTTCCGTC  GATCAAGCCA  ACCAAAGCAC  CATTCTCAGC
151 GGAAACGTCG  TCATCAGACA  GGGTACGCTC  AATATTTCCG  CCGCCCCGCT
201 CAATGTTACA  CGCGGC .GCG  AAAGCGGGCG  AATCCGTGAG  GGCGGGAAGT
251 TCGCCAGTCC  GCTTCAGCCA  GACATTTGGC  GCGGGCAAAG  GCACGGTTCG
301 CGGACAGGCA  AACAACGTTG  CTTATTTCAT  TGGCGGCAGC  ACCGTAGTCT
```

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTTGCCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNVT RGXQRRRIRE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCLFI CRQHRSLNR* CQSTARRRCR RRCGDYIQH Q NRSLYHQ RQH
151 KIRRKIRFQI RQGQRRYP AF EYAKIRIIP M PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m214.pep	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
a214	MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L					
	10	20	30	40	50	60
	70	80	90	100	110	120
m214.pep	NISAARVNVT RGRQRRRIRE GGRFASPLQ PDIGRRQRH GARTGKQRCLF IC RQHRSLNRX					
a214	NISAARVNVT RGRQRRRIRE GGRFASPLQ PDIGRRQRH GARTGKQRCLF IC RQHRSLNRX					
	70	80	90	100	110	120
	130	140	150			
m214.pep	CQSTARRRC RRRCGDYIQ H QNRSLYHQ RQH KI					
a214	CQSTARRRC RRRCGDYIQ H QNRSLYHQ RQH KIRRKIR FQIRQGRRYP AF EYAKIRIIP M					
	130	140	150	160	170	180
a214	PSETXTWFG RHLPTEILKRY L X					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTGC AAC
51  TTCTCCCGCT TTTGCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGTAC CACATTTAGC
151 GGCAATGTCA TCATCAGACA GGTACGCTC AACATTCCG CCTCGCGCGT
201 CAACGTCACA CGCGGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCCGTCCG CTTGAGCCAA ACGTTGGACG GGGGCAAGG GACGGTGCGC
301 GGTGAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGGCGGCG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAACTCT ATACCATCAA CGGCAGCAGC
451 AAATCGGGTG CGAAATCCGC TTCCAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
1  MIQKICKLFV LIVIFATSPA FALQSDSRRP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISASRVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 GQANNVTYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTINGST
151 KSGAKSASKT GRVSVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
151 GGAACGTCG TCATCAGACA GGTACGCTC AATATTCCG CCGCCGCGT

```

201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
 251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
 301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
 351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
 401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
 451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
 501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
 51 GNVVIRQGT L NISAARVNV T RGGKGGESV R AEGSPVRF S Q TLDGGKGT V R
 101 GQANNVAY S S AGSTVVL T GN AKVQRGGD V A EGAVITYN T K TEVYTISG S T
 151 KSGAKSASK S GRVSVVIQ P S STQKSE*

m214-1/g214-1 93.8% identity in 176 aa overlap

	10	20	30	40	50	60
m214-1.pep	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGS L	DQANQSTTFS	GNVVIRQGT L
g214-1	MIQKICKLFV	LIVIFATSP	FALQSDSRRP	IQIEADQGS L	DQANQSTTFS	GNVVIIRQGT L
	10	20	30	40	50	60
	70	80	90	100	110	120
m214-1.pep	NISAARVNV	TRGGKGGESV	RAEGSPVRF S	Q TLDGGKGT V	RQANNVAY S S	AGSTVVL T GN
g214-1	NISASRVNV	TRGGKGGESV	RAEGSPVRF S	Q TLDGGKGT V	RQANNVY S S	AGSTVVL T GN
	70	80	90	100	110	120
	130	140	150	160	170	
m214-1.pep	AKVQRGGD	VAEGAVITYN	TKTEVYTISG	STKSGAKSASK	S GRVSVVIQ P S	STQKSEX
g214-1	AKVQRGGD	VAEGAVITYN	TKTEVYTING	STKSGAKSASK	T GRVSVVIQ P S	STQKTEX
	130	140	150	160	170	

g214-1/p38685

sp|P38685|YHBN ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)
 >gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF_ol85 [Escherichia coli]
 >gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185
 Score = 97.1 bits (238), Expect = 6e-20
 Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQPIQIEADQGS L DQANQSTTFS GNVVIRQGT L NISAARVNVTR--GGKGG 76
 PAF A+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G
 Sbjct: 24 PAFAVTGD TDQPIHIESDQQSLDMQGNVVTFTGNVIVTQGTIKINADKVVVTRPGGEQ GK 83

Query: 77 ESVAEAGSPVRF S Q TLDGGKGT V RQANNVAY S S AGSTVVL T GN AKVQRGGD VAEGAVIT 136
 E + G P F Q D GK V G A+ + Y A VVLTGNA +Q+ +G IT
 Sbjct: 84 EVIDGYGKPATFYQM DNGK-PVEGHASQMHYELAKDFVVL T GNAYLQQVDSNIKGDKIT 142

Query: 137 YNTKTE 142
 Y K +
 Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

1 ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
 51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
 101 AGGCCGACCA AGGTTTCGCTC GATCAAGCCA ACCAAAGCAC CACATTCAGC
 151 GGAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCCGCGT
 201 CAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
 251 CGCCAGTCCG CTTAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCGC
 301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
 351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
 401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
 451 AAATCCGGCG CAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
 501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

51 GNVVIRQGTI NISAARVNVTR RGGKGGESVR AEGSPVRFSSQ TLDGGKGTVR
 101 GQANNVAYSS AGSTVVLTGN AKVQRGGDVA EGAVITYNTK TEVYTISGST
 151 KSGAKSASKS GRVSVVIQPS STQKSE*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKLFVLI	IAFFSASP	FALQSDSR	QPIQIEAD	QGSILDQ	ANQSTTF
m214-1	MIQKICKLFVLI	IAFFSASP	FALQSDSR	QPIQIEAD	QGSILDQ	ANQSTTF
	10	20	30	40	50	60
	70	80	90	100	110	120
a214-1.pep	NISAARVNVTR	RGGKGGESV	RAEGSPVR	FSSQTLDG	GKGTVRG	QANNVAYSS
m214-1	NISAARVNVTR	RGGKGGESV	RAEGSPVR	FSSQTLDG	GKGTVRG	QANNVAYSS
	70	80	90	100	110	120
	130	140	150	160	170	
a214-1.pep	AKVQRGGDVA	EGAVITYNT	KTTEVYTI	SGSTKSGA	KSASKSGR	VSVVIQPS
m214-1	AKVQRGGDVA	EGAVITYNT	KTTEVYTI	SGSTKSGA	KSASKSGR	VSVVIQPS
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq
 1 atgaaagtaa gatggcggta cggaaattgcg ttccattga tattggcgggt
 51 tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa
 101 tcgaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc
 151 ttggacggaa ggcggtttga cgaacagga tacttgaaag aacatttgag
 201 cgcgaaaggt gcgaaacagt ttcccgaata cagcgacatc cattttgatt
 251 cgccgcatct cgtgttcttc caagaaggca ggctgttgta cgaagtcggc
 301 agcgatgaag ccgtttacca taccgaaaac aaacagggtc tttttaaaaa
 351 caacgttggtg ctgacaaaaa ccgccgacgg caggcggcag gcgggtaaaag
 401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaaccc
 451 gatacgctcg tcagtttcca atatggcgcg tcgcacggtc aggcgggccc
 501 tatgacctac aaccacaaaa caggcatgtt gaacttctca tctaaagtga
 551 aagccgcgat ttatgatata aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep
 1 MKVRWRYGIA FPLILAVLALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS
 51 LDGRRFDEQG YLKEHLSAKG AKQFPENSID HFDSPLVFF QEGRLLYEVG
 101 SDEAVYHTEN KQVLFKNNVV LTKTADGRRQ AGKVETEKLH VDTESQYAQT
 151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKAAYDT KDM*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)
 1 ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT
 51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA
 101 GGCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTGAG CGCGAAGGGC
 151 GCGAAACAGT TTCCGAAAG CAGCGACATC CATTGATTGATT CGCCGCATCT
 201 CGTGTCTTTC CAAGAAGGCA GGTGTTGTA CGAAGTCGGC AGCGACGAAG
 251 CCGTTTACCA TACCGAAAAC AAACAGGTTT TTTTAAAAA CAACGTTGTG
 301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA
 351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCTG
 401 CAGTTTCCA ATATGGTGCA TCGCACGGTC AGGCGGGCGG CATGACTTAC
 451 GACCACAWWA CAGGCATGTT GAACCTCTCA TCTAAAGTGA AAGCCACGAT
 501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)
 1 ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG
 51 AKQFPESDI HFDSPLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNNVV
 101 LTKTADGKRQ AGKVEAEKLH VDTESQYAQT DTPVSFQYGA SHGQAGGMTY

151 DHXTGMLNFS SKVKATIYDT KDM*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40		
m215.pep		SLSAWLGR	ISEVEIEE	VLNPDEP	QYTMDSLDGRRFDEQG		
g215	MKVRWRYG	IAFPLILA	VALGSL	SAWLGR	ISEVEIEE	VLNPDEP	QYTMDSLDGRRFDEQG
	10	20	30	40	50	60	
	50	60	70	80	90	100	
m215.pep	YLKEHLS	AKGAKQ	FPESSD	IHFDS	PHLVFF	QEGRL	LYEVGSDEAVYHTENKQVLFKNNVV
g215	YLKEHLS	AKGAKQ	FPENS	DIHFDS	PHLVFF	QEGRL	LYEVGSDEAVYHTENKQVLFKNNVV
	70	80	90	100	110	120	
	110	120	130	140	150	160	
m215.pep	LTKTADG	KRQAGK	VEAEKL	HVDTES	QYAQT	DPVPS	FQYGASHGQAGGMTYDHXTGMLNFS
g215	LTKTADG	RRQAGK	VEKLV	HVDTES	QYAQT	DPVPS	FQYGASHGQAGGMTYNNHKTGMLNFS
	130	140	150	160	170	180	
	170						
m215.pep	SKVKATI	YDTKDMX					
g215	SKVKA	AIYDTKDM					
	190						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

```
a215.seq
1  ATGAAAGTAA  GATGGCGGTA  CGGAATTGCG  TTCCCATGTA  TATTGGCGGT
51  TTGCTTGGGC  AGCCTGTCCG  CATGGTTGGG  ACGCATCAGC  GAAGTCGAGA
101 TTGAAGAAGT  CAGGCTCAAT  CCCGACGAAC  CGCAATACAC  ATATGGACGA
151 TTGGATGGCA  GCGGTTTGA  CGAACAGGGA  TACTTGAAAG  AACATTGAG
201 TTCGAAGGGC  GCGAAACAGT  TTCCGAAAG  CAGCGACATT  CATTTCGACT
251 CACCGCATCT  CGTGTTCTTC  CAAGAAGGCA  GGTGTGTGTA  CGAAGTCGGC
301 AGCGATGAAT  CCGTTTACCA  TACCGAAAA  AAACAGGTTT  TTTTAAAAA
351 CAACGTTGTG  CTGACCAAAA  CCGCCGACGG  CAAACGCGAG  GCGGGTAAAG
401 TTGAAGCCGA  AAAGTCGCAC  GTCGATACCG  AATCTCAATA  TGCCCAAACC
451 GATACGCGTG  TCAGTTTCCA  ATATGGTGCA  TCGCACGGTC  AGGCGGGCGG
501 CATGACTTAC  GACCAAAAA  CAGGCATGTT  GAACTTCTCA  TCTAAAGTGA
551 AAGCCACGAT  TTATGATACA  AAAGATATGT  AA
```

This corresponds to the amino acid sequence <SEQ ID 756; ORF 215.a>:

a215.pep

1	<u>M</u> KVWRRYGIA	<u>F</u> PLILAVALG	<u>S</u> LSAWLGRIS	EVEIEEVRLN	PDEPQYTM	DG
51	LDGRRFDEQ	YLKEHLLSK	AKQFPSSDI	HFDSPHLVFF	QEGRLLYEV	G
101	SDEAVYHTN	KQVLFKNNV	LTKTADGKR	AGKVEAEKLH	VDTESQYAQT	
151	DTVPVSFOYA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIYDT	KDM*	

m215/a215 98.3% identity in 173 aa overlap

```

                                10      20      30      40
m215.pep                      SLSAWLGRISEVEIEEVR LNPDEPQYTMDSLDGRRFDEQG
                                |||||
a215      MKVRWRYGIAFPLILAVALGSLSAWLGRISEVEIEEVR LNPDEPQYTMDSLDGRRFDEQG
                                10      20      30      40      50      60
                                50      60      70      80      90     100
m215.pep      YLKEHL SAKGAKQFPESDDIHFDSPHLVFFOEGRLLYE VGSDEAVYHTENKOVLFKNNVV

```

```

|||||:|||||
a215      YLKEHLSSKGAKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNNVV
              70      80      90      100     110     120

              110     120     130     140     150     160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHXTGMLNFS
|||||
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVSFQYGASHGQAGGMTYDHKTGMLNFS
              130     140     150     160     170     180

              170
m215.pep  SKVKATIIDTKDMX
|||||
a215      SKVKATIIDTKDMX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtaccacgc gacgaaatca ccgccatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcatc accgcccgcc
101 ccgattcaac catggcgcgc catgccgata tccacatcac cgcacggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttggcggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301 aaacgcctgc ttttgcgcgt tgccgacatt atgcacaaag gcggcgccct
351 gcccgcgctc cgactcggca cgcccttgaa aggagccatc gtcagcatga
401 gcgagaaaag tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKDITLVC I TARP DSTMAR HADIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGA I VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGC CGGAAAT TGCAGCGGAA TTGgACAAAA
101 ACTTCGTCCT TCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGCGA TTTGGGTATG ATTGTGGACA rCGACGTGGT CGTCGCGATT
301 TCCAATTCCG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTCT TCCTGCTGCG CgcACGCGCG TTCACGCCCG
551 ACGATTTCGC CTTGAGCCAT CTGCGCGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GCGGCGCTGC CTGCCGTCCTG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTACCGG
801 TCTTTGATA GACGAAGTCA TGCATACGCA TCCTAAACC ATCTCCGCCG
851 AACGTCTGCG CACCGAAGCC CTGAAAGTCA TGAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLREIAAE LXKNFVLAAD ALLHCKGRVV

```

```

51  ITGMVKS GHI GRKMAATMAS TGTPAFFVHP AEAHGD LGM IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAP TTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHK G GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGR LKGVF
251 TDGDLRRL FQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

```

              70      80      90      100     110     120
m216.pep      TMASTGTPAFFVHPAEAAHGD LGMIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVCI
              ::|||:| ||||:|||||
g216           MISISSVPSDEITAIIPALKRKDITLVCI
              10      20      30

              130     140     150     160     170     180
m216.pep      TARPDMSTMARHADIHITASVSKEACPLGLAPTSTTAVMALGDALAVVLLRARAFTPD
|||||
g216           TARPDMSTMARHADIHITASVSQEACPLGLAPTSTTAVMALGDALAVVLLRARAFTPD
              40      50      60      70      80      90

              190     200     210     220     230     240
m216.pep      ALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGR
|| |||||
g216           ALIHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKGAIVSMSEKGLGMWAGTDGQRLS
              100     110     120     130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

a216.seq

```

1  ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGTT
51  GCACACCGAA GCGGAAGGCT TGC GCGAAAT TGC GCGCGGAT TTGGACGAAA
101 ACTTCGCCCT TGC GCGCGGAC GCGTTGTGTC ACTGCAAAGG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 CATGGCCTCG ACCGGCACGC CCGCGTTTTT CGTCCACCTT GCGGAAGCGG
251 CACACGGCGA TTTGGGCATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCGG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGCTGCG CGCCCGCGCG TTCACGCCCG
551 ACGACTTCGC CTTGAGCCAC CCTGCCGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GGCGGCTGC CTGCCGTCGG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCCG CCTGTTTCAA GAATGCGACA ATTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

a216.pep

```

1  MAMAGNEKYL DWAREVLHTE AEGLEIAAD LDENFALAAD ALLHCKGRVV
51  ITGMKSGHI GRKMAATMAS TGTPAFFVHP AEAHGD LGM IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAP TTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHK G GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGR LKGVF
251 TDGDLRRL FQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN

```

301 GLLVTDADGV LIGALNMHDL LAARIV*

m216/a216 97.2% identity in 326 aa overlap

	10	20	30	40	50	60
m216.pep	MAMAENKYLWAREVLHAEAEGLREIAAELXKNFVLAADALLHCKGRVITGMVKS GHI					
a216	MAMAGNEKYLWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVITGMKSGHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m216.pep	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIIPALKRKD					
a216	GRKMAATMASTGTPAFFVHPAEAAHGDLMIVDNDVVVAISNSGESDEIAAIIIPALKRKD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m216.pep	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
a216	ITLVCITARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m216.pep	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPPLKEAIVSMSEKGLGMLAVT					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPPLKEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m216.pep	DGQGRKLGVTFTDGLRRLFQECNFTGLSIDEVMHTHPKTI SAERLATEALKVMQANHVN					
a216	DGQGRKLGVTFTDGLRRLFQECNFTGLSIDEVMHTHPKTI SAERLATEALKVMQANHVN					
	250	260	270	280	290	300
	310	320				
m216.pep	GLLVTDADGVLIGALNMHDLAARIVX					
a216	GLLVTDADGVLIGALNMHDLAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggtatg acggtttgtt gcggcaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt tttcgaggtt ttggactgcc
101 ttttgggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccgga
151 acgcgccacc cattcgccga ccgtcgaggg ttgccgccat atccgggcaa
201 tatccgacag ggtttcgagg aaggcggaac aacgtccgaa catggcggtt
251 tgattcacgt cggcatacca cgcgctgaca tcttgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgcccgcga tttctccgtc caatcccaaa
401 tggacgttca aatcggaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgc aaacggcgca acacggcgcc ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttccagca agtcggacac gcaactcaac
551 gcataaaaaa acggttgccg gcggctgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgcggg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgataa ggggttcgata ttcgggggta a

```

This corresponds to the amino acid sequence <SEQ ID 764; ORF 217.ng>:

g217.pep..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPYPGNIRQ GFEEGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHPAQYH TVCRLLPGKQ LIRAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAQQQVGH ALQRIKKRLP AADFHVNRGI

```

201 RQCLRAGLRL SEHGFKRRI GFDIRG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 765>:

m217.seq

```

1  ATGGCGGATG ACGGTGTGCG GCGGCAACTG TCCGAAAAT TGCGCCAATT
51  CGGTTTCCGC CTCCATTG ACCCATTCGT TTCAAGGTT TTGGACTGAC
101 TTTTGGTCAT CGGCTTCAGC TTGAACAAT GTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTGCGCGA CCGTTGCGGG CTGCCGCCAT ATCCGTACAA
201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CATGGCGGTT
251 TGATTACAGT CGGCATACCA CGCGCTGACA TCCTGCCACA TCGGATTGCC
301 GCCTTTGGGC AGCATCCAGC CCAATATCAT GCGTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTCTCCGTC CAAACCCAG
401 TGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGTA AATCGTCTC
451 AGTCAGTCCG AAACGGCGCA ACACGGGCGC GGTTTCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGGCG GCGGCTGATT TTCACGCTG ACACGGAATA
601 CGGCAATGCC TCGCACCGG GctGCGCTG TCCGAACAG GCTTCGATA
651 AAGGCGTATA GGATTGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 766; ORF 217>:

m217.pep

```

1  MADDGVRRL SGKLRQFGR LFPDPFVKV LDXLLVIGFS LEQCFKQIPA
51  TRHPFADRCG LPPYPYNIRO GFEEGGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPVDVQIGN HVVQKRXLV
151 SQSETAQHGR GFXXKHKHFID FKSFAQQVEQ AXQSMKQRLA AADFHVXHGI
201 RQCLRTGLRL SEHGFDKRII GFDIRG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 217 shows 80.5% identity over a 226 aa overlap with a predicted ORF (ORF 217.ng) from *N. gonorrhoeae*:

m217/g217

	10	20	30	40	50	60
m217.pep	MADDGVRRLSGKLRQFGFRLFPDPFVKVLDXLLVIGFSLEQCFKQIPATRHFPADRCG					
g217	MADDGLLRQLSEKPSQSALFLPDPFVFEVLDCLLVIGPGLKQCFKQIPATRHFPADRRR					
	10	20	30	40	50	60
m217.pep	LPPYPYNIROGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
g217	LPPYPGNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
	70	80	90	100	110	120
m217.pep	LIRAAAHFSVQTPVDVQIGNHVQKRXLVLSQSETAQHGRGFXXKHKHFIDFKSAFQQVEQ					
g217	LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFQKREHFADFKTAFQOVGH					
	130	140	150	160	170	180
m217.pep	AXQSMKQRLAAADFHVXHGI RQCLRTGLRLSEHGFDKRIIGFDIRGX					
g217	ALQRIKKRLPAADFHVRNGIRQCLRAGLRLSEHGFKRRIIGFDIRG					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 767>:

a217.seq

```

1  GTGGCGGATG ACGGTGTGCA GCGGCAACTG TCCGAAAAT TGCGCCAATT
51  CGGTTTCCGC CTGCCATTG ACCCATTCGT TTTCGAGGCT TTGGACTGCC
101 TTTTGGTCAT CGCCTTCGAC TTGAACAAT GTTCAAGCA AATCCCGGCA
151 ACGCGCCACC CATTGCTCAA CCGTCGAGG TTGCCGCCAT ATCCGTACAA

```